(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
24 December 2003 (24.12.2003)

PCT

(10) International Publication Number
WO 03/106654 A2

(51) International Patent Classification[7]: C12N

(21) International Application Number: PCT/US03/19153

(22) International Filing Date: 16 June 2003 (16.06.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/389,299 14 June 2002 (14.06.2002) US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier application:
US 60/389,299 (CON)
Filed on 14 June 2002 (14.06.2002)

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 03/106654 A2

(54) Title: XYLANASES, NUCLEIC ADICS ENCODING THEM AND METHODS FOR MAKING AND USING THEM

(57) Abstract: The invention relates to xylanases and to polynucleotides encoding the xylanases. In addition, methods of designing new xylanases and methods of use thereof are also provided. The xylanases have increased activity and stability at increased pH and temperature.

XYLANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AND USING THEM

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of priority under 35 U.S.C. § 119(e) of U.S. Provisional Application No. 60/389,299, filed June 14, 2002. The aforementioned application is explicitly incorporated herein by reference in its entirety and for all purposes.

FIELD OF THE INVENTION

This invention relates generally to enzymes, polynucleotides encoding the enzymes, the use of such polynucleotides and polypeptides and more specifically to enzymes having xylanase activity, e.g., catalyzing hydrolysis of internal β-1,4-xylosidic linkages or endo- β-1,4-glucanase linkages.

BACKGROUND

Xylanases (e.g., endo-1,4-beta-xylanase, EC 3.2.1.8) hydrolyze internal β-1,4-xylosidic linkages in xylan to produce smaller molecular weight xylose and xylo-oligomers. Xylans are polysaccharides formed from 1,4-β-glycoside-linked D-xylopyranoses. Xylanases are of considerable commercial value, being used in the food industry, for baking and fruit and vegetable processing, breakdown of agricultural waste, in the manufacture of animal feed and in pulp and paper production. Xylanases are formed by fungi and bacteria.

Arabinoxylanase are major non-starch polysaccharides of cereals representing 2.5 – 7.1% w/w depending on variety and growth conditions. The physicochemical properties of this polysaccharide are such that it gives rise to viscous solutions or even gels under oxidative conditions. In addition, arabinoxylans have high water-binding capacity and may have a role in protein foam stability. All of these characteristics present problems for several industries including brewing, baking, animal nutrition and paper manufacturing. In brewing applications, the presence of xylan results in wort filterability and haze formation issues. In baking applications (especially for cookies and crackers), these arabinoxylans create sticky doughs that are difficult to machine and reduce biscuit size. In addition, this carbohydrate is implicated in rapid rehydration of the baked product resulting in loss of crispiness and reduced shelf-life. For monogastric animal feed applications with cereal diets, arabinoxylan is a major contributing factor to viscosity of gut contents and thereby adversely affects the digestibility of the feed and animal growth rate. For ruminant animals, these

polysaccharides represent substantial components of fiber intake and more complete digestion of arabinoxylans would facilitate higher feed conversion efficiencies.

Xylanases are currently used as additives (dough conditioners) in dough processing for the hydrolysis of water soluble arabinoxylan. In baking applications (especially for cookies and crackers), arabinoxylan creates sticky doughs that are difficult to machine and reduce biscuit size. In addition, this carbohydrate is implicated in rapid rehydration of the baked product resulting in loss of crispiness and reduced shelf-life.

The enhancement of xylan digestion in animal feed may improve the availability and digestibility of valuable carbohydrate and protein feed nutrients. For monogastric animal feed applications with cereal diets, arabinoxylan is a major contributing factor to viscosity of gut contents and thereby adversely affects the digestibility of the feed and animal growth rate. For ruminant animals, these polysaccharides represent substantial components of fiber intake and more complete digestion would facilitate higher feed conversion efficiencies. It is desirable for animal feed xylanases to be active in the animal stomach. This requires a feed enzyme to have high activity at 37 °C and at low pH for monogastrics (pH 2-4) and near neutral pH for ruminants (pH 6.5-7). The enzyme should also possess resistance to animal gut xylanases and stability at the higher temperatures involved in feed pelleting. As such, there is a need in the art for xylanase feed additives for monogastric feed with high specific activity, activity at 35-40°C and pH 2-4, half life greater than 30 minutes in SGF and a half-life > 5 minutes at 85°C in formulated state. For ruminant feed, there is a need for xylanase feed additives that have a high specific activity, activity at 35-40°C and pH 6.5-7.0, half life greater than 30 minutes in SRF and stability as a concentrated dry powder.

Xylanases are also used in a number of other applications. For example, xylanases are used in improving the quality and quantity of milk protein production in lactating cows (see, for example, Kung, L., et al, J. Dairy Science, 2000 Jan 83:115-122), increasing the amount of soluble saccharides in the stomach and small intestine of pigs (see, for example, van der Meulen, J. et al, Arch. Tierernahr, 2001 54:101-115), improving late egg production efficiency and egg yields in hens (see, for example, Jaroni, D., et al, Poult. Sci., 1999 June 78:841-847). Additionally, xylanases have been shown to be useful in biobleaching and treatment of chemical pulps (see, for example, U.S. Pat. No. 5,202,249), biobleaching and treatment of wood or paper pulps (see, for example, U.S. Pat. Nos. 5,179,021, 5,116,746, 5,407,827, 5,405,769, 5,395,765, 5,369,024, 5,457,045, 5,434,071,

5,498,534, 5,591,304, 5,645,686, 5,725,732, 5,759,840, 5,834,301, 5,871,730 and 6,057,438) in reducing lignin in wood and modifying wood (see, for example, U.S. Pat. Nos. 5,486,468 and 5,770,012) as flour, dough and bread improvers (see, for example, U.S. Pat. Nos. 5,108,765 and 5,306,633) as feed additives and/or supplements, as set forth above (see, for example, U.S. Pat. Nos. 5,432,074, 5,429,828, 5,612,055, 5,720,971, 5,981,233, 5,948,667, 6,099,844, 6,132,727 and 6,132,716), in manufacturing cellulose solutions (see, for example, U.S. Pat. No.5,760,211). Detergent compositions having xylanase activity are used for fruit, vegetables and/or mud and clay compounds (see, for example, U.S. Pat. No. 5,786,316).

Xylanases are also useful in a method of use and composition of a carbohydrase and/or a xylanase for the manufacture of an agent for the treatments and/or prophylaxis of coccidiosis. The manufactured agent can be in the form of a cereal-based animal feed. (see, for example, U.S. Pat. No. 5,624,678) Additional uses for xylanases include use in the production of water soluble dietary fiber (see, for example, U.S. Pat. No. 5,622,738), in improving the filterability, separation and production of starch (see, for example, U.S. Pat. Nos. 4,960,705 and 5,023,176), in the beverage industry in improving filterability of wort or beer (see, for example, U.S. Pat. No. 4,746,517), in an enzyme composition for promoting the secretion of milk of livestock and improving the quality of the milk (see, for example, U.S. Pat. No. 4,144,354), in reducing viscosity of plant material (see, for example, U.S. Pat. No. 5,874,274), in increasing viscosity or gel strength of food products such as jam, marmalade, jelly, juice, paste, soup, salsa, etc. (see, for example, U.S. Pat. No. 6,036,981). Xylanases may also be used in hydrolysis of hemicellulose for which it is selective, particularly in the presence of cellulose. Additionally, the cellulase rich retentate is suitable for the hydrolysis of cellulose (see, for example, U.S. Pat. No. 4,725,544).

Various uses of xylanases include the production of ethanol (see, for example, PCT Application Nos. WO0043496 and WO8100857), in transformation of a microbe that produces ethanol (see, for example, PCT Application No. WO99/46362), in production of oenological tannins and enzymatic composition (see, for example, PCT Application No. WO0164830), in stimulating the natural defenses of plants (see, for example, PCT Application No. WO0130161), in production of sugars from hemicellulose substrates (see, for example, PCT Application No. WO9203541), in the cleaning of fruit, vegetables, mud or clay containing soils (see, for example, PCT Application No. WO9613568), in cleaning beer filtration membranes (see, for example, PCT Application No. WO9623579), in a method of killing or inhibiting microbial cells (see, for example, PCT Application No. WO9732480) and in determining the characteristics of process waters from wood pulp

bleaching by using the ratios of two UV absorption measurements and comparing the spectra (see, for example, PCT Application No. WO9840721).

With regard to xylanases used in the paper and pulp industry, xylanases have been isolated from many sources. In particular, see U.S. Patents No. 6,083,733 and 6,140,095 and 6,346,407. In particular, it is noted that U.S. Patents No. 6,140,095 addresses alkali-tolerant xylanases. However, it is noted that there remains a need in the art for xylanases to be used in the paper and pulp industry where the enzyme is active in the temperature range of 65°C to 75°C and at a pH of approximately 10. Additionally, an enzyme of the invention useful in the paper and pulp industry would decrease the need for bleaching chemicals, such as chlorine dioxide.

The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

SUMMARY OF THE INVENTION

The invention provides isolated or recombinant nucleic acids comprising a nucleic acid sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary nucleic acid of the invention, e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID

NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000, 2050, 2100, 2200, 2250, 2300, 2350, 2400, 2450, 2500, or more residues, encodes at least one polypeptide having a xylanase activity, and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection.

Exemplary nucleic acids of the invention also include isolated or recombinant nucleic acids encoding a polypeptide having a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID

NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380, and subsequences thereof and variants thereof. In one aspect, the polypeptide has a xylanase activity.

In one aspect, the invention also provides xylanase-encoding nucleic acids with a common novelty in that they are derived from mixed cultures. The invention provides xylanase-encoding nucleic acids isolated from mixed cultures comprising a nucleic acid sequence having at least about 10, 15, 20, 25, 30, 35, 40, 45, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary nucleic acid of the invention, e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID

NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, or more.

In one aspect, the invention also provides xylanase-encoding nucleic acids with a common novelty in that they are derived from an environmental source, e.g., mixed environmental sources, a bacterial source and/or an archaeal source, see Table 3, below. In one aspect, the invention provides xylanase-encoding nucleic acids isolated from an environmental source, e.g., a mixed environmental source, a bacterial source and/or an archaeal source, comprising a nucleic acid sequence having at least about 10, 15, 20, 25, 30, 35, 40, 45, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary nucleic acid of the invention over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200 or more, residues, wherein the nucleic acid encodes at least one polypeptide having a xylanase activity, and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection.

In one aspect, the invention also provides xylanase-encoding nucleic acids with a common novelty in that they are derived from a common glycosidase family, e.g., family 5, 6, 8, 10, 11, 26 or 30, as set forth in Table 5, below.

In one aspect, the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

Another aspect of the invention is an isolated or recombinant nucleic acid including at least 10 consecutive bases of a nucleic acid sequence of the invention, sequences substantially identical thereto, and the sequences complementary thereto.

In one aspect, the xylanase activity comprises catalyzing hydrolysis of internal β-1,4-xylosidic linkages. In one aspect, the xylanase activity comprises an endo-1,4-beta-xylanase activity.

In one aspect, the xylanase activity comprises hydrolyzing a xylan to produce a smaller molecular weight xylose and xylo-oligomer. In one aspect, the xylan comprises an arabinoxylan, such as a water soluble arabinoxylan. The water soluble arabinoxylan can comprise a dough or a bread product.

In one aspect, the xylanase activity comprises hydrolyzing polysaccharides comprising 1,4-β-glycoside-linked D-xylopyranoses. In one aspect, the xylanase activity comprises hydrolyzing hemicelluloses. In one aspect, the xylanase activity comprises hydrolyzing hemicelluloses in a wood or paper pulp or a paper product. In one aspect, the invention provides methods for reducing lignin in a wood or wood product comprising contacting the wood or wood product with a polypeptide of the invention.

In one aspect, the xylanase activity comprises catalyzing hydrolysis of xylans in a beverage or a feed or a food product. The feed or food product can comprise a cereal-based animal feed, a wort or a beer, a milk or a milk product, a fruit or a vegetable. In one aspect, the invention provides a food, feed or beverage or a beverage precursor comprising a polypeptide of the invention. The food can be a dough or a bread product. The beverage or a beverage precursor can be a beer or a wort.

In one aspect, the invention provides methods of dough conditioning comprising contacting a dough or a bread product with at least one polypeptide of the invention under conditions sufficient for conditioning the dough. In one aspect, the invention provides methods of beverage production comprising administration of at least one polypeptide of the invention to a beverage or a beverage precursor under conditions sufficient for decreasing the viscosity of the beverage.

In one aspect, the xylanase activity comprises catalyzing hydrolysis of xylans in a cell, e.g., a plant cell or a microbial cell.

In one aspect, the isolated or recombinant nucleic acid encodes a polypeptide having a xylanase activity that is thermostable. The polypeptide can retain a xylanase activity under conditions comprising a temperature range of between about 37°C to about 95°C; between about 55°C to about 85°C, between about 70°C to about 95°C, or, between about 90°C to about 95°C.

In another aspect, the isolated or recombinant nucleic acid encodes a polypeptide having a xylanase activity that is thermotolerant. The polypeptide can retain a xylanase activity after exposure to a temperature in the range from greater than 37°C to about 95°C or anywhere in the range from greater than 55°C to about 85°C. The polypeptide can retain a xylanase activity after exposure to a temperature in the range between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more. In one aspect, the polypeptide retains a xylanase activity after exposure to a temperature in the range from greater than 90°C to about 95°C at pH 4.5.

The invention provides isolated or recombinant nucleic acids comprising a sequence that hybridizes under stringent conditions to a nucleic acid comprising a sequence of the invention, e.g., a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID

NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, or fragments or subsequences thereof. In one aspect, the nucleic acid encodes a polypeptide having a xylanase activity. The nucleic acid can be at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200 or more residues in length or the full length of the gene or transcript. In one aspect, the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes.

The invention provides a nucleic acid probe for identifying a nucleic acid encoding a polypeptide having a xylanase activity, wherein the probe comprises at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000 or more, consecutive bases of a sequence comprising a sequence of the invention, or fragments or subsequences

thereof, wherein the probe identifies the nucleic acid by binding or hybridization. The probe can comprise an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 consecutive bases of a sequence comprising a sequence of the invention, or fragments or subsequences thereof.

The invention provides a nucleic acid probe for identifying a nucleic acid encoding a polypeptide having a xylanase activity, wherein the probe comprises a nucleic acid comprising a sequence at least about 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000 or more residues having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to a nucleic acid of the invention, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection.

The probe can comprise an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 consecutive bases of a nucleic acid sequence of the invention, or a subsequence thereof.

The invention provides an amplification primer pair for amplifying a nucleic acid encoding a polypeptide having a xylanase activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence of the invention, or fragments or subsequences thereof. One or each member of the amplification primer sequence pair can comprise an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence, or about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence.

The invention provides amplification primer pairs, wherein the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of a nucleic acid of the invention, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of the complementary strand of the first member.

The invention provides xylanase-encoding nucleic acids generated by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. The invention provides xylanases generated by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. The invention

provides methods of making a xylanase by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. In one aspect, the amplification primer pair amplifies a nucleic acid from a library, e.g., a gene library, such as an environmental library.

The invention provides methods of amplifying a nucleic acid encoding a polypeptide having a xylanase activity comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic acid sequence of the invention, or fragments or subsequences thereof.

The invention provides expression cassettes comprising a nucleic acid of the invention or a subsequence thereof. In one aspect, the expression cassette can comprise the nucleic acid that is operably linked to a promoter. The promoter can be a viral, bacterial, mammalian or plant promoter. In one aspect, the plant promoter can be a potato, rice, corn, wheat, tobacco or barley promoter. The promoter can be a constitutive promoter. The constitutive promoter can comprise CaMV35S. In another aspect, the promoter can be an inducible promoter. In one aspect, the promoter can be a tissue-specific promoter or an environmentally regulated or a developmentally regulated promoter. Thus, the promoter can be, e.g., a seed-specific, a leaf-specific, a root-specific, a stem-specific or an abscission-induced promoter. In one aspect, the expression cassette can further comprise a plant or plant virus expression vector.

The invention provides cloning vehicles comprising an expression cassette (e.g., a vector) of the invention or a nucleic acid of the invention. The cloning vehicle can be a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome. The viral vector can comprise an adenovirus vector, a retroviral vector or an adeno-associated viral vector. The cloning vehicle can comprise a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

The invention provides transformed cell comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention, or a cloning vehicle of the invention. In one aspect, the transformed cell can be a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell. In one aspect, the plant cell can be a cereal, a potato, wheat, rice, corn, tobacco or barley cell.

The invention provides transgenic non-human animals comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention. In one aspect, the animal is a mouse.

The invention provides transgenic plants comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention. The transgenic plant can be a cereal plant, a corn plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant or a tobacco plant.

The invention provides transgenic seeds comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention. The transgenic seed can be a cereal plant, a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a peanut or a tobacco plant seed.

The invention provides an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a nucleic acid of the invention. The invention provides methods of inhibiting the translation of a xylanase message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a nucleic acid of the invention. In one aspect, the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

The invention provides methods of inhibiting the translation of a xylanase message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a nucleic acid of the invention. The invention provides double-stranded inhibitory RNA (RNAi) molecules comprising a subsequence of a sequence of the invention. In one aspect, the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length. The invention provides methods of inhibiting the expression of a xylanase in a cell comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (iRNA), wherein the RNA comprises a subsequence of a sequence of the invention.

The invention provides an isolated or recombinant polypeptide comprising an amino acid sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary polypeptide or peptide of the invention over a region of at least about 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350 or more residues, or over the full length of the polypeptide, and the sequence identities are determined

by analysis with a sequence comparison algorithm or by a visual inspection. Exemplary polypeptide or peptide sequences of the invention include SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334,

SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380, and subsequences thereof and variants thereof. Exemplary polypeptides also include fragments of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600 or more residues in length, or over the full length of an enzyme. Exemplary polypeptide or peptide sequences of the invention include sequence encoded by a nucleic acid of the invention. Exemplary polypeptide or peptide sequences of the invention include polypeptides or peptides specifically bound by an antibody of the invention. In one aspect, a polypeptide of the invention has at least one xylanase activity.

Another aspect of the invention provides an isolated or recombinant polypeptide or peptide including at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 or more consecutive bases of a polypeptide or peptide sequence of the invention, sequences substantially identical thereto, and the sequences complementary thereto. The peptide can be, e.g., an immunogenic fragment, a motif (e.g., a binding site), a signal sequence, a prepro sequence or an active site.

The invention provides isolated or recombinant nucleic acids comprising a sequence encoding a polypeptide having a xylanase activity and a signal sequence, wherein the nucleic acid comprises a sequence of the invention. The signal sequence can be derived from another xylanase or a non-xylanase (a heterologous) enzyme. The invention provides isolated or recombinant nucleic acids comprising a sequence encoding a polypeptide having a xylanase activity, wherein the sequence does not contain a signal sequence and the nucleic acid comprises a sequence of the invention.

In one aspect, the xylanase activity comprises catalyzing hydrolysis of internal β-1,4-xylosidic linkages. In one aspect, the xylanase activity comprises an endo-1,4-beta-xylanase activity. In one aspect, the xylanase activity comprises hydrolyzing a xylan to produce a smaller molecular weight xylose and xylo-oligomer. In one aspect, the xylan comprises an arabinoxylan, such as a water soluble arabinoxylan. The water soluble arabinoxylan can comprise a dough or a bread product.

In one aspect, the xylanase activity comprises hydrolyzing polysaccharides comprising 1,4-β-glycoside-linked D-xylopyranoses. In one aspect, the xylanase activity

comprises hydrolyzing hemicelluloses. In one aspect, the xylanase activity comprises hydrolyzing hemicelluloses in a wood or paper pulp or a paper product.

In one aspect, the xylanase activity comprises catalyzing hydrolysis of xylans in a feed or a food product. The feed or food product can comprise a cereal-based animal feed, a wort or a beer, a milk or a milk product, a fruit or a vegetable.

In one aspect, the xylanase activity comprises catalyzing hydrolysis of xylans in a cell, e.g., a plant cell or a microbial cell.

In one aspect, the xylanase activity is thermostable. The polypeptide can retain a xylanase activity under conditions comprising a temperature range of between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more. In another aspect, the xylanase activity can be thermotolerant. The polypeptide can retain a xylanase activity after exposure to a temperature in the range from greater than 37°C to about 95°C, or in the range from greater than 55°C to about 85°C. In one aspect, the polypeptide can retain a xylanase activity after exposure to a temperature in the range from greater than 90°C to about 95°C at pH 4.5.

In one aspect, the isolated or recombinant polypeptide can comprise the polypeptide of the invention that lacks a signal sequence. In one aspect, the isolated or recombinant polypeptide can comprise the polypeptide of the invention comprising a heterologous signal sequence, such as a heterologous xylanase or non-xylanase signal sequence.

In one aspect, the invention provides chimeric proteins comprising a first domain comprising a signal sequence of the invention and at least a second domain. The protein can be a fusion protein. The second domain can comprise an enzyme. The enzyme can be a xylanase.

The invention provides chimeric polypeptides comprising at least a first domain comprising signal peptide (SP), a prepro sequence and/or a catalytic domain (CD) of the invention and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP), prepro sequence and/ or catalytic domain (CD). In one aspect, the heterologous polypeptide or peptide is not a xylanase. The heterologous polypeptide or peptide can be amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP), prepro sequence and/or catalytic domain (CD).

The invention provides isolated or recombinant nucleic acids encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP), a prepro domain and/or a catalytic domain (CD) of the invention and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP), prepro domain and/ or catalytic domain (CD).

The invention provides isolated or recombinant signal sequences (e.g., signal peptides) consisting of a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43 or 1 to 44, of a polypeptide of the invention, e.g., SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244,

SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380.

In one aspect, the xylanase activity comprises a specific activity at about 37°C in the range from about 1 to about 1200 units per milligram of protein, or, about 100 to about 1000 units per milligram of protein. In another aspect, the xylanase activity comprises a specific activity from about 100 to about 1000 units per milligram of protein, or, from about 500 to about 750 units per milligram of protein. Alternatively, the xylanase activity comprises a specific activity at 37°C in the range from about 1 to about 750 units per milligram of protein, or, from about 500 to about 1200 units per milligram of protein. In one aspect, the xylanase activity comprises a specific activity at 37°C in the range from about 1 to about 500 units per milligram of protein, or, from about 750 to about 1000 units per milligram of protein. In another aspect, the xylanase activity comprises a specific activity at 37°C in the range from about 1 to about 250 units per milligram of protein. Alternatively, the xylanase activity comprises a specific activity at 37°C in the range from about 1 to about 100 units per milligram of protein. In another aspect, the thermotolerance comprises retention of at least half of the specific activity of the xylanase at 37°C after being heated to the elevated temperature. Alternatively, the thermotolerance can comprise retention of specific activity at 37°C in the range from about 1 to about 1200 units per milligram of protein, or, from about 500 to about 1000 units per milligram of protein, after being heated to the elevated temperature. In another aspect, the thermotolerance can comprise retention of specific activity at 37°C in the range from about 1 to about 500 units per milligram of protein after being heated to the elevated temperature.

The invention provides the isolated or recombinant polypeptide of the invention, wherein the polypeptide comprises at least one glycosylation site. In one aspect, glycosylation can be an N-linked glycosylation. In one aspect, the polypeptide can be glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

In one aspect, the polypeptide can retain a xylanase activity under conditions comprising about pH 6.5, pH 6, pH 5.5, pH 5, pH 4.5 or pH 4. In another aspect, the polypeptide can retain a xylanase activity under conditions comprising about pH 7, pH 7.5 pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10, pH 10.5 or pH 11. In one aspect, the polypeptide can retain a xylanase activity after exposure to conditions comprising about pH 6.5, pH 6, pH 5.5, pH 5, pH 4.5 or pH 4. In another aspect, the polypeptide can retain a xylanase activity after exposure to conditions comprising about pH 7, pH 7.5 pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10, pH 10.5 or pH 11.

The invention provides protein preparations comprising a polypeptide of the invention, wherein the protein preparation comprises a liquid, a solid or a gel.

The invention provides heterodimers comprising a polypeptide of the invention and a second protein or domain. The second member of the heterodimer can be a different phospholipase, a different enzyme or another protein. In one aspect, the second domain can be a polypeptide and the heterodimer can be a fusion protein. In one aspect, the second domain can be an epitope or a tag. In one aspect, the invention provides homodimers comprising a polypeptide of the invention.

The invention provides immobilized polypeptides having a xylanase activity, wherein the polypeptide comprises a polypeptide of the invention, a polypeptide encoded by a nucleic acid of the invention, or a polypeptide comprising a polypeptide of the invention and a second domain. In one aspect, the polypeptide can be immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

The invention provides arrays comprising an immobilized nucleic acid of the invention. The invention provides arrays comprising an antibody of the invention.

The invention provides isolated or recombinant antibodies that specifically bind to a polypeptide of the invention or to a polypeptide encoded by a nucleic acid of the invention. The antibody can be a monoclonal or a polyclonal antibody. The invention provides hybridomas comprising an antibody of the invention, e.g., an antibody that specifically binds to a polypeptide of the invention or to a polypeptide encoded by a nucleic acid of the invention.

The invention provides method of isolating or identifying a polypeptide having a xylanase activity comprising the steps of: (a) providing an antibody of the invention; (b) providing a sample comprising polypeptides; and (c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having a xylanase activity.

The invention provides methods of making an anti-xylanase antibody comprising administering to a non-human animal a nucleic acid of the invention or a polypeptide of the invention or subsequences thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-xylanase antibody. The invention provides methods of making an anti-xylanase immune comprising administering to a non-human animal a nucleic acid of the invention or a polypeptide of the invention or subsequences thereof in an amount sufficient to generate an immune response.

The invention provides methods of producing a recombinant polypeptide comprising the steps of: (a) providing a nucleic acid of the invention operably linked to a promoter; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide. In one aspect, the method can further comprise transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell.

The invention provides methods for identifying a polypeptide having a xylanase activity comprising the following steps: (a) providing a polypeptide of the invention; or a polypeptide encoded by a nucleic acid of the invention; (b) providing a xylanase substrate; and (c) contacting the polypeptide or a fragment or variant thereof of step (a) with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having a xylanase activity.

The invention provides methods for identifying a xylanase substrate comprising the following steps: (a) providing a polypeptide of the invention; or a polypeptide encoded by a nucleic acid of the invention; (b) providing a test substrate; and (c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of a reaction product identifies the test substrate as a xylanase substrate.

The invention provides methods of determining whether a test compound specifically binds to a polypeptide comprising the following steps: (a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid comprises a nucleic acid of the invention, or, providing a polypeptide of the invention; (b) providing a test compound; (c) contacting the polypeptide with the test compound; and (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

The invention provides methods for identifying a modulator of a xylanase activity comprising the following steps: (a) providing a polypeptide of the invention or a polypeptide encoded by a nucleic acid of the invention; (b) providing a test compound; (c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the xylanase, wherein a change in the xylanase activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the xylanase activity. In one aspect, the xylanase activity can be measured by providing a xylanase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product. A decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of xylanase activity. An increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of xylanase activity.

The invention provides computer systems comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence of the invention (e.g., a polypeptide encoded by a nucleic acid of the invention). In one aspect, the computer system can further comprise a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon. In another aspect, the sequence comparison algorithm comprises a computer program that indicates polymorphisms. In one aspect, the computer system can further comprise an identifier that identifies one or more features in said sequence. The invention provides computer readable media having stored thereon a polypeptide sequence or a nucleic acid sequence of the invention. The invention provides methods for identifying a feature in a sequence comprising the steps of: (a) reading the sequence using a computer program which

identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence of the invention; and (b) identifying one or more features in the sequence with the computer program. The invention provides methods for comparing a first sequence to a second sequence comprising the steps of: (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence of the invention; and (b) determining differences between the first sequence and the second sequence with the computer program. The step of determining differences between the first sequence and the second sequence can further comprise the step of identifying polymorphisms. In one aspect, the method can further comprise an identifier that identifies one or more features in a sequence. In another aspect, the method can comprise reading the first sequence using a computer program and identifying one or more features in the sequence.

The invention provides methods for isolating or recovering a nucleic acid encoding a polypeptide having a xylanase activity from an environmental sample comprising the steps of: (a) providing an amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide having a xylanase activity, wherein the primer pair is capable of amplifying a nucleic acid of the invention; (b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and, (c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide having a xylanase activity from an environmental sample. One or each member of the amplification primer sequence pair can comprise an oligonucleotide comprising at least about 10 to 50 consecutive bases of a sequence of the invention. In one aspect, the amplification primer sequence pair is an amplification pair of the invention.

The invention provides methods for isolating or recovering a nucleic acid encoding a polypeptide having a xylanase activity from an environmental sample comprising the steps of: (a) providing a polynucleotide probe comprising a nucleic acid of the invention or a subsequence thereof; (b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a); (c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and (d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a),

thereby isolating or recovering a nucleic acid encoding a polypeptide having a xylanase activity from an environmental sample. The environmental sample can comprise a water sample, a liquid sample, a soil sample, an air sample or a biological sample. In one aspect, the biological sample can be derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

The invention provides methods of generating a variant of a nucleic acid encoding a polypeptide having a xylanase activity comprising the steps of: (a) providing a template nucleic acid comprising a nucleic acid of the invention; and (b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid. In one aspect, the method can further comprise expressing the variant nucleic acid to generate a variant xylanase polypeptide. The modifications, additions or deletions can be introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly (e.g., GeneReassembly™, see, e.g., U.S. Patent No. 6,537,776), gene site saturated mutagenesis (GSSM™), synthetic ligation reassembly (SLR) or a combination thereof. In another aspect, the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

In one aspect, the method can be iteratively repeated until a xylanase having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced. In one aspect, the variant xylanase polypeptide is thermotolerant, and retains some activity after being exposed to an elevated temperature. In another aspect, the variant xylanase polypeptide has increased glycosylation as compared to the xylanase encoded by a template nucleic acid. Alternatively, the variant xylanase polypeptide has a xylanase activity under a high temperature, wherein the xylanase encoded by the template nucleic acid is not active under the high temperature. In one aspect, the method can be iteratively repeated until a xylanase coding sequence having an altered codon usage from that of the template nucleic acid is produced. In another aspect, the

method can be iteratively repeated until a xylanase gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

In one aspect, the invention provides isolated or recombinant nucleic acids comprising a sequence as set forth in SEQ ID NO: 189, wherein SEQ ID NO: 189 contains one or more of the following mutations: the nucleotides at positions 22 to 24 are TTC, the nucleotides at positions 31 to 33 are CAC, the nucleotides at positions 34 to 36 are TTG, the nucleotides at positions 49 to 51 are ATA, the nucleotides at positions 31 to 33 are CAT, the nucleotides at positions 67 to 69 are ACG, the nucleotides at positions 178 to 180 are CAC, the nucleotides at positions 190 to 192 are TGT, the nucleotides at positions 190 to 192 are GTA, the nucleotides at positions 190 to 192 are GTT, the nucleotides at positions 193 to 195 are GTG, the nucleotides at positions 202 to 204 are GCT, the nucleotides at positions 235 to 237 are CCA, or the nucleotides at positions 235 to 237 are CCC. In one aspect, the invention provides methods for making a nucleic acid comprising this sequence, wherein the mutations in SEQ ID NO: 189 are obtained by gene site saturated mutagenesis (GSSM™).

In one aspect, the invention provides isolated or recombinant nucleic acids comprising SEQ ID NO: 190, wherein SEQ ID NO: 190 contains one or more of the following mutations: the aspartic acid at amino acid position 8 is phenylalanine, the glutamine at amino acid position 11 is histidine, the asparagine at amino acid position 12 is leucine, the glycine at amino acid position 17 is isoleucine, the threonine at amino acid position 23 is threonine encoded by a codon other than the wild type codon, the glycine at amino acid position 60 is histidine, the proline at amino acid position 64 is cysteine, the proline at amino acid position 64 is valine, the serine at amino acid position 65 is valine, the glycine at amino acid position 68 is isoleucine, the glycine at amino acid position 68 is alanine, or the valine at amino acid position 79 is proline.

The invention provides methods for modifying codons in a nucleic acid encoding a polypeptide having a xylanase activity to increase its expression in a host cell, the method comprising the following steps: (a) providing a nucleic acid of the invention encoding a polypeptide having a xylanase activity; and, (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

The invention provides methods for modifying codons in a nucleic acid encoding a polypeptide having a xylanase activity; the method comprising the following steps: (a) providing a nucleic acid of the invention; and, (b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a xylanase.

The invention provides methods for modifying codons in a nucleic acid encoding a polypeptide having a xylanase activity to increase its expression in a host cell, the method comprising the following steps: (a) providing a nucleic acid of the invention encoding a xylanase polypeptide; and, (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

The invention provides methods for modifying a codon in a nucleic acid encoding a polypeptide having a xylanase activity to decrease its expression in a host cell, the method comprising the following steps: (a) providing a nucleic acid of the invention; and (b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell. In one aspect, the host cell can be a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

The invention provides methods for producing a library of nucleic acids encoding a plurality of modified xylanase active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps: (a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to a nucleic acid of the invention, and the nucleic acid encodes a xylanase active site or a xylanase substrate binding site; (b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and, (c) using the set of mutagenic

oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified xylanase active sites or substrate binding sites. In one aspect, the method comprises mutagenizing the first nucleic acid of step (a) by a method comprising an optimized directed evolution system, gene site-saturation mutagenesis (GSSM™), synthetic ligation reassembly (SLR), error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly (GeneReassembly™, U.S. Patent No. 6,537,776), gene site saturated mutagenesis (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof. In another aspect, the method comprises mutagenizing the first nucleic acid of step (a) or variants by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

The invention provides methods for making a small molecule comprising the following steps: (a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises a xylanase enzyme encoded by a nucleic acid of the invention; (b) providing a substrate for at least one of the enzymes of step (a); and (c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions. The invention provides methods for modifying a small molecule comprising the following steps: (a) providing a xylanase enzyme, wherein the enzyme comprises a polypeptide of the invention, or, a polypeptide encoded by a nucleic acid of the invention, or a subsequence thereof; (b) providing a small molecule; and (c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the xylanase enzyme, thereby modifying a small molecule by a xylanase enzymatic reaction. In one aspect, the method can comprise a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the xylanase enzyme. In one aspect, the method can comprise a plurality of additional enzymes under

conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the plurality of enzymatic reactions. In another aspect, the method can further comprise the step of testing the library to determine if a particular modified small molecule that exhibits a desired activity is present within the library. The step of testing the library can further comprise the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

The invention provides methods for determining a functional fragment of a xylanase enzyme comprising the steps of: (a) providing a xylanase enzyme, wherein the enzyme comprises a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention, or a subsequence thereof; and (b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for a xylanase activity, thereby determining a functional fragment of a xylanase enzyme. In one aspect, the xylanase activity is measured by providing a xylanase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

The invention provides methods for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis, the method comprising the following steps: (a) making a modified cell by modifying the genetic composition of a cell, wherein the genetic composition is modified by addition to the cell of a nucleic acid of the invention; (b) culturing the modified cell to generate a plurality of modified cells; (c) measuring at least one metabolic parameter of the cell by monitoring the cell culture of step (b) in real time; and, (d) analyzing the data of step (c) to determine if the measured parameter differs from a comparable measurement in an unmodified cell under similar conditions, thereby identifying an engineered phenotype in the cell using real-time metabolic flux analysis. In one aspect, the genetic composition of the cell can be modified by a method comprising deletion of a sequence or modification of a sequence in the cell, or, knocking out the expression of a gene. In one aspect, the method can further comprise selecting a cell comprising a newly engineered phenotype. In another aspect, the method can comprise culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.

The invention provides methods of increasing thermotolerance or thermostability of a xylanase polypeptide, the method comprising glycosylating a xylanase polypeptide, wherein the polypeptide comprises at least thirty contiguous amino acids of a polypeptide of the invention; or a polypeptide encoded by a nucleic acid sequence of the invention, thereby increasing the thermotolerance or thermostability of the xylanase polypeptide. In one aspect, the xylanase specific activity can be thermostable or thermotolerant at a temperature in the range from greater than about 37°C to about 95°C.

The invention provides methods for overexpressing a recombinant xylanase polypeptide in a cell comprising expressing a vector comprising a nucleic acid comprising a nucleic acid of the invention or a nucleic acid sequence of the invention, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection, wherein overexpression is effected by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

The invention provides methods of making a transgenic plant comprising the following steps: (a) introducing a heterologous nucleic acid sequence into the cell, wherein the heterologous nucleic sequence comprises a nucleic acid sequence of the invention, thereby producing a transformed plant cell; and (b) producing a transgenic plant from the transformed cell. In one aspect, the step (a) can further comprise introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts. In another aspect, the step (a) can further comprise introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment. Alternatively, the step (a) can further comprise introducing the heterologous nucleic acid sequence into the plant cell DNA using an *Agrobacterium tumefaciens* host. In one aspect, the plant cell can be a potato, corn, rice, wheat, tobacco, or barley cell.

The invention provides methods of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps: (a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a nucleic acid of the invention; (b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell. The invention provides methods of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps: (a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence of the invention; (b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

The invention provides methods for hydrolyzing, breaking up or disrupting a xylan-comprising composition comprising the following steps: (a) providing a polypeptide of the invention having a xylanase activity, or a polypeptide encoded by a nucleic acid of the invention; (b) providing a composition comprising a xylan; and (c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the xylanase hydrolyzes, breaks up or disrupts the xylan-comprising composition. In one aspect, the composition comprises a plant cell, a bacterial cell, a yeast cell, an insect cell, or an animal cell. Thus, the composition can comprise any plant or plant part, any xylan-containing food or feed, a waste product and the like. The invention provides methods for liquefying or removing a xylan-comprising composition comprising the following steps: (a) providing a polypeptide of the invention having a xylanase activity, or a polypeptide encoded by a nucleic acid of the invention; (b) providing a composition comprising a xylan; and (c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the xylanase removes, softens or liquefies the xylan-comprising composition.

The invention provides detergent compositions comprising a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention, wherein the polypeptide has a xylanase activity. The xylanase can be a nonsurface-active xylanase or a surface-active xylanase. The xylanase can be formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel form, a paste or a slurry form. The invention provides methods for washing an object comprising the following steps: (a) providing a composition comprising a polypeptide of the invention having a xylanase activity, or a polypeptide encoded by a nucleic acid of the invention; (b) providing an object; and (c) contacting the polypeptide of step (a) and the object of step (b) under conditions wherein the composition can wash the object.

The invention provides textiles or fabrics, including, e.g., threads, comprising a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention. In one aspect, the textiles or fabrics comprise xylan-containing fibers. The invention provides methods for treating a textile or fabric (e.g., removing a stain from a composition) comprising the following steps: (a) providing a composition comprising a polypeptide of the invention having a xylanase activity, or a polypeptide encoded by a nucleic acid of the invention; (b) providing a textile or fabric comprising a xylan; and (c) contacting the polypeptide of step (a) and the composition of step (b) under conditions wherein the xylanase can treat the textile or fabric (e.g., remove the stain). The invention provides methods for improving the finish of a fabric comprising the following steps: (a) providing a composition

comprising a polypeptide of the invention having a xylanase activity, or a polypeptide encoded by a nucleic acid of the invention; (b) providing a fabric; and (c) contacting the polypeptide of step (a) and the fabric of step (b) under conditions wherein the polypeptide can treat the fabric thereby improving the finish of the fabric. In one aspect, the fabric is a wool or a silk.

The invention provides feeds or foods comprising a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention. The invention provides methods for hydrolyzing xylans in a feed or a food prior to consumption by an animal comprising the following steps: (a) obtaining a feed material comprising a xylanase of the invention, or a xylanase encoded by a nucleic acid of the invention; and (b) adding the polypeptide of step (a) to the feed or food material in an amount sufficient for a sufficient time period to cause hydrolysis of the xylan and formation of a treated food or feed, thereby hydrolyzing the xylans in the food or the feed prior to consumption by the animal. In one aspect, the invention provides methods for hydrolyzing xylans in a feed or a food after consumption by an animal comprising the following steps: (a) obtaining a feed material comprising a xylanase of the invention, or a xylanase encoded by a nucleic acid of the invention; (b) adding the polypeptide of step (a) to the feed or food material; and (c) administering the feed or food material to the animal, wherein after consumption, the xylanase causes hydrolysis of xylans in the feed or food in the digestive tract of the animal. The food or the feed can be, e.g., a cereal, a grain, a corn and the like.

The invention provides food or nutritional supplements for an animal comprising a polypeptide of the invention, e.g., a polypeptide encoded by the nucleic acid of the invention. In one aspect, the polypeptide in the food or nutritional supplement can be glycosylated. The invention provides edible enzyme delivery matrices comprising a polypeptide of the invention, e.g., a polypeptide encoded by the nucleic acid of the invention. In one aspect, the delivery matrix comprises a pellet. In one aspect, the polypeptide can be glycosylated. In one aspect, the xylanase activity is thermotolerant. In another aspect, the xylanase activity is thermostable.

The invention provides a food, a feed or a nutritional supplement comprising a polypeptide of the invention. The invention provides methods for utilizing a xylanase as a nutritional supplement in an animal diet, the method comprising: preparing a nutritional supplement containing a xylanase enzyme comprising at least thirty contiguous amino acids of a polypeptide of the invention; and administering the nutritional supplement to an animal to increase utilization of a xylan contained in a feed or a food ingested by the animal. The

animal can be a human, a ruminant or a monogastric animal. The xylanase enzyme can be prepared by expression of a polynucleotide encoding the xylanase in an organism selected from the group consisting of a bacterium, a yeast, a plant, an insect, a fungus and an animal. The organism can be selected from the group consisting of an *S. pombe, S. cerevisiae, Pichia pastoris, Pseudomonas* sp., *E. coli, Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

The invention provides edible enzyme delivery matrix comprising a thermostable recombinant xylanase enzyme, e.g., a polypeptide of the invention. The invention provides methods for delivering a xylanase supplement to an animal, the method comprising: preparing an edible enzyme delivery matrix in the form of pellets comprising a granulate edible carrier and a thermostable recombinant xylanase enzyme, wherein the pellets readily disperse the xylanase enzyme contained therein into aqueous media, and administering the edible enzyme delivery matrix to the animal. The recombinant xylanase enzyme can comprise a polypeptide of the invention. The granulate edible carrier can comprise a carrier selected from the group consisting of a grain germ, a grain germ that is spent of oil, a hay, an alfalfa, a timothy, a soy hull, a sunflower seed meal and a wheat midd. The edible carrier can comprise grain germ that is spent of oil. The xylanase enzyme can be glycosylated to provide thermostability at pelletizing conditions. The delivery matrix can be formed by pelletizing a mixture comprising a grain germ and a xylanase. The pelletizing conditions can include application of steam. The pelletizing conditions can comprise application of a temperature in excess of about 80°C for about 5 minutes and the enzyme retains a specific activity of at least 350 to about 900 units per milligram of enzyme.

The invention provides methods for improving texture and flavor of a dairy product comprising the following steps: (a) providing a polypeptide of the invention having a xylanase activity, or a xylanase encoded by a nucleic acid of the invention; (b) providing a dairy product; and (c) contacting the polypeptide of step (a) and the dairy product of step (b) under conditions wherein the xylanase can improve the texture or flavor of the dairy product. In one aspect, the dairy product comprises a cheese or a yogurt. The invention provides dairy products comprising a xylanase of the invention, or is encoded by a nucleic acid of the invention.

The invention provides methods for improving the extraction of oil from an oil-rich plant material comprising the following steps: (a) providing a polypeptide of the invention having a xylanase activity, or a xylanase encoded by a nucleic acid of the invention; (b) providing an oil-rich plant material; and (c) contacting the polypeptide of step (a) and the oil-rich plant material. In one aspect, the oil-rich plant material comprises an oil-

rich seed. The oil can be a soybean oil, an olive oil, a rapeseed (canola) oil or a sunflower oil.

The invention provides methods for preparing a fruit or vegetable juice, syrup, puree or extract comprising the following steps: (a) providing a polypeptide of the invention having a xylanase activity, or a xylanase encoded by a nucleic acid of the invention; (b) providing a composition or a liquid comprising a fruit or vegetable material; and (c) contacting the polypeptide of step (a) and the composition, thereby preparing the fruit or vegetable juice, syrup, puree or extract.

The invention provides papers or paper products or paper pulp comprising a xylanase of the invention, or a polypeptide encoded by a nucleic acid of the invention. The invention provides methods for treating a paper or a paper or wood pulp comprising the following steps: (a) providing a polypeptide of the invention having a xylanase activity, or a xylanase encoded by a nucleic acid of the invention; (b) providing a composition comprising a paper or a paper or wood pulp; and (c) contacting the polypeptide of step (a) and the composition of step (b) under conditions wherein the xylanase can treat the paper or paper or wood pulp. In one aspect, the pharmaceutical composition acts as a digestive aid or an anti-microbial (e.g., against *Salmonella*). In one aspect, the treatment is prophylactic. In one aspect, the invention provides oral care products comprising a polypeptide of the invention having a xylanase activity, or a xylanase encoded by a nucleic acid of the invention. The oral care product can comprise a toothpaste, a dental cream, a gel or a tooth powder, an odontic, a mouth wash, a pre- or post brushing rinse formulation, a chewing gum, a lozenge or a candy. The invention provides contact lens cleaning compositions comprising a polypeptide of the invention having a xylanase activity, or a xylanase encoded by a nucleic acid of the invention.

In one aspect, the invention provides methods for eliminating or protecting animals from a microorganism comprising a xylan comprising administering a polypeptide of the invention. The microorganism can be a bacterium comprising a xylan, e.g., *Salmonella*.

The invention provides an isolated nucleic acid having a sequence as set forth in SEQ ID NO.:189 and variants thereof having at least 50% sequence identity to SEQ ID NO.:189 and encoding polypeptides having xylanase activity. In one aspect, the polypeptide has a xylanase activity, e.g., a thermostable xylanase activity.

The invention provides isolated or recombinant nucleic acids comprising SEQ ID NO:189, wherein SEQ ID NO:189 comprises one or more or all of the following sequence variations: the nucleotides at positions 22 to 24 are TTC, the nucleotides at positions 22 to 24

are TTT, the nucleotides at positions 31 to 33 are CAC, the nucleotides at positions 31 to 33 are CAT, the nucleotides at positions 34 to 36 are TTG, the nucleotides at positions 34 to 36 are TTA, the nucleotides at positions 34 to 36 are CTC, the nucleotides at positions 34 to 36 are CTT, the nucleotides at positions 34 to 36 are CTA, the nucleotides at positions 34 to 36 are CTG, the nucleotides at positions 49 to 51 are ATA, the nucleotides at positions 49 to 51 are ATT, the nucleotides at positions 49 to 51 are ATC, the nucleotides at positions 178 to 180 are CAC, the nucleotides at positions 178 to 180 are CAT, the nucleotides at positions 190 to 192 are TGT, the nucleotides at positions 190 to 192 are TGC, the nucleotides at positions 190 to 192 are GTA, the nucleotides at positions 190 to 192 are GTT, the nucleotides at positions 190 to 192 are GTC, the nucleotides at positions 190 to 192 are GTG, the nucleotides at positions 193 to 195 are GTG, the nucleotides at positions 193 to 195 are GTC, the nucleotides at positions 193 to 195 are GTA, the nucleotides at positions 193 to 195 are GTT, the nucleotides at positions 202 to 204 are ATA, the nucleotides at positions 202 to 204 are ATT, the nucleotides at positions 202 to 204 are ATC, the nucleotides at positions 202 to 204 are GCT, the nucleotides at positions 202 to 204 are GCG, the nucleotides at positions 202 to 204 are GCC, the nucleotides at positions 202 to 204 are GCA, the nucleotides at positions 235 to 237 are CCA, the nucleotides at positions 235 to 237 are CCC, or the nucleotides at positions 235 to 237 are CCG.

The invention provides isolated or recombinant polypeptides comprising an amino acid sequence comprising SEQ ID NO:190, wherein SEQ ID NO:190 comprises one or more or all of the following sequence variations: the aspartic acid at amino acid position 8 is phenylalanine, the glutamine at amino acid position 11 is histidine, the asparagine at amino acid position 12 is leucine, the glycine at amino acid position 17 is isoleucine, the threonine at amino acid position 23 is threonine encoded by a codon other than the wild type codon, the glycine at amino acid position 60 is histidine, the proline at amino acid position 64 is cysteine, the proline at amino acid position 64 is valine, the serine at amino acid position 65 is valine, the glycine at amino acid position 68 is isoleucine, the glycine at amino acid position 68 is alanine, or the serine at amino acid position 79 is proline. In one aspect, the polypeptide has a xylanase activity, e.g., a thermostable xylanase activity.

The invention provides isolated or recombinant nucleic acids comprising SEQ ID NO: 189, wherein SEQ ID NO:189 comprises one or more or all sequence variations set forth in Table 1 or Table 2. The invention provides isolated or recombinant polypeptides encoded by nucleic acids comprising SEQ ID NO: 189, wherein SEQ ID NO:189 comprises

one or more or all sequence variations set forth in Table 1 or Table 2. In one aspect, the polypeptide has a xylanase activity, e.g., a thermostable xylanase activity.

The invention provides isolated or recombinant nucleic acids comprising SEQ ID NO:379, wherein SEQ ID NO:379 comprises one or more or all of the following sequence variations: the nucleotides at positions 22 to 24 are TTC, the nucleotides at positions 31 to 33 are CAC, the nucleotides at positions 49 to 51 are ATA, the nucleotides at positions 178 to 180 are CAC, the nucleotides at positions 193 to 195 are GTG, the nucleotides at positions 202 to 204 are GCT.

The invention provides isolated or recombinant polypeptides comprising SEQ ID NO:380, wherein SEQ ID NO:380 comprises one or more or all of the following sequence variations: D8F, Q11H, G17I, G60H, S65V and/or G68A. In one aspect, the polypeptide has a xylanase activity, e.g., a thermostable xylanase activity.

The isolated or recombinant nucleic acids of the invention are also referred to as "Group A nucleic acid sequences". The invention provides an isolated nucleic acid including at least 10 consecutive bases of a sequence as set forth in Group A nucleic acid sequences, sequences substantially identical thereto and the sequences complementary thereto.

The isolated or recombinant polypeptides of the invention, which include functional fragments of the exemplary sequences of the invention, are also referred to as "Group B amino acid sequences". Another aspect of the invention is an isolated or recombinant nucleic acid encoding a polypeptide having at least 10 consecutive amino acids of a sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto. In yet another aspect, the invention provides a purified polypeptide having a sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto. Another aspect of the invention is an isolated or purified antibody that specifically binds to a polypeptide having a sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto.

Another aspect of the invention is an isolated or purified antibody or binding fragment thereof, which specifically binds to a polypeptide having at least 10 consecutive amino acids of one of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto.

Another aspect of the invention is a method of making a polypeptide having a sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto. The method includes introducing a nucleic acid encoding the polypeptide into a host

cell, wherein the nucleic acid is operably linked to a promoter and culturing the host cell under conditions that allow expression of the nucleic acid. Another aspect of the invention is a method of making a polypeptide having at least 10 amino acids of a sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto. The method includes introducing a nucleic acid encoding the polypeptide into a host cell, wherein the nucleic acid is operably linked to a promoter and culturing the host cell under conditions that allow expression of the nucleic acid, thereby producing the polypeptide.

Another aspect of the invention is a method of generating a variant including obtaining a nucleic acid having a sequence as set forth in Group A nucleic acid sequences, sequences substantially identical thereto, sequences complementary to the sequences of Group A nucleic acid sequences, fragments comprising at least 30 consecutive nucleotides of the foregoing sequences and changing one or more nucleotides in the sequence to another nucleotide, deleting one or more nucleotides in the sequence, or adding one or more nucleotides to the sequence.

Another aspect of the invention is a computer readable medium having stored thereon a sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto.

Another aspect of the invention is a computer system including a processor and a data storage device wherein the data storage device has stored thereon a sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide having a sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto.

Another aspect of the invention is a method for comparing a first sequence to a reference sequence wherein the first sequence is a nucleic acid having a sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide code of Group B amino acid sequences and sequences substantially identical thereto. The method includes reading the first sequence and the reference sequence through use of a computer program that compares sequences; and determining differences between the first sequence and the reference sequence with the computer program.

Another aspect of the invention is a method for identifying a feature in a sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide having a sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto, including reading the sequence through the use of a

computer program which identifies features in sequences; and identifying features in the sequence with the computer program.

Yet another aspect of the invention is a method of catalyzing the breakdown of xylan or a derivative thereof, comprising the step of contacting a sample containing xylan or the derivative thereof with a polypeptide of Group B amino acid sequences and sequences substantially identical thereto under conditions which facilitate the breakdown of the xylan.

Another aspect of the invention is an assay for identifying fragments or variants of Group B amino acid sequences and sequences substantially identical thereto, which retain the enzymatic function of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto. The assay includes contacting the polypeptide of Group B amino acid sequences, sequences substantially identical thereto, or polypeptide fragment or variant with a substrate molecule under conditions which allow the polypeptide fragment or variant to function and detecting either a decrease in the level of substrate or an increase in the level of the specific reaction product of the reaction between the polypeptide and substrate thereby identifying a fragment or variant of such sequences.

Another aspect of the invention is a nucleic acid probe of an oligonucleotide from about 10 to 50 nucleotides in length and having a segment of at least 10 contiguous nucleotides that is at least 50% complementary to a nucleic acid target region of a nucleic acid sequence selected from the group consisting of Group A nucleic acid sequences; and which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex.

Another aspect of the invention is a polynucleotide probe for isolation or identification of xylanase genes having a sequence which is the same as, or fully complementary to at least a fragment of one of Group A nucleic acid sequences.

In still another aspect, the invention provides a protein preparation comprising a polypeptide having an amino acid sequence selected from Group B amino acid sequences and sequences substantially identical thereto wherein the protein preparation is a liquid.

Still another aspect of the invention provides a protein preparation comprising a polypeptide having an amino acid sequence selected from Group B amino acid sequences and sequences substantially identical thereto wherein the polypeptide is a solid.

Yet another aspect of the invention provides a method for modifying small molecules, comprising the step of mixing at least one polypeptide encoded by a polynucleotide selected from Group A nucleic acid sequences, sequences substantially identical thereto and the sequences complementary thereto with at least one small molecule,

to produce at least one modified small molecule via at least one biocatalytic reaction, where the at least one polypeptide has xylanase activity.

Another aspect of the invention is a cloning vector of a sequence that encodes a polypeptide having xylanase activity, said sequence being selected from Group A nucleic acid sequences, sequences substantially identical thereto and the sequences complementary thereto.

Another aspect of the invention is a host cell comprising a sequence that encodes a polypeptide having xylanase activity, said sequence being selected from Group A nucleic acid sequences, sequences substantially identical thereto and the sequences complementary thereto.

In yet another aspect, the invention provides an expression vector capable of replicating in a host cell comprising a polynucleotide having a sequence selected Group A nucleic acid sequences, sequences substantially identical thereto, sequences complementary thereto and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.

In another aspect, the invention provides a method of dough conditioning comprising contacting dough with at least one polypeptide of Group B amino acid sequences and sequences substantially identical thereto under conditions sufficient for conditioning the dough.

Another aspect of the invention is a method of beverage production comprising administration of at least one polypeptide of Group B amino acid sequences and sequences substantially identical thereto under conditions sufficient for decreasing the viscosity of wort or beer.

The xylanases of the invention are used to break down the high molecular weight arabinoxylans in animal feed. Adding the xylanases of the invention stimulates growth rates by improving digestibility, which also improves the quality of the animal litter. Xylanase functions through the gastro-intestinal tract to reduce intestinal viscosity and increase diffusion of pancreatic enzymes. Additionally, the xylanases of the invention may be used in the treatment of endosperm cell walls of feed grains and vegetable proteins. In one aspect of the invention, the novel xylanases of the invention are administered to an animal in order to increase the utilization of the xylan in the food. This activity of the xylanases of the invention may be used to break down insoluble cell wall material, liberating nutrients in the cell walls, which then become available to the animal. It also changes hemicellulose to

nutritive sugars so that nutrients formerly trapped within the cell walls are released. Xylanase also produces compounds that may be a nutritive source for the ruminal microflora.

Another aspect of the invention provides a method for utilizing xylanase as a nutritional supplement in the diets of animals, comprising preparation of a nutritional supplement containing a recombinant xylanase enzyme comprising at least thirty contiguous amino acids of Group B amino acid sequences and sequences substantially identical thereto and administering the nutritional supplement to an animal to increase the utilization of xylan contained in food ingested by the animal.

In another aspect of the invention, a method for delivering a xylanase supplement to an animal is provided, where the method comprises preparing an edible enzyme delivery matrix in the form of pellets comprising a granulate edible carrier and a thermostable recombinant xylanase enzyme, wherein the particles readily disperse the xylanase enzyme contained therein into aqueous media, and administering the edible enzyme delivery matrix to the animal. The granulate edible carrier may comprise a carrier selected from the group consisting of grain germ that is spent of oil, hay, alfalfa, timothy, soy hull, sunflower seed meal and wheat midd. The xylanase enzyme may have an amino acid sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto.

In another aspect, the invention provides an isolated nucleic acid comprising a sequence that encodes a polypeptide having xylanase activity, wherein the sequence is selected from Group A nucleic acid sequences, sequences substantially identical thereto and the sequences complementary thereto, wherein the sequence contains a signal sequence. The invention also provides an isolated nucleic acid comprising a sequence that encodes a polypeptide having xylanase activity, wherein the sequence is selected from Group A nucleic acid sequences, sequences substantially identical thereto and the sequences complementary thereto, wherein the sequence contains a signal sequence from another xylanase. Additionally, the invention provides an isolated nucleic acid comprising a sequence that encodes a polypeptide having xylanase activity, wherein the sequence is selected from Group A nucleic acid sequences, sequences substantially identical thereto and the sequences complementary thereto wherein the sequence does not contain a signal sequence.

Still another aspect of the invention provides an isolated nucleic acid that is a mutation of SEQ ID NO: 189. Yet another aspect provides an amino acid sequence that is a mutation of SEQ ID NO: 190.

The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

All publications, patents, patent applications, GenBank sequences and ATCC deposits, cited herein are hereby expressly incorporated by reference for all purposes.

BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings are illustrative of aspects of the invention and are not meant to limit the scope of the invention as encompassed by the claims.

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

Figure 1 is a block diagram of a computer system.

Figure 2 is a flow diagram illustrating one aspect of a process for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database.

Figure 3 is a flow diagram illustrating one aspect of a process in a computer for determining whether two sequences are homologous.

Figure 4 is a flow diagram illustrating one aspect of an identifier process 300 for detecting the presence of a feature in a sequence.

Figure 5 is a graph comparing activity of the wild type sequence (SEQ ID NOS: 189 and 190) to the 8x mutant (SEQ ID NOS:375, 376), a combination of mutants D, F, H, I, S, V, X and AA in Table 1.

Figure 6A illustrates the nine single site amino acid mutants of SEQ ID NO:378 (encoded by SEQ ID NO:377) as generated by Gene Site Saturation Mutagenesis (GSSM™) of SEQ ID NO:190 (encoded by SEQ ID NO:189), as described in detail in Example 5, below.

Figure 6B illustrates the unfolding of SEQ ID NO:190 and SEQ ID NO:378 in melting temperature transition midpoint (Tm) experiments as determined by DSC for each enzyme, as described in detail in Example 5, below.

Figure 7A illustrates the pH and temperature activity profiles for the enzymes SEQ ID NO:190 and SEQ ID NO:378, as described in detail in Example 5, below.

Figure 7B illustrates the rate/temperature activity optima for the enzymes SEQ ID NO:190 and SEQ ID NO:378, as described in detail in Example 5, below.

Figure 7C illustrates the thermal tolerance/ residual activity for the enzymes SEQ ID NO:190 and SEQ ID NO:378, as described in detail in Example 5, below.

Figure 8A illustrates the GeneReassembly™ library of all possible combinations of the 9 GSSM™ point mutations that was constructed and screened for variants with improved thermal tolerance and activity, as described in detail in Example 5, below.

Figure 8B illustrates the relative activity of the "6X-2" variant and "9X" variant (SEQ ID NO:378) compared to SEQ ID NO:190 ("wild-type") at a temperature optimum and pH 6.0, as described in detail in Example 5, below.

Figure 9A illustrates the fingerprints obtained after hydrolysis of oligoxylans (Xyl)3, (Xyl)4, (Xyl)5 and (Xyl)6 by the SEQ ID NO:190 ("wild-type") and the "9X" variant (SEQ ID NO:378) enzymes, as described in detail in Example 5, below.

Figure 9B illustrates the fingerprints obtained after hydrolysis of Beechwood xylan by the SEQ ID NO:190 ("wild-type") and the "9X" variant (SEQ ID NO:378) enzymes, as described in detail in Example 5, below.

Figure 10A is a schematic diagram illustrating the level of thermal stability (represented by Tm) improvement over SEQ ID NO:190 ("wild-type") obtained by GSSM™ evolution, as described in detail in Example 5, below.

Figure 10B illustrates a "fitness diagram" of enzyme improvement in the form of SEQ ID NO:378 and SEQ ID NO:380, as obtained by combining GSSM™ and GeneReassembly™ technologies, as described in detail in Example 5, below.

Figure 11 is a schematic flow diagram of an exemplary routine screening protocol to determine whether a xylanase of the invention is useful in pretreating paper pulp, as described in detail in Example 6, below.

Like reference symbols in the various drawings indicate like elements.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to xylanases and polynucleotides encoding them and methods of making and using them. Xylanase activity of the polypeptides of the invention encompasses enzymes having hydrolase activity, for example, enzymes capable of hydrolyzing glycosidic linkages present in xylan, e.g., catalyzing hydrolysis of internal β-1,4-xylosidic linkages. The xylanases of the invention can be used to make and/or process foods, feeds, nutritional supplements, textiles, detergents and the like. The xylanases of the

invention can be used in pharmaceutical compositions and dietary aids. Xylanases of the invention are particularly useful in baking, animal feed, beverage and paper processes.

Definitions

The term "antibody" includes a peptide or polypeptide derived from, modeled after or substantially encoded by an immunoglobulin gene or immunoglobulin genes, or fragments thereof, capable of specifically binding an antigen or epitope, see, e.g. Fundamental Immunology, Third Edition, W.E. Paul, ed., Raven Press, N.Y. (1993); Wilson (1994) J. Immunol. Methods 175:267-273; Yarmush (1992) J. Biochem. Biophys. Methods 25:85-97. The term antibody includes antigen-binding portions, i.e., "antigen binding sites," (e.g., fragments, subsequences, complementarity determining regions (CDRs)) that retain capacity to bind antigen, including (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a F(ab')2 fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward et al., (1989) Nature 341:544-546), which consists of a VH domain; and (vi) an isolated complementarity determining region (CDR). Single chain antibodies are also included by reference in the term "antibody."

The terms "array" or "microarray" or "biochip" or "chip" as used herein is a plurality of target elements, each target element comprising a defined amount of one or more polypeptides (including antibodies) or nucleic acids immobilized onto a defined area of a substrate surface, as discussed in further detail, below.

As used herein, the terms "computer," "computer program" and "processor" are used in their broadest general contexts and incorporate all such devices, as described in detail, below. A "coding sequence of" or a "sequence encodes" a particular polypeptide or protein, is a nucleic acid sequence which is transcribed and translated into a polypeptide or protein when placed under the control of appropriate regulatory sequences.

The phrases "nucleic acid" or "nucleic acid sequence" as used herein refer to an oligonucleotide, nucleotide, polynucleotide, or to a fragment of any of these, to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent a sense or antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material, natural or synthetic in origin. The phrases "nucleic acid" or "nucleic acid sequence" includes oligonucleotide, nucleotide, polynucleotide, or to a fragment of any of these, to DNA or RNA (e.g., mRNA, rRNA, tRNA, iRNA) of genomic or synthetic origin

which may be single-stranded or double-stranded and may represent a sense or antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material, natural or synthetic in origin, including, e.g., iRNA, ribonucleoproteins (e.g., e.g., double stranded iRNAs, e.g., iRNPs). The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogues of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones, see e.g., Mata (1997) Toxicol. Appl. Pharmacol. 144:189-197; Strauss-Soukup (1997) Biochemistry 36:8692-8698; Samstag (1996) Antisense Nucleic Acid Drug Dev 6:153-156. "Oligonucleotide" includes either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands that may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide can ligate to a fragment that has not been dephosphorylated.

A "coding sequence of" or a "nucleotide sequence encoding" a particular polypeptide or protein, is a nucleic acid sequence which is transcribed and translated into a polypeptide or protein when placed under the control of appropriate regulatory sequences.

The term "gene" means the segment of DNA involved in producing a polypeptide chain; it includes regions preceding and following the coding region (leader and trailer) as well as, where applicable, intervening sequences (introns) between individual coding segments (exons). "Operably linked" as used herein refers to a functional relationship between two or more nucleic acid (e.g., DNA) segments. Typically, it refers to the functional relationship of transcriptional regulatory sequence to a transcribed sequence. For example, a promoter is operably linked to a coding sequence, such as a nucleic acid of the invention, if it stimulates or modulates the transcription of the coding sequence in an appropriate host cell or other expression system. Generally, promoter transcriptional regulatory sequences that are operably linked to a transcribed sequence are physically contiguous to the transcribed sequence, i.e., they are cis-acting. However, some transcriptional regulatory sequences, such as enhancers, need not be physically contiguous or located in close proximity to the coding sequences whose transcription they enhance.

The term "expression cassette" as used herein refers to a nucleotide sequence which is capable of affecting expression of a structural gene (i.e., a protein coding sequence, such as a xylanase of the invention) in a host compatible with such sequences. Expression cassettes include at least a promoter operably linked with the polypeptide coding sequence; and, optionally, with other sequences, e.g., transcription termination signals. Additional

factors necessary or helpful in effecting expression may also be used, e.g., enhancers. Thus, expression cassettes also include plasmids, expression vectors, recombinant viruses, any form of recombinant "naked DNA" vector, and the like. A "vector" comprises a nucleic acid that can infect, transfect, transiently or permanently transduce a cell. It will be recognized that a vector can be a naked nucleic acid, or a nucleic acid complexed with protein or lipid. The vector optionally comprises viral or bacterial nucleic acids and/or proteins, and/or membranes (e.g., a cell membrane, a viral lipid envelope, etc.). Vectors include, but are not limited to replicons (e.g., RNA replicons, bacteriophages) to which fragments of DNA may be attached and become replicated. Vectors thus include, but are not limited to RNA, autonomous self-replicating circular or linear DNA or RNA (e.g., plasmids, viruses, and the like, see, e.g., U.S. Patent No. 5,217,879), and include both the expression and non-expression plasmids. Where a recombinant microorganism or cell culture is described as hosting an "expression vector" this includes both extra-chromosomal circular and linear DNA and DNA that has been incorporated into the host chromosome(s). Where a vector is being maintained by a host cell, the vector may either be stably replicated by the cells during mitosis as an autonomous structure, or is incorporated within the host's genome.

As used herein, the term "promoter" includes all sequences capable of driving transcription of a coding sequence in a cell, e.g., a plant cell. Thus, promoters used in the constructs of the invention include *cis*-acting transcriptional control elements and regulatory sequences that are involved in regulating or modulating the timing and/or rate of transcription of a gene. For example, a promoter can be a *cis*-acting transcriptional control element, including an enhancer, a promoter, a transcription terminator, an origin of replication, a chromosomal integration sequence, 5' and 3' untranslated regions, or an intronic sequence, which are involved in transcriptional regulation. These cis-acting sequences typically interact with proteins or other biomolecules to carry out (turn on/off, regulate, modulate, etc.) transcription. "Constitutive" promoters are those that drive expression continuously under most environmental conditions and states of development or cell differentiation. "Inducible" or "regulatable" promoters direct expression of the nucleic acid of the invention under the influence of environmental conditions or developmental conditions. Examples of environmental conditions that may affect transcription by inducible promoters include anaerobic conditions, elevated temperature, drought, or the presence of light.

"Tissue-specific" promoters are transcriptional control elements that are only active in particular cells or tissues or organs, e.g., in plants or animals. Tissue-specific regulation may be achieved by certain intrinsic factors that ensure that genes encoding

proteins specific to a given tissue are expressed. Such factors are known to exist in mammals and plants so as to allow for specific tissues to develop.

The term "plant" includes whole plants, plant parts (e.g., leaves, stems, flowers, roots, etc.), plant protoplasts, seeds and plant cells and progeny of same. The class of plants which can be used in the method of the invention is generally as broad as the class of higher plants amenable to transformation techniques, including angiosperms (monocotyledonous and dicotyledonous plants), as well as gymnosperms. It includes plants of a variety of ploidy levels, including polyploid, diploid, haploid and hemizygous states. As used herein, the term "transgenic plant" includes plants or plant cells into which a heterologous nucleic acid sequence has been inserted, e.g., the nucleic acids and various recombinant constructs (e.g., expression cassettes) of the invention.

"Plasmids" can be commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. Equivalent plasmids to those described herein are known in the art and will be apparent to the ordinarily skilled artisan.

"Amino acid" or "amino acid sequence" as used herein refer to an oligopeptide, peptide, polypeptide, or protein sequence, or to a fragment, portion, or subunit of any of these and to naturally occurring or synthetic molecules.

"Amino acid" or "amino acid sequence" include an oligopeptide, peptide, polypeptide, or protein sequence, or to a fragment, portion, or subunit of any of these, and to naturally occurring or synthetic molecules. The term "polypeptide" as used herein, refers to amino acids joined to each other by peptide bonds or modified peptide bonds, *i.e.*, peptide isosteres and may contain modified amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as post-translational processing, or by chemical modification techniques that are well known in the art. Modifications can occur anywhere in the polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also a given polypeptide may have many types of modifications. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of a phosphytidylinositol, cross-linking cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of

pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristolyation, oxidation, pegylation, xylan hydrolase processing, phosphorylation, prenylation, racemization, selenoylation, sulfation and transfer-RNA mediated addition of amino acids to protein such as arginylation. (*See* Creighton, T.E., Proteins – Structure and Molecular Properties 2nd Ed., W.H. Freeman and Company, New York (1993); *Posttranslational Covalent Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York, pp. 1-12 (1983)). The peptides and polypeptides of the invention also include all "mimetic" and "peptidomimetic" forms, as described in further detail, below.

As used herein, the term "isolated" means that the material is removed from its original environment (*e.g.*, the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition and still be isolated in that such vector or composition is not part of its natural environment. As used herein, the term "purified" does not require absolute purity; rather, it is intended as a relative definition. Individual nucleic acids obtained from a library have been conventionally purified to electrophoretic homogeneity. The sequences obtained from these clones could not be obtained directly either from the library or from total human DNA. The purified nucleic acids of the invention have been purified from the remainder of the genomic DNA in the organism by at least 10^4-10^6 fold. However, the term "purified" also includes nucleic acids that have been purified from the remainder of the genomic DNA or from other sequences in a library or other environment by at least one order of magnitude, typically two or three orders and more typically four or five orders of magnitude.

As used herein, the term "recombinant" means that the nucleic acid is adjacent to a "backbone" nucleic acid to which it is not adjacent in its natural environment. Additionally, to be "enriched" the nucleic acids will represent 5% or more of the number of nucleic acid inserts in a population of nucleic acid backbone molecules. Backbone molecules according to the invention include nucleic acids such as expression vectors, self-replicating nucleic acids, viruses, integrating nucleic acids and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. Typically, the enriched nucleic acids represent 15% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. More typically, the enriched nucleic acids represent 50% or more of the number of nucleic acid inserts

in the population of recombinant backbone molecules. In a one aspect, the enriched nucleic acids represent 90% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules.

"Recombinant" polypeptides or proteins refer to polypeptides or proteins produced by recombinant DNA techniques; *i.e.*, produced from cells transformed by an exogenous DNA construct encoding the desired polypeptide or protein. "Synthetic" polypeptides or protein are those prepared by chemical synthesis. Solid-phase chemical peptide synthesis methods can also be used to synthesize the polypeptide or fragments of the invention. Such method have been known in the art since the early 1960's (Merrifield, R. B., *J. Am. Chem. Soc.*, 85:2149-2154, 1963) (See also Stewart, J. M. and Young, J. D., Solid Phase Peptide Synthesis, 2nd Ed., Pierce Chemical Co., Rockford, Ill., pp. 11-12)) and have recently been employed in commercially available laboratory peptide design and synthesis kits (Cambridge Research Biochemicals). Such commercially available laboratory kits have generally utilized the teachings of H. M. Geysen *et al, Proc. Natl. Acad. Sci., USA*, 81:3998 (1984) and provide for synthesizing peptides upon the tips of a multitude of "rods" or "pins" all of which are connected to a single plate. When such a system is utilized, a plate of rods or pins is inverted and inserted into a second plate of corresponding wells or reservoirs, which contain solutions for attaching or anchoring an appropriate amino acid to the pin's or rod's tips. By repeating such a process step, *i.e.*, inverting and inserting the rod's and pin's tips into appropriate solutions, amino acids are built into desired peptides. In addition, a number of available FMOC peptide synthesis systems are available. For example, assembly of a polypeptide or fragment can be carried out on a solid support using an Applied Biosystems, Inc. Model 431A automated peptide synthesizer. Such equipment provides ready access to the peptides of the invention, either by direct synthesis or by synthesis of a series of fragments that can be coupled using other known techniques.

A promoter sequence is "operably linked to" a coding sequence when RNA polymerase which initiates transcription at the promoter will transcribe the coding sequence into mRNA.

"Plasmids" are designated by a lower case "p" preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described herein are known in the art and will be apparent to the ordinarily skilled artisan.

"Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 μg of plasmid or DNA fragment is used with about 2 units of enzyme in about 20 μl of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 μg of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37°C are ordinarily used, but may vary in accordance with the supplier's instructions. After digestion, gel electrophoresis may be performed to isolate the desired fragment.

The phrase "substantially identical" in the context of two nucleic acids or polypeptides, refers to two or more sequences that have, e.g., at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more nucleotide or amino acid residue (sequence) identity, when compared and aligned for maximum correspondence, as measured using one of the known sequence comparison algorithms or by visual inspection. Typically, the substantial identity exists over a region of at least about 100 residues and most commonly the sequences are substantially identical over at least about 150-200 residues. In some aspects, the sequences are substantially identical over the entire length of the coding regions.

Additionally a "substantially identical" amino acid sequence is a sequence that differs from a reference sequence by one or more conservative or non-conservative amino acid substitutions, deletions, or insertions, particularly when such a substitution occurs at a site that is not the active site of the molecule and provided that the polypeptide essentially retains its functional properties. A conservative amino acid substitution, for example, substitutes one amino acid for another of the same class (*e.g.*, substitution of one hydrophobic amino acid, such as isoleucine, valine, leucine, or methionine, for another, or substitution of one polar amino acid for another, such as substitution of arginine for lysine, glutamic acid for aspartic acid or glutamine for asparagine). One or more amino acids can be deleted, for example, from a xylanase polypeptide, resulting in modification of the structure of the polypeptide, without significantly altering its biological activity. For example, amino- or

carboxyl-terminal amino acids that are not required for xylanase biological activity can be removed. Modified polypeptide sequences of the invention can be assayed for xylanase biological activity by any number of methods, including contacting the modified polypeptide sequence with a xylanase substrate and determining whether the modified polypeptide decreases the amount of specific substrate in the assay or increases the bioproducts of the enzymatic reaction of a functional xylanase polypeptide with the substrate.

"Fragments" as used herein are a portion of a naturally occurring protein which can exist in at least two different conformations. Fragments can have the same or substantially the same amino acid sequence as the naturally occurring protein. "Substantially the same" means that an amino acid sequence is largely, but not entirely, the same, but retains at least one functional activity of the sequence to which it is related. In general two amino acid sequences are "substantially the same" or "substantially homologous" if they are at least about 85% identical. Fragments which have different three dimensional structures as the naturally occurring protein are also included. An example of this, is a "pro-form" molecule, such as a low activity proprotein that can be modified by cleavage to produce a mature enzyme with significantly higher activity.

"Hybridization" refers to the process by which a nucleic acid strand joins with a complementary strand through base pairing. Hybridization reactions can be sensitive and selective so that a particular sequence of interest can be identified even in samples in which it is present at low concentrations. Suitably stringent conditions can be defined by, for example, the concentrations of salt or formamide in the prehybridization and hybridization solutions, or by the hybridization temperature and are well known in the art. In particular, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature. In alternative aspects, nucleic acids of the invention are defined by their ability to hybridize under various stringency conditions (e.g., high, medium, and low), as set forth herein.

For example, hybridization under high stringency conditions could occur in about 50% formamide at about 37°C to 42°C. Hybridization could occur under reduced stringency conditions in about 35% to 25% formamide at about 30°C to 35°C. In particular, hybridization could occur under high stringency conditions at 42°C in 50% formamide, 5X SSPE, 0.3% SDS and 200 n/ml sheared and denatured salmon sperm DNA. Hybridization could occur under reduced stringency conditions as described above, but in 35% formamide at a reduced temperature of 35°C. The temperature range corresponding to a particular level of stringency can be further narrowed by calculating the purine to pyrimidine ratio of the

nucleic acid of interest and adjusting the temperature accordingly. Variations on the above ranges and conditions are well known in the art.

The term "variant" refers to polynucleotides or polypeptides of the invention modified at one or more base pairs, codons, introns, exons, or amino acid residues (respectively) yet still retain the biological activity of a xylanase of the invention. Variants can be produced by any number of means included methods such as, for example, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly (e.g., GeneReassembly™, see, e.g., U.S. Patent No. 6,537,776), GSSM™ and any combination thereof.

Table 1 and Table 2 list variants obtained by mutating SEQ ID NO:189 (encoding SEQ ID NO:190) by GSSM™. The invention provides nucleic acids having one or more, or all, of the sequences as set forth in Tables 1 and 2, i.e., nucleic acids having sequences that are variants of SEQ ID NO:189, where the variations are set forth in Table 1 and Table 2, and the polypeptides that are encoded by these variants.

These GSSM™ variants (set forth in Tables 1 and 2) were tested for thermal tolerance (see Examples, below). Mutants D, F, G, H, I, J, K, S, T, U, V, W, X, Y, Z, AA , DD and EE were found to have the highest thermal tolerance among the mutants in Table 1. Mutants may also be combined to form a larger mutant. For example, mutants D, F, H, I, S, V, X and AA of Table 1 were combined to form a larger mutant termed "8x" with a sequence as set forth in SEQ ID NO:375 (polypeptide encoding nucleic acid) and SEQ ID NO:376 (amino acid sequence). Figure 5 is a graph comparing the activity of the wild type sequence (SEQ ID NOS: 189 and 190) to the 8x mutant (SEQ ID NOS: 259 and 260). In comparing the wild type and the 8x mutant, it was discovered that the optimal temperature for both was 65°C and that the optimal pH for both was 5.5. The wild type sequence was found to maintain its stability for less than 1 minute at 65°C, while the 8x mutant (SEQ ID NOS:375, 376) was found to maintain its stability for more than 10 minutes at 85°C. The substrate used was AZO-AZO-xylan. In one aspect, the 8x mutant (SEQ ID NOS:375, 376) was evolved by GSSM™. In another aspect, the wild type is a GSSM™ parent for thermal tolerance evolution.

Table 1

Mutant	Mutation	Wild type Seq	GSSM™ Seq
A	A2F	GCC	TTT
B	A2D	GCC	GAC
C	A5H	GCT	CAC
D	D8F	GAC	TTC
E	Q11L	CAA	CTC
F	Q11H	CAA	CAC
G	N12L	AAT	TTG
H	N12L	AAT	TTG
I	G17I	GGT	ATA
J	Q11H,T23T	CAA,ACC	CAT,ACG
K	Q11H	CAA	CAT
L	S26P	TCT	CCG
M	S26P	TCT	CCA
N	S35F	TCA	TTT
O	No Change	GTT	GTA
P	A51P	GCA	CCG
Q	A51P	GCA	CCG
R	G60R	GGA	CGC
S	G60H	GGA	CAC
T	G60H	GGA	CAC
U	P64C	CCG	TGT
V	P64V	CCG	GTA
W	P64V	CCG	GTT
X	S65V	TCC	GTG
Y	Q11H	CAA	CAT
Z	G68I	GGA	ATA
AA	G68A	GGA	GCT
BB	A71G	GCT	GGA
CC	No Change	AAT	AAC
DD	S79P	TCA	CCA
EE	S79P	TCA	CCC
FF	T95S	ACT	TCT
GG	Y98P	TAT	CCG
HH	T114S	ACT	AGC
II	No Change	AAC	AAC
JJ	No Change	AGG	AGA
KK	I142L	ATT	CTG
LL	S151I	AGC	ATC
MM	S138T,S151A	TCG,AGC	ACG,GCG
NN	K158R	AAG	CGG
OO	K160V,V172I	AAA,GTA	GTT,ATA

The codon variants as set forth in Table 2 that produced variants (of SEQ ID NO:189) with the best variation or "improvement" over "wild type" (SEQ ID NO:189) in thermal tolerance are highlighted. As noted above, the invention provides nucleic acids, and the polypeptides that encode them, comprising one, several or all or the variations set forth in Table 2 and Table 1.

Table 2

Mutation	Wild type Sequence	GSSM™ Sequence	Other codons also coding for same changed amino acid
A2F	GCC	TTT	TTC
A2D	GCC	GAC	GAT
A5H	GCT	CAC	CAT
D8F	GAC	TTC	TTT
Q11L	CAA	CTC	TTA, TTG, CTT, CTA, CTG
Q11H	CAA	CAC, CAT	-
N12L	AAT	TTG	TTA, CTC, CTT, CTA, CTG
G17I	GGT	ATA	ATT, ATC
T23T	ACC	ACG	ACT, ACC, ACA
S26P	TCT	CCG, CCA	CCC
S35F	TCA	TTT	TTC
A51P	GCA	CCG	CCC, CCA
G60R	GGA	CGC	CGT, CGA, CGG, AGA, AGG
G60H	GGA	CAC	CAT
P64C	CCG	TGT	TGC
P64V	CCG	GTA, GTT	GTC, GTG
S65V	TCC	GTC	GTC, GTA, GTT
G68I	GGA	ATA	ATT, ATC
G68A	GGA	GCT	GCG, GCC, GCA
A71G	GCT	GGA	GGT, GGC, GGG
S79P	TCA	CCA, CCG	CCG
T95S	ACT	TCT	TCC, TCA, TCG, AGT, AGC
Y98P	TAT	CCG	CCC, CCA
T114S	ACT	AGC	TCC, TCA, TCG, AGT, TCT
I142L	ATT	CTG	TTA, CTC, CTT, CTA, TTG
S151I	AGC	ATC	ATT, ATA
S138T	TCG	ACG	ACT, ACC, ACA
S151A	AGC	GCG	GCT, GCC, GCA
K158R	AAG	CGG	CGT, CGA, CGC, AGA, AGG
K160V	AAA	GTT	GTC, GTA, GTG
V172I	GTA	ATA	ATT, ATC

In one aspect the amino acid sequence of an amino acid sequence (SEQ ID NO: 208) of Group B amino acid sequences is modified by a single amino acid mutation. In a specific aspect, that mutation is an asparagine to aspartic acid mutation. The resulting amino acid sequence and corresponding nucleic acid sequence are set forth as SEQ ID NO:252 and SEQ ID NO:251, respectively. Single amino acid mutations with an improvement in the pH optimum of the enzyme, such as the mutation of SEQ ID NO:208, have been shown in the art with respect to xylanases. (See, for example, Joshi, M., Sidhu, G., Pot, I., Brayer, G., Withers, S., McIntosh, L., J. Mol. Bio. 299, 255-279 (2000).) It is also noted that in such single amino acid mutations, portions of the sequences may be removed in the subcloning process. For example, SEQ ID NO:207 and SEQ ID NO:251 differ in only

one nucleotide, over the area that the sequences align. However, it is noted that a 78 nucleotide area at the N-terminus of SEQ ID NO:207 was removed from the N-terminus of SEQ ID NO:251 in the subcloning. Additionally, the first three nucleotides in SEQ ID NO:251 were changed to ATG and then the point mutation was made at the sixth nucleotide in SEQ ID NO:251.

The term "saturation mutagenesis", "gene site saturated mutagenesis" or "GSSM™" includes a method that uses degenerate oligonucleotide primers to introduce point mutations into a polynucleotide, as described in detail, below.

The term "optimized directed evolution system" or "optimized directed evolution" includes a method for reassembling fragments of related nucleic acid sequences, e.g., related genes, and explained in detail, below.

The term "synthetic ligation reassembly" or "SLR" includes a method of ligating oligonucleotide fragments in a non-stochastic fashion, and explained in detail, below.

Generating and Manipulating Nucleic Acids

The invention provides nucleic acids (e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193,

SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379; nucleic acids encoding polypeptides as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID

NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380), including expression cassettes such as expression vectors, encoding the polypeptides of the invention. The invention also includes methods for discovering new xylanase sequences using the nucleic acids of the invention. The invention also includes methods for inhibiting the expression of xylanase genes, transcripts and polypeptides using the nucleic acids of the invention. Also provided are methods for modifying the nucleic acids of the invention by, e.g., synthetic ligation reassembly, optimized directed evolution system and/or saturation mutagenesis.

The nucleic acids of the invention can be made, isolated and/or manipulated by, e.g., cloning and expression of cDNA libraries, amplification of message or genomic DNA by PCR, and the like. For example, the following exemplary sequences of the invention were initially derived from the following sources:

Table 3

SEQ ID	SOURCE
1, 2	Bacteria
101, 102	Environmental
103, 104	Bacteria
105, 106	Environmental
107, 108	Bacteria
109, 110	Environmental
11, 12	Environmental
111, 112	Environmental
113, 114	Environmental
115, 116	Environmental
117, 118	Environmental
119, 120	Environmental
121, 122	Environmental
123, 124	Environmental
125, 126	Environmental
127, 128	Environmental
129, 130	Bacteria
13, 14	Environmental
131, 132	Environmental
133, 134	Environmental
135, 136	Environmental
137, 138	Environmental
139, 140	Environmental
141, 142	Environmental
143, 144	Bacteria
145, 146	Eukaryote
147, 148	Environmental
149, 150	Environmental
15, 16	Environmental
151, 152	Environmental
153, 154	Environmental
155, 156	Environmental
157, 158	Environmental
159, 160	Environmental
161, 162	Environmental
163, 164	Environmental
165, 166	Environmental
167, 168	Environmental
169, 170	Environmental
17, 18	Bacteria
171, 172	Environmental
173, 174	Environmental
175, 176	Environmental
177, 178	Environmental
179, 180	Environmental
181, 182	Environmental
183, 184	Environmental
185, 186	Environmental

187, 188	Environmental
189, 190	Environmental
19, 20	Environmental
191, 192	Environmental
193, 194	Environmental
195, 196	Environmental
197, 198	Environmental
199, 200	Environmental
201, 202	Environmental
203, 204	Environmental
205, 206	Environmental
207, 208	Environmental
209, 210	Environmental
21, 22	Environmental
211, 212	Environmental
213, 214	Environmental
215, 216	Environmental
217, 218	Environmental
219, 220	Environmental
221, 222	Environmental
223, 224	Environmental
225, 226	Environmental
227, 228	Environmental
229, 230	Environmental
23, 24	Environmental
231, 232	Bacteria
233, 234	Environmental
235, 236	Environmental
237, 238	Environmental
239, 240	Environmental
241, 242	Environmental
243, 244	Environmental
245, 246	Environmental
247, 248	Environmental
249, 250	Environmental
25, 26	Environmental
251, 252	Environmental
253, 254	Environmental
255, 256	Environmental
257, 258	Environmental
259, 260	Environmental
261, 262	Environmental
263, 264	Environmental
265, 266	Environmental
267, 268	Bacteria
269, 270	Environmental
27, 28	Environmental
271, 272	Environmental
273, 274	Environmental
275, 276	Environmental

277, 278	Environmental
279, 280	Environmental
281, 282	Environmental
283, 284	Environmental
285, 286	Environmental
287, 288	Environmental
289, 290	Environmental
29, 30	Archaea
291, 292	Environmental
293, 294	Environmental
295, 296	Environmental
297, 298	Environmental
299, 300	Environmental
3, 4	Environmental
301, 302	Environmental
303, 304	Environmental
305, 306	Bacteria
307, 308	Environmental
309, 310	Environmental
31, 32	Environmental
311, 312	Environmental
313, 314	Bacteria
315, 316	Environmental
317, 318	Environmental
319, 320	Environmental
321, 322	Environmental
323, 324	Environmental
325, 326	Environmental
327, 328	Environmental
329, 330	Environmental
33, 34	Environmental
331, 332	Environmental
333, 334	Environmental
335, 336	Environmental
337, 338	Environmental
339, 340	Environmental
341, 342	Environmental
343, 344	Environmental
345, 346	Environmental
347, 348	Environmental
349, 350	Environmental
35, 36	Environmental
351, 352	Environmental
353, 354	Environmental
355, 356	Environmental
357, 358	Environmental
359, 360	Environmental
361, 362	Environmental
363, 364	Environmental
365, 366	Environmental

367, 368	Environmental
369, 370	Environmental
37, 38	Environmental
371, 372	Environmental
373, 374	Environmental
375, 376	Artificial
377, 378	Artificial
39, 40	Environmental
41, 42	Environmental
43, 44	Environmental
45, 46	Environmental
47, 48	Environmental
49, 50	Environmental
5, 6	Environmental
51, 52	Environmental
53, 54	Bacteria
55, 56	Environmental
57, 58	Environmental
59, 60	Environmental
61, 62	Environmental
63, 64	Environmental
65, 66	Environmental
67, 68	Environmental
69, 70	Environmental
7, 8	Environmental
71, 72	Environmental
73, 74	Environmental
75, 76	Environmental
77, 78	Environmental
79, 80	Environmental
81, 82	Environmental
83, 84	Environmental
85, 86	Bacteria
87, 88	Environmental
89, 90	Bacteria
9, 10	Environmental
91, 92	Environmental
93, 94	Environmental
95, 96	Environmental
97, 98	Environmental
99, 100	Environmental

In one aspect, the invention also provides xylanase-encoding nucleic acids with a common novelty in that they are derived from an environmental source, or a bacterial source, or an archaeal source.

In practicing the methods of the invention, homologous genes can be modified by manipulating a template nucleic acid, as described herein. The invention can be practiced

in conjunction with any method or protocol or device known in the art, which are well described in the scientific and patent literature.

One aspect of the invention is an isolated nucleic acid comprising one of the sequences of Group A nucleic acid sequences and sequences substantially identical thereto, the sequences complementary thereto, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of a Group A nucleic acid sequence (or the sequences complementary thereto). The isolated, nucleic acids may comprise DNA, including cDNA, genomic DNA and synthetic DNA. The DNA may be double-stranded or single-stranded and if single stranded may be the coding strand or non-coding (anti-sense) strand. Alternatively, the isolated nucleic acids may comprise RNA.

As discussed in more detail below, the isolated nucleic acids of one of the Group A nucleic acid sequences and sequences substantially identical thereto, may be used to prepare one of the polypeptides of a Group B amino acid sequence and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of one of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto.

Accordingly, another aspect of the invention is an isolated nucleic acid which encodes one of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of one of the polypeptides of the Group B amino acid sequences. The coding sequences of these nucleic acids may be identical to one of the coding sequences of one of the nucleic acids of Group A nucleic acid sequences, or a fragment thereof or may be different coding sequences which encode one of the polypeptides of Group B amino acid sequences, sequences substantially identical thereto and fragments having at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of one of the polypeptides of Group B amino acid sequences, as a result of the redundancy or degeneracy of the genetic code. The genetic code is well known to those of skill in the art and can be obtained, for example, on page 214 of B. Lewin, Genes VI, Oxford University Press, 1997.

The isolated nucleic acid which encodes one of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, may include, but is not limited to: only the coding sequence of one of Group A nucleic acid sequences and sequences substantially identical thereto and additional coding sequences, such as leader sequences or

proprotein sequences and non-coding sequences, such as introns or non-coding sequences 5' and/or 3' of the coding sequence. Thus, as used herein, the term "polynucleotide encoding a polypeptide" encompasses a polynucleotide which includes only the coding sequence for the polypeptide as well as a polynucleotide which includes additional coding and/or non-coding sequence.

Alternatively, the nucleic acid sequences of Group A nucleic acid sequences and sequences substantially identical thereto, may be mutagenized using conventional techniques, such as site directed mutagenesis, or other techniques familiar to those skilled in the art, to introduce silent changes into the polynucleotides of Group A nucleic acid sequences and sequences substantially identical thereto. As used herein, "silent changes" include, for example, changes which do not alter the amino acid sequence encoded by the polynucleotide. Such changes may be desirable in order to increase the level of the polypeptide produced by host cells containing a vector encoding the polypeptide by introducing codons or codon pairs which occur frequently in the host organism.

The invention also relates to polynucleotides which have nucleotide changes which result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptides of Group B amino acid sequences and sequences substantially identical thereto. Such nucleotide changes may be introduced using techniques such as site directed mutagenesis, random chemical mutagenesis, exonuclease III deletion and other recombinant DNA techniques. Alternatively, such nucleotide changes may be naturally occurring allelic variants which are isolated by identifying nucleic acids which specifically hybridize to probes comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of Group A nucleic acid sequences and sequences substantially identical thereto (or the sequences complementary thereto) under conditions of high, moderate, or low stringency as provided herein.

General Techniques

The nucleic acids used to practice this invention, whether RNA, iRNA, antisense nucleic acid, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed/ generated recombinantly. Recombinant polypeptides (e.g., xylanases) generated from these nucleic acids can be individually isolated or cloned and tested for a desired activity. Any recombinant expression system can be used, including bacterial, mammalian, yeast, insect or plant cell expression systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, e.g., Adams (1983) J. Am. Chem. Soc. 105:661; Belousov (1997) Nucleic Acids Res. 25:3440-3444; Frenkel (1995) Free Radic. Biol. Med. 19:373-380; Blommers (1994) Biochemistry 33:7886-7896; Narang (1979) Meth. Enzymol. 68:90; Brown (1979) Meth. Enzymol. 68:109; Beaucage (1981) Tetra. Lett. 22:1859; U.S. Patent No. 4,458,066.

Techniques for the manipulation of nucleic acids, such as, e.g., subcloning, labeling probes (e.g., random-primer labeling using Klenow polymerase, nick translation, amplification), sequencing, hybridization and the like are well described in the scientific and patent literature, see, e.g., Sambrook, ed., MOLECULAR CLONING: A LABORATORY MANUAL (2ND ED.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989); CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); LABORATORY TECHNIQUES IN BIOCHEMISTRY AND MOLECULAR BIOLOGY: HYBRIDIZATION WITH NUCLEIC ACID PROBES, Part I. Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Another useful means of obtaining and manipulating nucleic acids used to practice the methods of the invention is to clone from genomic samples, and, if desired, screen and re-clone inserts isolated or amplified from, e.g., genomic clones or cDNA clones. Sources of nucleic acid used in the methods of the invention include genomic or cDNA libraries contained in, e.g., mammalian artificial chromosomes (MACs), see, e.g., U.S. Patent Nos. 5,721,118; 6,025,155; human artificial chromosomes, see, e.g., Rosenfeld (1997) Nat. Genet. 15:333-335; yeast artificial chromosomes (YAC); bacterial artificial chromosomes (BAC); P1 artificial chromosomes, see, e.g., Woon (1998) Genomics 50:306-316; P1-derived vectors (PACs), see, e.g., Kern (1997) Biotechniques 23:120-124; cosmids, recombinant viruses, phages or plasmids.

In one aspect, a nucleic acid encoding a polypeptide of the invention is assembled in appropriate phase with a leader sequence capable of directing secretion of the translated polypeptide or fragment thereof.

The invention provides fusion proteins and nucleic acids encoding them. A polypeptide of the invention can be fused to a heterologous peptide or polypeptide, such as N-terminal identification peptides which impart desired characteristics, such as increased stability or simplified purification. Peptides and polypeptides of the invention can also be synthesized and expressed as fusion proteins with one or more additional domains linked thereto for, e.g., producing a more immunogenic peptide, to more readily isolate a

recombinantly synthesized peptide, to identify and isolate antibodies and antibody-expressing B cells, and the like. Detection and purification facilitating domains include, e.g., metal chelating peptides such as polyhistidine tracts and histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA). The inclusion of a cleavable linker sequences such as Factor Xa or enterokinase (Invitrogen, San Diego CA) between a purification domain and the motif-comprising peptide or polypeptide to facilitate purification. For example, an expression vector can include an epitope-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin and an enterokinase cleavage site (see e.g., Williams (1995) Biochemistry 34:1787-1797; Dobeli (1998) Protein Expr. Purif. 12:404-414). The histidine residues facilitate detection and purification while the enterokinase cleavage site provides a means for purifying the epitope from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature, see e.g., Kroll (1993) DNA Cell. Biol., 12:441-53.

Transcriptional and translational control sequences

The invention provides nucleic acid (e.g., DNA) sequences of the invention operatively linked to expression (e.g., transcriptional or translational) control sequence(s), e.g., promoters or enhancers, to direct or modulate RNA synthesis/ expression. The expression control sequence can be in an expression vector. Exemplary bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, PL and trp. Exemplary eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein I.

Promoters suitable for expressing a polypeptide in bacteria include the *E. coli* lac or trp promoters, the lacI promoter, the lacZ promoter, the T3 promoter, the T7 promoter, the gpt promoter, the lambda PR promoter, the lambda PL promoter, promoters from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), and the acid phosphatase promoter. Eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, heat shock promoters, the early and late SV40 promoter, LTRs from retroviruses, and the mouse metallothionein-I promoter. Other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses may also be used. Promoters suitable for expressing the polypeptide or fragment thereof in bacteria

include the *E. coli lac* or *trp* promoters, the *lacI* promoter, the *lacZ* promoter, the *T3* promoter, the *T7* promoter, the *gpt* promoter, the *lambda* P_R promoter, the *lambda* P_L promoter, promoters from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK) and the acid phosphatase promoter. Fungal promoters include the α factor promoter. Eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, heat shock promoters, the early and late SV40 promoter, LTRs from retroviruses and the mouse metallothionein-I promoter. Other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses may also be used.

Tissue-Specific Plant Promoters

The invention provides expression cassettes that can be expressed in a tissue-specific manner, e.g., that can express a xylanase of the invention in a tissue-specific manner. The invention also provides plants or seeds that express a xylanase of the invention in a tissue-specific manner. The tissue-specificity can be seed specific, stem specific, leaf specific, root specific, fruit specific and the like.

In one aspect, a constitutive promoter such as the CaMV 35S promoter can be used for expression in specific parts of the plant or seed or throughout the plant. For example, for overexpression, a plant promoter fragment can be employed which will direct expression of a nucleic acid in some or all tissues of a plant, e.g., a regenerated plant. Such promoters are referred to herein as "constitutive" promoters and are active under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35S transcription initiation region, the 1'- or 2'- promoter derived from T-DNA of *Agrobacterium tumefaciens*, and other transcription initiation regions from various plant genes known to those of skill. Such genes include, e.g., *ACT11* from *Arabidopsis* (Huang (1996) *Plant Mol. Biol.* 33:125-139); *Cat3* from *Arabidopsis* (GenBank No. U43147, Zhong (1996) *Mol. Gen. Genet.* 251:196-203); the gene encoding stearoyl-acyl carrier protein desaturase from *Brassica napus* (Genbank No. X74782, Solocombe (1994) *Plant Physiol.* 104:1167-1176); *GPc1* from maize (GenBank No. X15596; Martinez (1989) *J. Mol. Biol* 208:551-565); the *Gpc2* from maize (GenBank No. U45855, Manjunath (1997) *Plant Mol. Biol.* 33:97-112); plant promoters described in U.S. Patent Nos. 4,962,028; 5,633,440.

The invention uses tissue-specific or constitutive promoters derived from viruses which can include, *e.g.*, the tobamovirus subgenomic promoter (Kumagai (1995)

Proc. Natl. Acad. Sci. USA 92:1679-1683; the rice tungro bacilliform virus (RTBV), which replicates only in phloem cells in infected rice plants, with its promoter which drives strong phloem-specific reporter gene expression; the cassava vein mosaic virus (CVMV) promoter, with highest activity in vascular elements, in leaf mesophyll cells, and in root tips (Verdaguer (1996) Plant Mol. Biol. 31:1129-1139).

Alternatively, the plant promoter may direct expression of xylanase-expressing nucleic acid in a specific tissue, organ or cell type (*i.e.* tissue-specific promoters) or may be otherwise under more precise environmental or developmental control or under the control of an inducible promoter. Examples of environmental conditions that may affect transcription include anaerobic conditions, elevated temperature, the presence of light, or sprayed with chemicals/hormones. For example, the invention incorporates the drought-inducible promoter of maize (Busk (1997) supra); the cold, drought, and high salt inducible promoter from potato (Kirch (1997) Plant Mol. Biol. 33:897 909).

Tissue-specific promoters can promote transcription only within a certain time frame of developmental stage within that tissue. See, e.g., Blazquez (1998) Plant Cell 10:791-800, characterizing the *Arabidopsis* LEAFY gene promoter. See also Cardon (1997) *Plant J* 12:367-77, describing the transcription factor SPL3, which recognizes a conserved sequence motif in the promoter region of the *A. thaliana* floral meristem identity gene AP1; and Mandel (1995) Plant Molecular Biology, Vol. 29, pp 995-1004, describing the meristem promoter eIF4. Tissue specific promoters which are active throughout the life cycle of a particular tissue can be used. In one aspect, the nucleic acids of the invention are operably linked to a promoter active primarily only in cotton fiber cells. In one aspect, the nucleic acids of the invention are operably linked to a promoter active primarily during the stages of cotton fiber cell elongation, e.g., as described by Rinehart (1996) supra. The nucleic acids can be operably linked to the Fbl2A gene promoter to be preferentially expressed in cotton fiber cells (Ibid) . See also, John (1997) Proc. Natl. Acad. Sci. USA 89:5769-5773; John, et al., U.S. Patent Nos. 5,608,148 and 5,602,321, describing cotton fiber-specific promoters and methods for the construction of transgenic cotton plants. Root-specific promoters may also be used to express the nucleic acids of the invention. Examples of root-specific promoters include the promoter from the alcohol dehydrogenase gene (DeLisle (1990) Int. Rev. Cytol. 123:39-60). Other promoters that can be used to express the nucleic acids of the invention include, e.g., ovule-specific, embryo-specific, endosperm-specific, integument-specific, seed coat-specific promoters, or some combination thereof; a leaf-specific promoter (see, e.g., Busk (1997) Plant J. 11:1285 1295, describing a leaf-specific promoter in maize); the ORF13

promoter from *Agrobacterium rhizogenes* (which exhibits high activity in roots, see, e.g., Hansen (1997) supra); a maize pollen specific promoter (see, e.g., Guerrero (1990) Mol. Gen. Genet. 224:161 168); a tomato promoter active during fruit ripening, senescence and abscission of leaves and, to a lesser extent, of flowers can be used (see, e.g., Blume (1997) Plant J. 12:731 746); a pistil-specific promoter from the potato SK2 gene (see, e.g., Ficker (1997) Plant Mol. Biol. 35:425 431); the Blec4 gene from pea, which is active in epidermal tissue of vegetative and floral shoot apices of transgenic alfalfa making it a useful tool to target the expression of foreign genes to the epidermal layer of actively growing shoots or fibers; the ovule-specific BEL1 gene (see, e.g., Reiser (1995) Cell 83:735-742, GenBank No. U39944); and/or, the promoter in Klee, U.S. Patent No. 5,589,583, describing a plant promoter region is capable of conferring high levels of transcription in meristematic tissue and/or rapidly dividing cells.

Alternatively, plant promoters which are inducible upon exposure to plant hormones, such as auxins, are used to express the nucleic acids of the invention. For example, the invention can use the auxin-response elements E1 promoter fragment (AuxREs) in the soybean (*Glycine max* L.) (Liu (1997) Plant Physiol. 115:397-407); the auxin-responsive *Arabidopsis* GST6 promoter (also responsive to salicylic acid and hydrogen peroxide) (Chen (1996) Plant J. 10: 955-966); the auxin-inducible parC promoter from tobacco (Sakai (1996) 37:906-913); a plant biotin response element (Streit (1997) Mol. Plant Microbe Interact. 10:933-937); and, the promoter responsive to the stress hormone abscisic acid (Sheen (1996) Science 274:1900-1902).

The nucleic acids of the invention can also be operably linked to plant promoters which are inducible upon exposure to chemicals reagents which can be applied to the plant, such as herbicides or antibiotics. For example, the maize In2-2 promoter, activated by benzenesulfonamide herbicide safeners, can be used (De Veylder (1997) Plant Cell Physiol. 38:568-577); application of different herbicide safeners induces distinct gene expression patterns, including expression in the root, hydathodes, and the shoot apical meristem. Coding sequence can be under the control of, *e.g.*, a tetracycline-inducible promoter, *e.g.*, as described with transgenic tobacco plants containing the *Avena sativa* L. (oat) arginine decarboxylase gene (Masgrau (1997) Plant J. 11:465-473); or, a salicylic acid-responsive element (Stange (1997) Plant J. 11:1315-1324). Using chemically- (*e.g.*, hormone- or pesticide-) induced promoters, *i.e.*, promoter responsive to a chemical which can be applied to the transgenic plant in the field, expression of a polypeptide of the invention can be induced at a particular stage of development of the plant. Thus, the invention also

provides for transgenic plants containing an inducible gene encoding for polypeptides of the invention whose host range is limited to target plant species, such as corn, rice, barley, wheat, potato or other crops, inducible at any stage of development of the crop.

One of skill will recognize that a tissue-specific plant promoter may drive expression of operably linked sequences in tissues other than the target tissue. Thus, a tissue-specific promoter is one that drives expression preferentially in the target tissue or cell type, but may also lead to some expression in other tissues as well.

The nucleic acids of the invention can also be operably linked to plant promoters which are inducible upon exposure to chemicals reagents. These reagents include, e.g., herbicides, synthetic auxins, or antibiotics which can be applied, e.g., sprayed, onto transgenic plants. Inducible expression of the xylanase-producing nucleic acids of the invention will allow the grower to select plants with the optimal xylanase expression and/or activity. The development of plant parts can thus controlled. In this way the invention provides the means to facilitate the harvesting of plants and plant parts. For example, in various embodiments, the maize In2-2 promoter, activated by benzenesulfonamide herbicide safeners, is used (De Veylder (1997) Plant Cell Physiol. 38:568-577); application of different herbicide safeners induces distinct gene expression patterns, including expression in the root, hydathodes, and the shoot apical meristem. Coding sequences of the invention are also under the control of a tetracycline-inducible promoter, e.g., as described with transgenic tobacco plants containing the *Avena sativa* L. (oat) arginine decarboxylase gene (Masgrau (1997) Plant J. 11:465-473); or, a salicylic acid-responsive element (Stange (1997) Plant J. 11:1315-1324).

In some aspects, proper polypeptide expression may require polyadenylation region at the 3'-end of the coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant (or animal or other) genes, or from genes in the *Agrobacterial* T-DNA.

Expression vectors and cloning vehicles

The invention provides expression vectors and cloning vehicles comprising nucleic acids of the invention, e.g., sequences encoding the xylanases of the invention. Expression vectors and cloning vehicles of the invention can comprise viral particles, baculovirus, phage, plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, viral DNA (e.g., vaccinia, adenovirus, foul pox virus, pseudorabies and derivatives of SV40), P1-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other

vectors specific for specific hosts of interest (such as bacillus, Aspergillus and yeast). Vectors of the invention can include chromosomal, non-chromosomal and synthetic DNA sequences. Large numbers of suitable vectors are known to those of skill in the art, and are commercially available. Exemplary vectors are include: bacterial: pQE vectors (Qiagen), pBluescript plasmids, pNH vectors, (lambda-ZAP vectors (Stratagene); ptrc99a, pKK223-3, pDR540, pRIT2T (Pharmacia); Eukaryotic: pXT1, pSG5 (Stratagene), pSVK3, pBPV, pMSG, pSVLSV40 (Pharmacia). However, any other plasmid or other vector may be used so long as they are replicable and viable in the host. Low copy number or high copy number vectors may be employed with the present invention.

The expression vector can comprise a promoter, a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. Mammalian expression vectors can comprise an origin of replication, any necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking non-transcribed sequences. In some aspects, DNA sequences derived from the SV40 splice and polyadenylation sites may be used to provide the required non-transcribed genetic elements.

In one aspect, the expression vectors contain one or more selectable marker genes to permit selection of host cells containing the vector. Such selectable markers include genes encoding dihydrofolate reductase or genes conferring neomycin resistance for eukaryotic cell culture, genes conferring tetracycline or ampicillin resistance in *E. coli*, and the *S. cerevisiae* TRP1 gene. Promoter regions can be selected from any desired gene using chloramphenicol transferase (CAT) vectors or other vectors with selectable markers.

Vectors for expressing the polypeptide or fragment thereof in eukaryotic cells can also contain enhancers to increase expression levels. Enhancers are cis-acting elements of DNA, usually from about 10 to about 300 bp in length that act on a promoter to increase its transcription. Examples include the SV40 enhancer on the late side of the replication origin bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and the adenovirus enhancers.

A nucleic acid sequence can be inserted into a vector by a variety of procedures. In general, the sequence is ligated to the desired position in the vector following digestion of the insert and the vector with appropriate restriction endonucleases. Alternatively, blunt ends in both the insert and the vector may be ligated. A variety of cloning techniques are known in the art, e.g., as described in Ausubel and Sambrook. Such procedures and others are deemed to be within the scope of those skilled in the art.

The vector can be in the form of a plasmid, a viral particle, or a phage. Other vectors include chromosomal, non-chromosomal and synthetic DNA sequences, derivatives of SV40; bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. A variety of cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by, e.g., Sambrook.

Particular bacterial vectors which can be used include the commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017), pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden), GEM1 (Promega Biotec, Madison, WI, USA) pQE70, pQE60, pQE-9 (Qiagen), pD10, psiX174 pBluescript II KS, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene), ptrc99a, pKK223-3, pKK233-3, DR540, pRIT5 (Pharmacia), pKK232-8 and pCM7. Particular eukaryotic vectors include pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). However, any other vector may be used as long as it is replicable and viable in the host cell.

The nucleic acids of the invention can be expressed in expression cassettes, vectors or viruses and transiently or stably expressed in plant cells and seeds. One exemplary transient expression system uses episomal expression systems, e.g., cauliflower mosaic virus (CaMV) viral RNA generated in the nucleus by transcription of an episomal mini-chromosome containing supercoiled DNA, see, e.g., Covey (1990) Proc. Natl. Acad. Sci. USA 87:1633-1637. Alternatively, coding sequences, i.e., all or sub-fragments of sequences of the invention can be inserted into a plant host cell genome becoming an integral part of the host chromosomal DNA. Sense or antisense transcripts can be expressed in this manner. A vector comprising the sequences (e.g., promoters or coding regions) from nucleic acids of the invention can comprise a marker gene that confers a selectable phenotype on a plant cell or a seed. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

Expression vectors capable of expressing nucleic acids and proteins in plants are well known in the art, and can include, *e.g.*, vectors from *Agrobacterium* spp., potato virus X (see, *e.g.*, Angell (1997) EMBO J. 16:3675-3684), tobacco mosaic virus (see, *e.g.*, Casper (1996) Gene 173:69-73), tomato bushy stunt virus (see, *e.g.*, Hillman (1989) Virology 169:42-50), tobacco etch virus (see, *e.g.*, Dolja (1997) Virology 234:243-252), bean golden mosaic virus (see, *e.g.*, Morinaga (1993) Microbiol Immunol. 37:471-476), cauliflower mosaic virus (see, *e.g.*, Cecchini (1997) Mol. Plant Microbe Interact. 10:1094-1101), maize

Ac/Ds transposable element (see, *e.g.*, Rubin (1997) Mol. Cell. Biol. 17:6294-6302; Kunze (1996) Curr. Top. Microbiol. Immunol. 204:161-194), and the maize suppressor-mutator (Spm) transposable element (see, *e.g.*, Schlappi (1996) Plant Mol. Biol. 32:717-725); and derivatives thereof.

In one aspect, the expression vector can have two replication systems to allow it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector can contain at least one sequence homologous to the host cell genome. It can contain two homologous sequences which flank the expression construct. The integrating vector can be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

Expression vectors of the invention may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed, e.g., genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers can also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct RNA synthesis. Particular named bacterial promoters include *lacI*, *lacZ*, *T3*, *T7*, *gpt*, *lambda* P_R, P_L and *trp*. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. Promoter regions can be selected from any desired gene using chloramphenicol transferase (CAT) vectors or other vectors with selectable markers. In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

Mammalian expression vectors may also comprise an origin of replication, any necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences and 5' flanking nontranscribed sequences. In some

aspects, DNA sequences derived from the SV40 splice and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Vectors for expressing the polypeptide or fragment thereof in eukaryotic cells may also contain enhancers to increase expression levels. Enhancers are cis-acting elements of DNA, usually from about 10 to about 300 bp in length that act on a promoter to increase its transcription. Examples include the SV40 enhancer on the late side of the replication origin bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin and the adenovirus enhancers.

In addition, the expression vectors typically contain one or more selectable marker genes to permit selection of host cells containing the vector. Such selectable markers include genes encoding dihydrofolate reductase or genes conferring neomycin resistance for eukaryotic cell culture, genes conferring tetracycline or ampicillin resistance in *E. coli* and the *S. cerevisiae TRP1* gene.

In some aspects, the nucleic acid encoding one of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, or fragments comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof is assembled in appropriate phase with a leader sequence capable of directing secretion of the translated polypeptide or fragment thereof. Optionally, the nucleic acid can encode a fusion polypeptide in which one of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof is fused to heterologous peptides or polypeptides, such as N-terminal identification peptides which impart desired characteristics, such as increased stability or simplified purification.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is ligated to the desired position in the vector following digestion of the insert and the vector with appropriate restriction endonucleases. Alternatively, blunt ends in both the insert and the vector may be ligated. A variety of cloning techniques are disclosed in Ausubel *et al.* Current Protocols in Molecular Biology, John Wiley 503 Sons, Inc. 1997 and Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2nd Ed., Cold Spring Harbor Laboratory Press (1989. Such procedures and others are deemed to be within the scope of those skilled in the art.

The vector may be, for example, in the form of a plasmid, a viral particle, or a phage. Other vectors include chromosomal, nonchromosomal and synthetic DNA sequences, derivatives of SV40; bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors

derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus and pseudorabies. A variety of cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, N.Y., (1989).

Host cells and transformed cells

The invention also provides a transformed cell comprising a nucleic acid sequence of the invention, e.g., a sequence encoding a xylanase of the invention, or a vector of the invention. The host cell may be any of the host cells familiar to those skilled in the art, including prokaryotic cells, eukaryotic cells, such as bacterial cells, fungal cells, yeast cells, mammalian cells, insect cells, or plant cells. Exemplary bacterial cells include *E. coli*, *Streptomyces*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*. Exemplary insect cells include *Drosophila S2* and *Spodoptera Sf9*. Exemplary animal cells include CHO, COS or Bowes melanoma or any mouse or human cell line. The selection of an appropriate host is within the abilities of those skilled in the art. Techniques for transforming a wide variety of higher plant species are well known and described in the technical and scientific literature. See, e.g., Weising (1988) Ann. Rev. Genet. 22:421-477; U.S. Patent No. 5,750,870.

The vector can be introduced into the host cells using any of a variety of techniques, including transformation, transfection, transduction, viral infection, gene guns, or Ti-mediated gene transfer. Particular methods include calcium phosphate transfection, DEAE-Dextran mediated transfection, lipofection, or electroporation (Davis, L., Dibner, M., Battey, I., Basic Methods in Molecular Biology, (1986)).

In one aspect, the nucleic acids or vectors of the invention are introduced into the cells for screening, thus, the nucleic acids enter the cells in a manner suitable for subsequent expression of the nucleic acid. The method of introduction is largely dictated by the targeted cell type. Exemplary methods include $CaPO_4$ precipitation, liposome fusion, lipofection (e.g., LIPOFECTIN™), electroporation, viral infection, etc. The candidate nucleic acids may stably integrate into the genome of the host cell (for example, with retroviral introduction) or may exist either transiently or stably in the cytoplasm (i.e. through the use of traditional plasmids, utilizing standard regulatory sequences, selection markers, etc.). As many pharmaceutically important screens require human or model mammalian cell targets, retroviral vectors capable of transfecting such targets are can be used.

Where appropriate, the engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (e.g., temperature shift or chemical induction) and the cells may be cultured for an additional period to allow them to produce the desired polypeptide or fragment thereof.

Cells can be harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract is retained for further purification. Microbial cells employed for expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such methods are well known to those skilled in the art. The expressed polypeptide or fragment thereof can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. If desired, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Depending upon the host employed in a recombinant production procedure, the polypeptides produced by host cells containing the vector may be glycosylated or may be non-glycosylated. Polypeptides of the invention may or may not also include an initial methionine amino acid residue.

Cell-free translation systems can also be employed to produce a polypeptide of the invention. Cell-free translation systems can use mRNAs transcribed from a DNA construct comprising a promoter operably linked to a nucleic acid encoding the polypeptide or fragment thereof. In some aspects, the DNA construct may be linearized prior to conducting an in vitro transcription reaction. The transcribed mRNA is then incubated with an appropriate cell-free translation extract, such as a rabbit reticulocyte extract, to produce the desired polypeptide or fragment thereof.

The expression vectors can contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate

reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

Host cells containing the polynucleotides of interest, e.g., nucleic acids of the invention, can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression and will be apparent to the ordinarily skilled artisan. The clones which are identified as having the specified enzyme activity may then be sequenced to identify the polynucleotide sequence encoding an enzyme having the enhanced activity.

The invention provides a method for overexpressing a recombinant xylanase in a cell comprising expressing a vector comprising a nucleic acid of the invention, e.g., a nucleic acid comprising a nucleic acid sequence with at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to a sequence of Group A nucleic acid sequences over a region of at least about 100 residues, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection, or, a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence as set forth in Group A nucleic acid sequences, or a subsequence thereof. The overexpression can be effected by any means, e.g., use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

The nucleic acids of the invention can be expressed, or overexpressed, in any in vitro or in vivo expression system. Any cell culture systems can be employed to express, or over-express, recombinant protein, including bacterial, insect, yeast, fungal or mammalian cultures. Over-expression can be effected by appropriate choice of promoters, enhancers, vectors (e.g., use of replicon vectors, dicistronic vectors (see, e.g., Gurtu (1996) Biochem. Biophys. Res. Commun. 229:295-8), media, culture systems and the like. In one aspect, gene amplification using selection markers, e.g., glutamine synthetase (see, e.g., Sanders (1987) Dev. Biol. Stand. 66:55-63), in cell systems are used to overexpress the polypeptides of the invention.

Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes EP 0659215 (W0 9403612 A1) (Nevalainen *et al.*); Lapidot, A., Mechaly, A., Shoham, Y., "Overexpression and single-step purification of a thermostable

xylanase from *Bacillus stearothermophilus* T-6," J. Biotechnol. Nov 51:259-64 (1996); Lüthi, E., Jasmat, N.B., Bergquist, P.L., "Xylanase from the extremely thermophilic bacterium *Caldocellum saccharolyticum*: overexpression of the gene in *Escherichia coli* and characterization of the gene product," Appl. Environ. Microbiol. Sep 56:2677-83 (1990); and Sung, W.L., Luk, C.K., Zahab, D.M., Wakarchuk, W., "Overexpression of the *Bacillus subtilis* and *circulans* xylanases in *Escherichia coli*," Protein Expr. Purif. Jun 4:200-6 (1993), although these references do not teach the inventive enzymes of the instant application.

The host cell may be any of the host cells familiar to those skilled in the art, including prokaryotic cells, eukaryotic cells, mammalian cells, insect cells, or plant cells. As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Streptomyces*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera Pseudomonas, Streptomyces and Staphylococcus, fungal cells, such as yeast, insect cells such as *Drosophila S2* and *Spodoptera Sf9*, animal cells such as CHO, COS or Bowes melanoma and adenoviruses. The selection of an appropriate host is within the abilities of those skilled in the art.

The vector may be introduced into the host cells using any of a variety of techniques, including transformation, transfection, transduction, viral infection, gene guns, or Ti-mediated gene transfer. Particular methods include calcium phosphate transfection, DEAE-Dextran mediated transfection, lipofection, or electroporation (Davis, L., Dibner, M., Battey, I., Basic Methods in Molecular Biology, (1986)).

Where appropriate, the engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (*e.g.*, temperature shift or chemical induction) and the cells may be cultured for an additional period to allow them to produce the desired polypeptide or fragment thereof.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means and the resulting crude extract is retained for further purification. Microbial cells employed for expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such methods are well known to those skilled in the art. The expressed polypeptide or fragment thereof can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation

exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. If desired, high performance liquid chromatography (HPLC) can be employed for final purification steps.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts (described by Gluzman, Cell, 23:175, 1981) and other cell lines capable of expressing proteins from a compatible vector, such as the C127, 3T3, CHO, HeLa and BHK cell lines.

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Depending upon the host employed in a recombinant production procedure, the polypeptides produced by host cells containing the vector may be glycosylated or may be non-glycosylated. Polypeptides of the invention may or may not also include an initial methionine amino acid residue.

Alternatively, the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof can be synthetically produced by conventional peptide synthesizers. In other aspects, fragments or portions of the polypeptides may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, the fragments may be employed as intermediates for producing the full-length polypeptides.

Cell-free translation systems can also be employed to produce one of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof using mRNAs transcribed from a DNA construct comprising a promoter operably linked to a nucleic acid encoding the polypeptide or fragment thereof. In some aspects, the DNA construct may be linearized prior to conducting an *in vitro* transcription reaction. The transcribed mRNA is then incubated with an appropriate cell-free translation extract, such as a rabbit reticulocyte extract, to produce the desired polypeptide or fragment thereof.

Amplification of Nucleic Acids

In practicing the invention, nucleic acids of the invention and nucleic acids encoding the xylanases of the invention, or modified nucleic acids of the invention, can be reproduced by amplification. Amplification can also be used to clone or modify the nucleic acids of the invention. Thus, the invention provides amplification primer sequence pairs for amplifying nucleic acids of the invention. One of skill in the art can design amplification primer sequence pairs for any part of or the full length of these sequences.

In one aspect, the invention provides a nucleic acid amplified by a primer pair of the invention, e.g., a primer pair as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 residues of a nucleic acid of the invention, and about the first (the 5') 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 residues of the complementary strand.

The invention provides an amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide having a xylanase activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence of the invention, or fragments or subsequences thereof. One or each member of the amplification primer sequence pair can comprise an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence, or about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 consecutive bases of the sequence. The invention provides amplification primer pairs, wherein the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 residues of a nucleic acid of the invention, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 residues of the complementary strand of the first member. The invention provides xylanases generated by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. The invention provides methods of making a xylanase by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. In one aspect, the amplification primer pair amplifies a nucleic acid from a library, e.g., a gene library, such as an environmental library.

Amplification reactions can also be used to quantify the amount of nucleic acid in a sample (such as the amount of message in a cell sample), label the nucleic acid (e.g., to apply it to an array or a blot), detect the nucleic acid, or quantify the amount of a specific nucleic acid in a sample. In one aspect of the invention, message isolated from a cell or a cDNA library are amplified.

The skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (see, e.g., PCR PROTOCOLS, A GUIDE TO METHODS AND APPLICATIONS, ed. Innis, Academic Press, N.Y. (1990) and PCR STRATEGIES (1995), ed. Innis, Academic Press, Inc., N.Y., ligase chain reaction (LCR) (see, e.g., Wu (1989) Genomics 4:560; Landegren (1988) Science 241:1077; Barringer (1990) Gene 89:117); transcription amplification (see, e.g., Kwoh (1989) Proc. Natl. Acad. Sci. USA 86:1173); and, self-sustained sequence replication (see, e.g., Guatelli (1990) Proc. Natl. Acad. Sci. USA 87:1874); Q Beta replicase amplification (see, e.g., Smith (1997) J. Clin. Microbiol. 35:1477-1491), automated Q-beta replicase amplification assay (see, e.g., Burg (1996) Mol. Cell. Probes 10:257-271) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger (1987) Methods Enzymol. 152:307-316; Sambrook; Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan (1995) Biotechnology 13:563-564.

Determining the degree of sequence identity

The invention provides nucleic acids comprising sequences having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary nucleic acid of the invention (e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID

NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379) over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550 or more, residues. The invention provides polypeptides comprising sequences having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary polypeptide of the invention. The extent of sequence identity (homology) may be determined using any computer program and

associated parameters, including those described herein, such as BLAST 2.2.2. or FASTA version 3.0t78, with the default parameters.

The nucleic acid sequences are also referred to as "Group A" nucleic acid sequences, which include sequences substantially identical thereto, as well as sequences homologous to Group A nucleic acid sequences and fragments thereof and sequences complementary to all of the preceding sequences. Nucleic acid sequences of the invention can comprise at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of an exemplary sequence of the invention (e.g., Group A nucleic acid sequences) and sequences substantially identical thereto. Homologous sequences and fragments of Group A nucleic acid sequences and sequences substantially identical thereto, refer to a sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, or 50% homology to these sequences. Homology may be determined using any of the computer programs and parameters described herein, including FASTA version 3.0t78 with the default parameters. Homologous sequences also include RNA sequences in which uridines replace the thymines in the nucleic acid sequences as set forth in the Group A nucleic acid sequences. The homologous sequences may be obtained using any of the procedures described herein or may result from the correction of a sequencing error. It will be appreciated that the nucleic acid sequences as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, can be represented in the traditional single character format (See the inside back cover of Stryer, Lubert. Biochemistry, 3rd Ed., W. H Freeman & Co., New York.) or in any other format which records the identity of the nucleotides in a sequence.

Various sequence comparison programs identified elsewhere in this patent specification are particularly contemplated for use in this aspect of the invention. Protein and/or nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA and CLUSTALW (Pearson and Lipman, Proc. Natl. Acad. Sci. USA 85(8):2444-2448, 1988; Altschul *et al.*, J. Mol. Biol. 215(3):403-410, 1990; Thompson *et al.*, Nucleic Acids Res. 22(2):4673-4680, 1994; Higgins *et al.*, Methods Enzymol. 266:383-402, 1996; Altschul *et al.*, J. Mol. Biol. 215(3):403-410, 1990; Altschul *et al.*, Nature Genetics 3:266-272, 1993).

Homology or identity is often measured using sequence analysis software (*e.g.*, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705). Such software matches

similar sequences by assigning degrees of homology to various deletions, substitutions and other modifications. The terms "homology" and "identity" in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same when compared and aligned for maximum correspondence over a comparison window or designated region as measured using any number of sequence comparison algorithms or by manual alignment and visual inspection.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequence for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol 48:443, 1970, by the search for similarity method of person & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection. Other algorithms for determining homology or identity include, for example, in addition to a BLAST program (Basic Local Alignment Search Tool at the National Center for Biological Information), ALIGN, AMAS (Analysis of Multiply Aligned Sequences), AMPS (Protein Multiple Sequence Alignment), ASSET (Aligned Segment Statistical Evaluation Tool), BANDS, BESTSCOR, BIOSCAN (Biological Sequence Comparative Analysis Node), BLIMPS (BLocks IMProved Searcher), FASTA, Intervals & Points, BMB, CLUSTAL V, CLUSTAL W, CONSENSUS, LCONSENSUS, WCONSENSUS, Smith-Waterman algorithm, DARWIN, Las Vegas algorithm, FNAT (Forced Nucleotide Alignment Tool), Framealign, Framesearch,

DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis Package), GAP (Global Alignment Program), GENAL, GIBBS, GenQuest, ISSC (Sensitive Sequence Comparison), LALIGN (Local Sequence Alignment), LCP (Local Content Program), MACAW (Multiple Alignment Construction & Analysis Workbench), MAP (Multiple Alignment Program), MBLKP, MBLKN, PIMA (Pattern-Induced Multi-sequence Alignment), SAGA (Sequence Alignment by Genetic Algorithm) and WHAT-IF. Such alignment programs can also be used to screen genome databases to identify polynucleotide sequences having substantially identical sequences. A number of genome databases are available, for example, a substantial portion of the human genome is available as part of the Human Genome Sequencing Project (J. Roach, http://weber.u.Washington.edu/~roach/human_ genome_ progress 2.html) (Gibbs, 1995). At least twenty-one other genomes have already been sequenced, including, for example, *M. genitalium* (Fraser *et al.*, 1995), M. jannaschii (Bult *et al.*, 1996), *H. influenzae* (Fleischmann *et al.*, 1995), *E. coli* (Blattner *et al.*, 1997) and yeast (*S. cerevisiae*) (Mewes *et al.*, 1997) and *D. melanogaster* (Adams *et al.*, 2000). Significant progress has also been made in sequencing the genomes of model organism, such as mouse, *C. elegans* and *Arabadopsis sp*. Several databases containing genomic information annotated with some functional information are maintained by different organization and are accessible via the internet

One example of a useful algorithm is BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, Nuc. Acids Res. 25:3389-3402, 1977 and Altschul *et al.*, J. Mol. Biol. 215:403-410, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al., supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X

determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3 and expectations (E) of 10 and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N= -4 and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, *e.g.*, Karlin & Altschul, Proc. Natl. Acad. Sci. USA 90:5873, 1993). One measure of similarity provided by BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a references sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01 and most preferably less than about 0.001.

In one aspect, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") In particular, five specific BLAST programs are used to perform the following task:

(1) BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;

(2) BLASTN compares a nucleotide query sequence against a nucleotide sequence database;

(3) BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;

(4) TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and

(5) TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet *et al.*, Science 256:1443-1445, 1992; Henikoff and Henikoff, Proteins 17:49-61, 1993). Less preferably, the

PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure,* Washington: National Biomedical Research Foundation). BLAST programs are accessible through the U.S. National Library of Medicine.

The parameters used with the above algorithms may be adapted depending on the sequence length and degree of homology studied. In some aspects, the parameters may be the default parameters used by the algorithms in the absence of instructions from the user.

Computer systems and computer program products

To determine and identify sequence identities, structural homologies, motifs and the like in silico, a nucleic acid or polypeptide sequence of the invention can be stored, recorded, and manipulated on any medium which can be read and accessed by a computer.

Accordingly, the invention provides computers, computer systems, computer readable mediums, computer programs products and the like recorded or stored thereon the nucleic acid and polypeptide sequences of the invention. As used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. A skilled artisan can readily adopt any known methods for recording information on a computer readable medium to generate manufactures comprising one or more of the nucleic acid and/or polypeptide sequences of the invention.

The polypeptides of the invention include the polypeptide sequences of Group B amino acid sequences, the exemplary sequences of the invention, and sequences substantially identical thereto, and fragments of any of the preceding sequences. Substantially identical, or homologous, polypeptide sequences refer to a polypeptide sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary sequence of the invention, e.g., a polypeptide sequences of the Group B amino acid sequences.

Homology may be determined using any of the computer programs and parameters described herein, including FASTA version 3.0t78 with the default parameters or with any modified parameters. The homologous sequences may be obtained using any of the procedures described herein or may result from the correction of a sequencing error. The polypeptide fragments comprise at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150,

200, 250, 300, 350, 400, 450, 500 or more consecutive amino acids of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto. It will be appreciated that the polypeptide codes as set forth in Group B amino acid sequences and sequences substantially identical thereto, can be represented in the traditional single character format or three letter format (See the inside back cover of Stryer, Lubert. Biochemistry, 3rd Ed., W. H Freeman & Co., New York.) or in any other format which relates the identity of the polypeptides in a sequence.

A nucleic acid or polypeptide sequence of the invention can be stored, recorded and manipulated on any medium which can be read and accessed by a computer. As used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. A skilled artisan can readily adopt any of the presently known methods for recording information on a computer readable medium to generate manufactures comprising one or more of the nucleic acid sequences as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, one or more of the polypeptide sequences as set forth in Group B amino acid sequences and sequences substantially identical thereto. Another aspect of the invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, or 20 or more nucleic acid sequences as set forth in Group A nucleic acid sequences and sequences substantially identical thereto.

Another aspect of the invention is a computer readable medium having recorded thereon one or more of the nucleic acid sequences as set forth in Group A nucleic acid sequences and sequences substantially identical thereto. Another aspect of the invention is a computer readable medium having recorded thereon one or more of the polypeptide sequences as set forth in Group B amino acid sequences and sequences substantially identical thereto. Another aspect of the invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, or 20 or more of the sequences as set forth above.

Computer readable media include magnetically readable media, optically readable media, electronically readable media and magnetic/optical media. For example, the computer readable media may be a hard disk, a floppy disk, a magnetic tape, CD-ROM, Digital Versatile Disk (DVD), Random Access Memory (RAM), or Read Only Memory (ROM) as well as other types of other media known to those skilled in the art.

Aspects of the invention include systems (*e.g.*, internet based systems), particularly computer systems which store and manipulate the sequence information described herein. One example of a computer system 100 is illustrated in block diagram form in Figure 1. As used herein, "a computer system" refers to the hardware components, software components

and data storage components used to analyze a nucleotide sequence of a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in the Group B amino acid sequences. The computer system 100 typically includes a processor for processing, accessing and manipulating the sequence data. The processor 105 can be any well-known type of central processing unit, such as, for example, the Pentium III from Intel Corporation, or similar processor from Sun, Motorola, Compaq, AMD or International Business Machines.

Typically the computer system 100 is a general purpose system that comprises the processor 105 and one or more internal data storage components 110 for storing data and one or more data retrieving devices for retrieving the data stored on the data storage components. A skilled artisan can readily appreciate that any one of the currently available computer systems are suitable.

In one particular aspect, the computer system 100 includes a processor 105 connected to a bus which is connected to a main memory 115 (preferably implemented as RAM) and one or more internal data storage devices 110, such as a hard drive and/or other computer readable media having data recorded thereon. In some aspects, the computer system 100 further includes one or more data retrieving device 118 for reading the data stored on the internal data storage devices 110.

The data retrieving device 118 may represent, for example, a floppy disk drive, a compact disk drive, a magnetic tape drive, or a modem capable of connection to a remote data storage system (*e.g.*, via the internet) etc. In some aspects, the internal data storage device 110 is a removable computer readable medium such as a floppy disk, a compact disk, a magnetic tape, etc. containing control logic and/or data recorded thereon. The computer system 100 may advantageously include or be programmed by appropriate software for reading the control logic and/or the data from the data storage component once inserted in the data retrieving device.

The computer system 100 includes a display 120 which is used to display output to a computer user. It should also be noted that the computer system 100 can be linked to other computer systems 125a-c in a network or wide area network to provide centralized access to the computer system 100.

Software for accessing and processing the nucleotide sequences of a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto, (such as search tools, compare tools and modeling tools etc.) may reside in main memory 115 during execution.

In some aspects, the computer system 100 may further comprise a sequence comparison algorithm for comparing a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto, stored on a computer readable medium to a reference nucleotide or polypeptide sequence(s) stored on a computer readable medium. A "sequence comparison algorithm" refers to one or more programs which are implemented (locally or remotely) on the computer system 100 to compare a nucleotide sequence with other nucleotide sequences and/or compounds stored within a data storage means. For example, the sequence comparison algorithm may compare the nucleotide sequences of a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto, stored on a computer readable medium to reference sequences stored on a computer readable medium to identify homologies or structural motifs.

Figure 2 is a flow diagram illustrating one aspect of a process 200 for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database. The database of sequences can be a private database stored within the computer system 100, or a public database such as GENBANK that is available through the Internet.

The process 200 begins at a start state 201 and then moves to a state 202 wherein the new sequence to be compared is stored to a memory in a computer system 100. As discussed above, the memory could be any type of memory, including RAM or an internal storage device.

The process 200 then moves to a state 204 wherein a database of sequences is opened for analysis and comparison. The process 200 then moves to a state 206 wherein the first sequence stored in the database is read into a memory on the computer. A comparison is then performed at a state 210 to determine if the first sequence is the same as the second sequence. It is important to note that this step is not limited to performing an exact comparison between the new sequence and the first sequence in the database. Well-known methods are known to those of skill in the art for comparing two nucleotide or protein sequences, even if they are not identical. For example, gaps can be introduced into one sequence in order to raise the homology level between the two tested sequences. The parameters that control whether gaps or other features are introduced into a sequence during comparison are normally entered by the user of the computer system.

Once a comparison of the two sequences has been performed at the state 210, a determination is made at a decision state 210 whether the two sequences are the same. Of course, the term "same" is not limited to sequences that are absolutely identical. Sequences that are within the homology parameters entered by the user will be marked as "same" in the process 200.

If a determination is made that the two sequences are the same, the process 200 moves to a state 214 wherein the name of the sequence from the database is displayed to the user. This state notifies the user that the sequence with the displayed name fulfills the homology constraints that were entered. Once the name of the stored sequence is displayed to the user, the process 200 moves to a decision state 218 wherein a determination is made whether more sequences exist in the database. If no more sequences exist in the database, then the process 200 terminates at an end state 220. However, if more sequences do exist in the database, then the process 200 moves to a state 224 wherein a pointer is moved to the next sequence in the database so that it can be compared to the new sequence. In this manner, the new sequence is aligned and compared with every sequence in the database.

It should be noted that if a determination had been made at the decision state 212 that the sequences were not homologous, then the process 200 would move immediately to the decision state 218 in order to determine if any other sequences were available in the database for comparison.

Accordingly, one aspect of the invention is a computer system comprising a processor, a data storage device having stored thereon a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto, a data storage device having retrievably stored thereon reference nucleotide sequences or polypeptide sequences to be compared to a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto and a sequence comparer for conducting the comparison. The sequence comparer may indicate a homology level between the sequences compared or identify structural motifs in the above described nucleic acid code of Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto, or it may identify structural motifs in sequences which are compared to these nucleic acid codes and polypeptide codes. In some aspects, the data storage device may have stored thereon the

sequences of at least 2, 5, 10, 15, 20, 25, 30 or 40 or more of the nucleic acid sequences as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or the polypeptide sequences as set forth in Group B amino acid sequences and sequences substantially identical thereto.

Another aspect of the invention is a method for determining the level of homology between a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto and a reference nucleotide sequence. The method including reading the nucleic acid code or the polypeptide code and the reference nucleotide or polypeptide sequence through the use of a computer program which determines homology levels and determining homology between the nucleic acid code or polypeptide code and the reference nucleotide or polypeptide sequence with the computer program. The computer program may be any of a number of computer programs for determining homology levels, including those specifically enumerated herein, (*e.g.*, BLAST2N with the default parameters or with any modified parameters). The method may be implemented using the computer systems described above. The method may also be performed by reading at least 2, 5, 10, 15, 20, 25, 30 or 40 or more of the above described nucleic acid sequences as set forth in the Group A nucleic acid sequences, or the polypeptide sequences as set forth in the Group B amino acid sequences through use of the computer program and determining homology between the nucleic acid codes or polypeptide codes and reference nucleotide sequences or polypeptide sequences.

Figure 3 is a flow diagram illustrating one aspect of a process 250 in a computer for determining whether two sequences are homologous. The process 250 begins at a start state 252 and then moves to a state 254 wherein a first sequence to be compared is stored to a memory. The second sequence to be compared is then stored to a memory at a state 256. The process 250 then moves to a state 260 wherein the first character in the first sequence is read and then to a state 262 wherein the first character of the second sequence is read. It should be understood that if the sequence is a nucleotide sequence, then the character would normally be either A, T, C, G or U. If the sequence is a protein sequence, then it is preferably in the single letter amino acid code so that the first and sequence sequences can be easily compared.

A determination is then made at a decision state 264 whether the two characters are the same. If they are the same, then the process 250 moves to a state 268 wherein the next characters in the first and second sequences are read. A determination is

then made whether the next characters are the same. If they are, then the process 250 continues this loop until two characters are not the same. If a determination is made that the next two characters are not the same, the process 250 moves to a decision state 274 to determine whether there are any more characters either sequence to read.

If there are not any more characters to read, then the process 250 moves to a state 276 wherein the level of homology between the first and second sequences is displayed to the user. The level of homology is determined by calculating the proportion of characters between the sequences that were the same out of the total number of sequences in the first sequence. Thus, if every character in a first 100 nucleotide sequence aligned with a every character in a second sequence, the homology level would be 100%.

Alternatively, the computer program may be a computer program which compares the nucleotide sequences of a nucleic acid sequence as set forth in the invention, to one or more reference nucleotide sequences in order to determine whether the nucleic acid code of Group A nucleic acid sequences and sequences substantially identical thereto, differs from a reference nucleic acid sequence at one or more positions. Optionally such a program records the length and identity of inserted, deleted or substituted nucleotides with respect to the sequence of either the reference polynucleotide or a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto. In one aspect, the computer program may be a program which determines whether a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, contains a single nucleotide polymorphism (SNP) with respect to a reference nucleotide sequence.

Accordingly, another aspect of the invention is a method for determining whether a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, differs at one or more nucleotides from a reference nucleotide sequence comprising the steps of reading the nucleic acid code and the reference nucleotide sequence through use of a computer program which identifies differences between nucleic acid sequences and identifying differences between the nucleic acid code and the reference nucleotide sequence with the computer program. In some aspects, the computer program is a program which identifies single nucleotide polymorphisms. The method may be implemented by the computer systems described above and the method illustrated in Figure 3. The method may also be performed by reading at least 2, 5, 10, 15, 20, 25, 30, or 40 or more of the nucleic acid sequences as set forth in Group A nucleic acid sequences and sequences substantially identical thereto and the reference nucleotide sequences through the use of the

computer program and identifying differences between the nucleic acid codes and the reference nucleotide sequences with the computer program.

In other aspects the computer based system may further comprise an identifier for identifying features within a nucleic acid sequence as set forth in the Group A nucleic acid sequences or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto.

An "identifier" refers to one or more programs which identifies certain features within a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto. In one aspect, the identifier may comprise a program which identifies an open reading frame in a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto.

Figure 4 is a flow diagram illustrating one aspect of an identifier process 300 for detecting the presence of a feature in a sequence. The process 300 begins at a start state 302 and then moves to a state 304 wherein a first sequence that is to be checked for features is stored to a memory 115 in the computer system 100. The process 300 then moves to a state 306 wherein a database of sequence features is opened. Such a database would include a list of each feature's attributes along with the name of the feature. For example, a feature name could be "Initiation Codon" and the attribute would be "ATG". Another example would be the feature name "TAATAA Box" and the feature attribute would be "TAATAA". An example of such a database is produced by the University of Wisconsin Genetics Computer Group. Alternatively, the features may be structural polypeptide motifs such as alpha helices, beta sheets, or functional polypeptide motifs such as enzymatic active sites, helix-turn-helix motifs or other motifs known to those skilled in the art.

Once the database of features is opened at the state 306, the process 300 moves to a state 308 wherein the first feature is read from the database. A comparison of the attribute of the first feature with the first sequence is then made at a state 310. A determination is then made at a decision state 316 whether the attribute of the feature was found in the first sequence. If the attribute was found, then the process 300 moves to a state 318 wherein the name of the found feature is displayed to the user.

The process 300 then moves to a decision state 320 wherein a determination is made whether move features exist in the database. If no more features do exist, then the process 300 terminates at an end state 324. However, if more features do exist in the

database, then the process 300 reads the next sequence feature at a state 326 and loops back to the state 310 wherein the attribute of the next feature is compared against the first sequence. It should be noted, that if the feature attribute is not found in the first sequence at the decision state 316, the process 300 moves directly to the decision state 320 in order to determine if any more features exist in the database.

Accordingly, another aspect of the invention is a method of identifying a feature within a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto, comprising reading the nucleic acid code(s) or polypeptide code(s) through the use of a computer program which identifies features therein and identifying features within the nucleic acid code(s) with the computer program. In one aspect, computer program comprises a computer program which identifies open reading frames. The method may be performed by reading a single sequence or at least 2, 5, 10, 15, 20, 25, 30, or 40 of the nucleic acid sequences as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or the polypeptide sequences as set forth in Group B amino acid sequences and sequences substantially identical thereto, through the use of the computer program and identifying features within the nucleic acid codes or polypeptide codes with the computer program.

A nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto, may be stored and manipulated in a variety of data processor programs in a variety of formats. For example, a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto, may be stored as text in a word processing file, such as Microsoft WORD™ or WORDPERFECT™ or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2™, SYBASE™, or ORACLE™. In addition, many computer programs and databases may be used as sequence comparison algorithms, identifiers, or sources of reference nucleotide sequences or polypeptide sequences to be compared to a nucleic acid sequence as set forth in Group A nucleic acid sequences and sequences substantially identical thereto, or a polypeptide sequence as set forth in Group B amino acid sequences and sequences substantially identical thereto. The following list is intended not to limit the invention but to provide guidance to programs and databases which are useful with the nucleic acid sequences as set forth in Group A nucleic acid

sequences and sequences substantially identical thereto, or the polypeptide sequences as set forth in Group B amino acid sequences and sequences substantially identical thereto.

The programs and databases which may be used include, but are not limited to: MacPattern (EMBL), DiscoveryBase (Molecular Applications Group), GeneMine (Molecular Applications Group), Look (Molecular Applications Group), MacLook (Molecular Applications Group), BLAST and BLAST2 (NCBI), BLASTN and BLASTX (Altschul et al, J. Mol. Biol. 215: 403, 1990), FASTA (Pearson and Lipman, Proc. Natl. Acad. Sci. USA, 85: 2444, 1988), FASTDB (Brutlag *et al.* Comp. App. Biosci. 6:237-245, 1990), Catalyst (Molecular Simulations Inc.), Catalyst/SHAPE (Molecular Simulations Inc.), Cerius^2.DBAccess (Molecular Simulations Inc.), HypoGen (Molecular Simulations Inc.), Insight II, (Molecular Simulations Inc.), Discover (Molecular Simulations Inc.), CHARMm (Molecular Simulations Inc.), Felix (Molecular Simulations Inc.), DelPhi, (Molecular Simulations Inc.), QuanteMM, (Molecular Simulations Inc.), Homology (Molecular Simulations Inc.), Modeler (Molecular Simulations Inc.), ISIS (Molecular Simulations Inc.), Quanta/Protein Design (Molecular Simulations Inc.), WebLab (Molecular Simulations Inc.), WebLab Diversity Explorer (Molecular Simulations Inc.), Gene Explorer (Molecular Simulations Inc.), SeqFold (Molecular Simulations Inc.), the MDL Available Chemicals Directory database, the MDL Drug Data Report data base, the Comprehensive Medicinal Chemistry database, Derwents's World Drug Index database, the BioByteMasterFile database, the Genbank database and the Genseqn database. Many other programs and data bases would be apparent to one of skill in the art given the present disclosure.

Motifs which may be detected using the above programs include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites, ubiquitination sites, alpha helices and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites and enzymatic cleavage sites.

Hybridization of nucleic acids

The invention provides isolated or recombinant nucleic acids that hybridize under stringent conditions to an exemplary sequence of the invention (e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45,

SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379). The stringent conditions can be highly stringent conditions, medium stringent conditions and/or

low stringent conditions, including the high and reduced stringency conditions described herein. In one aspect, it is the stringency of the wash conditions that set forth the conditions which determine whether a nucleic acid is within the scope of the invention, as discussed below.

In alternative aspects, nucleic acids of the invention as defined by their ability to hybridize under stringent conditions can be between about five residues and the full length of nucleic acid of the invention; e.g., they can be at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 55, 60, 65, 70, 75, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, or more, residues in length. Nucleic acids shorter than full length are also included. These nucleic acids can be useful as, e.g., hybridization probes, labeling probes, PCR oligonucleotide probes, iRNA (single or double stranded), antisense or sequences encoding antibody binding peptides (epitopes), motifs, active sites and the like.

In one aspect, nucleic acids of the invention are defined by their ability to hybridize under high stringency comprises conditions of about 50% formamide at about 37°C to 42°C. In one aspect, nucleic acids of the invention are defined by their ability to hybridize under reduced stringency comprising conditions in about 35% to 25% formamide at about 30°C to 35°C.

Alternatively, nucleic acids of the invention are defined by their ability to hybridize under high stringency comprising conditions at 42°C in 50% formamide, 5X SSPE, 0.3% SDS, and a repetitive sequence blocking nucleic acid, such as cot-1 or salmon sperm DNA (e.g., 200 n/ml sheared and denatured salmon sperm DNA). In one aspect, nucleic acids of the invention are defined by their ability to hybridize under reduced stringency conditions comprising 35% formamide at a reduced temperature of 35°C.

In nucleic acid hybridization reactions, the conditions used to achieve a particular level of stringency will vary, depending on the nature of the nucleic acids being hybridized. For example, the length, degree of complementarity, nucleotide sequence composition (*e.g.*, GC v. AT content) and nucleic acid type (*e.g.*, RNA v. DNA) of the hybridizing regions of the nucleic acids can be considered in selecting hybridization conditions. An additional consideration is whether one of the nucleic acids is immobilized, for example, on a filter.

Hybridization may be carried out under conditions of low stringency, moderate stringency or high stringency. As an example of nucleic acid hybridization, a polymer membrane containing immobilized denatured nucleic acids is first prehybridized for 30

minutes at 45°C in a solution consisting of 0.9 M NaCl, 50 mM NaH_2PO_4, pH 7.0, 5.0 mM Na_2EDTA, 0.5% SDS, 10X Denhardt's and 0.5 mg/ml polyriboadenylic acid. Approximately $2 X 10^7$ cpm (specific activity 4-9 X 10^8 cpm/ug) of ^{32}P end-labeled oligonucleotide probe are then added to the solution. After 12-16 hours of incubation, the membrane is washed for 30 minutes at room temperature in 1X SET (150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na_2EDTA) containing 0.5% SDS, followed by a 30 minute wash in fresh 1X SET at T_m-10°C for the oligonucleotide probe. The membrane is then exposed to autoradiographic film for detection of hybridization signals.

All of the foregoing hybridizations would be considered to be under conditions of high stringency.

Following hybridization, a filter can be washed to remove any non-specifically bound detectable probe. The stringency used to wash the filters can also be varied depending on the nature of the nucleic acids being hybridized, the length of the nucleic acids being hybridized, the degree of complementarity, the nucleotide sequence composition (*e.g.*, GC v. AT content) and the nucleic acid type (*e.g.*, RNA v. DNA). Examples of progressively higher stringency condition washes are as follows: 2X SSC, 0.1% SDS at room temperature for 15 minutes (low stringency); 0.1X SSC, 0.5% SDS at room temperature for 30 minutes to 1 hour (moderate stringency); 0.1X SSC, 0.5% SDS for 15 to 30 minutes at between the hybridization temperature and 68°C (high stringency); and 0.15M NaCl for 15 minutes at 72°C (very high stringency). A final low stringency wash can be conducted in 0.1X SSC at room temperature. The examples above are merely illustrative of one set of conditions that can be used to wash filters. One of skill in the art would know that there are numerous recipes for different stringency washes. Some other examples are given below.

Nucleic acids which have hybridized to the probe are identified by autoradiography or other conventional techniques.

The above procedure may be modified to identify nucleic acids having decreasing levels of homology to the probe sequence. For example, to obtain nucleic acids of decreasing homology to the detectable probe, less stringent conditions may be used. For example, the hybridization temperature may be decreased in increments of 5°C from 68°C to 42°C in a hybridization buffer having a Na+ concentration of approximately 1M. Following hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be "moderate" conditions above 50°C and "low" conditions below 50°C. A specific example of "moderate" hybridization conditions is

when the above hybridization is conducted at 55°C. A specific example of "low stringency" hybridization conditions is when the above hybridization is conducted at 45°C.

Alternatively, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50°C. These conditions are considered to be "moderate" conditions above 25% formamide and "low" conditions below 25% formamide. A specific example of "moderate" hybridization conditions is when the above hybridization is conducted at 30% formamide. A specific example of "low stringency" hybridization conditions is when the above hybridization is conducted at 10% formamide.

However, the selection of a hybridization format is not critical - it is the stringency of the wash conditions that set forth the conditions which determine whether a nucleic acid is within the scope of the invention. Wash conditions used to identify nucleic acids within the scope of the invention include, e.g.: a salt concentration of about 0.02 molar at pH 7 and a temperature of at least about 50°C or about 55°C to about 60°C; or, a salt concentration of about 0.15 M NaCl at 72°C for about 15 minutes; or, a salt concentration of about 0.2X SSC at a temperature of at least about 50°C or about 55°C to about 60°C for about 15 to about 20 minutes; or, the hybridization complex is washed twice with a solution with a salt concentration of about 2X SSC containing 0.1% SDS at room temperature for 15 minutes and then washed twice by 0.1X SSC containing 0.1% SDS at 68oC for 15 minutes; or, equivalent conditions. See Sambrook, Tijssen and Ausubel for a description of SSC buffer and equivalent conditions.

These methods may be used to isolate nucleic acids of the invention. For example, the preceding methods may be used to isolate nucleic acids having a sequence with at least about 97%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, or at least 50% homology to a nucleic acid sequence selected from the group consisting of one of the sequences of Group A nucleic acid sequences and sequences substantially identical thereto, or fragments comprising at least about 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases thereof and the sequences complementary thereto. Homology may be measured using the alignment algorithm. For example, the homologous polynucleotides may have a coding sequence which is a naturally occurring allelic variant of one of the coding sequences

described herein. Such allelic variants may have a substitution, deletion or addition of one or more nucleotides when compared to the nucleic acids of Group A nucleic acid sequences or the sequences complementary thereto.

Additionally, the above procedures may be used to isolate nucleic acids which encode polypeptides having at least about 99%, 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, or at least 50% homology to a polypeptide having the sequence of one of Group B amino acid sequences and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined using a sequence alignment algorithm (*e.g.*, such as the FASTA version 3.0t78 algorithm with the default parameters).

Oligonucleotides probes and methods for using them

The invention also provides nucleic acid probes that can be used, e.g., for identifying nucleic acids encoding a polypeptide with a xylanase activity or fragments thereof or for identifying xylanase genes. In one aspect, the probe comprises at least 10 consecutive bases of a nucleic acid of the invention. Alternatively, a probe of the invention can be at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 110, 120, 130, 150 or about 10 to 50, about 20 to 60 about 30 to 70, consecutive bases of a sequence as set forth in a nucleic acid of the invention. The probes identify a nucleic acid by binding and/or hybridization. The probes can be used in arrays of the invention, see discussion below, including, e.g., capillary arrays. The probes of the invention can also be used to isolate other nucleic acids or polypeptides.

The isolated nucleic acids of Group A nucleic acid sequences and sequences substantially identical thereto, the sequences complementary thereto, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of Group A nucleic acid sequences and sequences substantially identical thereto, or the sequences complementary thereto may also be used as probes to determine whether a biological sample, such as a soil sample, contains an organism having a nucleic acid sequence of the invention or an organism from which the nucleic acid was obtained. In such procedures, a biological sample potentially harboring the organism from which the nucleic acid was isolated is obtained and nucleic acids are obtained from the sample. The nucleic acids are contacted with the probe under conditions which permit the probe to specifically hybridize to any complementary sequences from which are present therein.

Where necessary, conditions which permit the probe to specifically hybridize to complementary sequences may be determined by placing the probe in contact with complementary sequences from samples known to contain the complementary sequence as well as control sequences which do not contain the complementary sequence. Hybridization conditions, such as the salt concentration of the hybridization buffer, the formamide concentration of the hybridization buffer, or the hybridization temperature, may be varied to identify conditions which allow the probe to hybridize specifically to complementary nucleic acids.

If the sample contains the organism from which the nucleic acid was isolated, specific hybridization of the probe is then detected. Hybridization may be detected by labeling the probe with a detectable agent such as a radioactive isotope, a fluorescent dye or an enzyme capable of catalyzing the formation of a detectable product.

Many methods for using the labeled probes to detect the presence of complementary nucleic acids in a sample are familiar to those skilled in the art. These include Southern Blots, Northern Blots, colony hybridization procedures and dot blots. Protocols for each of these procedures are provided in Ausubel *et al.* Current Protocols in Molecular Biology, John Wiley 503 Sons, Inc. (1997) and Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2nd Ed., Cold Spring Harbor Laboratory Press (1989.

Alternatively, more than one probe (at least one of which is capable of specifically hybridizing to any complementary sequences which are present in the nucleic acid sample), may be used in an amplification reaction to determine whether the sample contains an organism containing a nucleic acid sequence of the invention (*e.g.*, an organism from which the nucleic acid was isolated). Typically, the probes comprise oligonucleotides. In one aspect, the amplification reaction may comprise a PCR reaction. PCR protocols are described in Ausubel and Sambrook, *supra*. Alternatively, the amplification may comprise a ligase chain reaction, 3SR, or strand displacement reaction. (See Barany, F., "The Ligase Chain Reaction in a PCR World", *PCR Methods and Applications* 1:5-16, 1991; E. Fahy *et al.*, "Self-sustained Sequence Replication (3SR): An Isothermal Transcription-based Amplification System Alternative to PCR", *PCR Methods and Applications* 1:25-33, 1991; and Walker G.T. *et al.*, "Strand Displacement Amplification-an Isothermal *in vitro* DNA Amplification Technique", *Nucleic Acid Research* 20:1691-1696, 1992). In such procedures, the nucleic acids in the sample are contacted with the probes, the amplification reaction is performed and any resulting amplification product is detected. The amplification product may be detected by performing gel electrophoresis on the reaction products and staining the gel with an intercalator such as

ethidium bromide. Alternatively, one or more of the probes may be labeled with a radioactive isotope and the presence of a radioactive amplification product may be detected by autoradiography after gel electrophoresis.

Probes derived from sequences near the ends of the sequences of Group A nucleic acid sequences and sequences substantially identical thereto, may also be used in chromosome walking procedures to identify clones containing genomic sequences located adjacent to the sequences of Group A nucleic acid sequences and sequences substantially identical thereto. Such methods allow the isolation of genes which encode additional proteins from the host organism.

The isolated nucleic acids of Group A nucleic acid sequences and sequences substantially identical thereto, the sequences complementary thereto, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of Group A nucleic acid sequences and sequences substantially identical thereto, or the sequences complementary thereto may be used as probes to identify and isolate related nucleic acids. In some aspects, the related nucleic acids may be cDNAs or genomic DNAs from organisms other than the one from which the nucleic acid was isolated. For example, the other organisms may be related organisms. In such procedures, a nucleic acid sample is contacted with the probe under conditions which permit the probe to specifically hybridize to related sequences. Hybridization of the probe to nucleic acids from the related organism is then detected using any of the methods described above.

By varying the stringency of the hybridization conditions used to identify nucleic acids, such as cDNAs or genomic DNAs, which hybridize to the detectable probe, nucleic acids having different levels of homology to the probe can be identified and isolated. Stringency may be varied by conducting the hybridization at varying temperatures below the melting temperatures of the probes. The melting temperature, T_m, is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly complementary probe. Very stringent conditions are selected to be equal to or about 5°C lower than the T_m for a particular probe. The melting temperature of the probe may be calculated using the following formulas:

For probes between 14 and 70 nucleotides in length the melting temperature (T_m) is calculated using the formula: T_m=81.5+16.6(log [Na+])+0.41(fraction G+C)-(600/N) where N is the length of the probe.

If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation: T_m=81.5+16.6(log [Na+])+0.41(fraction G+C)-(0.63% formamide)-(600/N) where N is the length of the probe.

Prehybridization may be carried out in 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100μg denatured fragmented salmon sperm DNA or 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100μg denatured fragmented salmon sperm DNA, 50% formamide. The formulas for SSC and Denhardt's solutions are listed in Sambrook *et al.*, *supra*.

Hybridization is conducted by adding the detectable probe to the prehybridization solutions listed above. Where the probe comprises double stranded DNA, it is denatured before addition to the hybridization solution. The filter is contacted with the hybridization solution for a sufficient period of time to allow the probe to hybridize to cDNAs or genomic DNAs containing sequences complementary thereto or homologous thereto. For probes over 200 nucleotides in length, the hybridization may be carried out at 15-25°C below the T_m. For shorter probes, such as oligonucleotide probes, the hybridization may be conducted at 5-10°C below the T_m. Typically, for hybridizations in 6X SSC, the hybridization is conducted at approximately 68°C. Usually, for hybridizations in 50% formamide containing solutions, the hybridization is conducted at approximately 42°C.

Inhibiting Expression of Xylanases

The invention provides nucleic acids complementary to (e.g., antisense sequences to) the nucleic acids of the invention, e.g., xylanase-encoding nucleic acids. Antisense sequences are capable of inhibiting the transport, splicing or transcription of xylanase-encoding genes. The inhibition can be effected through the targeting of genomic DNA or messenger RNA. The transcription or function of targeted nucleic acid can be inhibited, for example, by hybridization and/or cleavage. One particularly useful set of inhibitors provided by the present invention includes oligonucleotides which are able to either bind xylanase gene or message, in either case preventing or inhibiting the production or function of xylanase. The association can be through sequence specific hybridization. Another useful class of inhibitors includes oligonucleotides which cause inactivation or cleavage of xylanase message. The oligonucleotide can have enzyme activity which causes such cleavage, such as ribozymes. The oligonucleotide can be chemically modified or conjugated to an enzyme or composition capable of cleaving the complementary nucleic acid. A pool of many different such oligonucleotides can be screened for those with the desired activity. Thus, the invention provides various compositions for the inhibition of xylanase

expression on a nucleic acid and/or protein level, e.g., antisense, iRNA and ribozymes comprising xylanase sequences of the invention and the anti-xylanase antibodies of the invention.

Inhibition of xylanase expression can have a variety of industrial applications. For example, inhibition of xylanase expression can slow or prevent spoilage. Spoilage can occur when polysaccharides, e.g., structural polysaccharides, are enzymatically degraded. This can lead to the deterioration, or rot, of fruits and vegetables. In one aspect, use of compositions of the invention that inhibit the expression and/or activity of xylanases, e.g., antibodies, antisense oligonucleotides, ribozymes and RNAi, are used to slow or prevent spoilage. Thus, in one aspect, the invention provides methods and compositions comprising application onto a plant or plant product (e.g., a cereal, a grain, a fruit, seed, root, leaf, etc.) antibodies, antisense oligonucleotides, ribozymes and RNAi of the invention to slow or prevent spoilage. These compositions also can be expressed by the plant (e.g., a transgenic plant) or another organism (e.g., a bacterium or other microorganism transformed with a xylanase gene of the invention).

The compositions of the invention for the inhibition of xylanase expression (e.g., antisense, iRNA, ribozymes, antibodies) can be used as pharmaceutical compositions, e.g., as anti-pathogen agents or in other therapies, e.g., as anti-microbials for, e.g., *Salmonella*.

Antisense Oligonucleotides

The invention provides antisense oligonucleotides capable of binding xylanase message which can inhibit xylan hydrolase activity (e.g., catalyzing hydrolysis of internal β-1,4-xylosidic linkages) by targeting mRNA. Strategies for designing antisense oligonucleotides are well described in the scientific and patent literature, and the skilled artisan can design such xylanase oligonucleotides using the novel reagents of the invention. For example, gene walking/ RNA mapping protocols to screen for effective antisense oligonucleotides are well known in the art, see, e.g., Ho (2000) Methods Enzymol. 314:168-183, describing an RNA mapping assay, which is based on standard molecular techniques to provide an easy and reliable method for potent antisense sequence selection. See also Smith (2000) Eur. J. Pharm. Sci. 11:191-198.

Naturally occurring nucleic acids are used as antisense oligonucleotides. The antisense oligonucleotides can be of any length; for example, in alternative aspects, the antisense oligonucleotides are between about 5 to 100, about 10 to 80, about 15 to 60, about

18 to 40. The optimal length can be determined by routine screening. The antisense oligonucleotides can be present at any concentration. The optimal concentration can be determined by routine screening. A wide variety of synthetic, non-naturally occurring nucleotide and nucleic acid analogues are known which can address this potential problem. For example, peptide nucleic acids (PNAs) containing non-ionic backbones, such as N-(2-aminoethyl) glycine units can be used. Antisense oligonucleotides having phosphorothioate linkages can also be used, as described in WO 97/03211; WO 96/39154; Mata (1997) Toxicol Appl Pharmacol 144:189-197; Antisense Therapeutics, ed. Agrawal (Humana Press, Totowa, N.J., 1996). Antisense oligonucleotides having synthetic DNA backbone analogues provided by the invention can also include phosphoro-dithioate, methylphosphonate, phosphoramidate, alkyl phosphotriester, sulfamate, 3'-thioacetal, methylene(methylimino), 3'-N-carbamate, and morpholino carbamate nucleic acids, as described above.

Combinatorial chemistry methodology can be used to create vast numbers of oligonucleotides that can be rapidly screened for specific oligonucleotides that have appropriate binding affinities and specificities toward any target, such as the sense and antisense xylanase sequences of the invention (see, e.g., Gold (1995) J. of Biol. Chem. 270:13581-13584).

Inhibitory Ribozymes

The invention provides ribozymes capable of binding xylanase message. These ribozymes can inhibit xylanase activity by, e.g., targeting mRNA. Strategies for designing ribozymes and selecting the xylanase-specific antisense sequence for targeting are well described in the scientific and patent literature, and the skilled artisan can design such ribozymes using the novel reagents of the invention. Ribozymes act by binding to a target RNA through the target RNA binding portion of a ribozyme which is held in close proximity to an enzymatic portion of the RNA that cleaves the target RNA. Thus, the ribozyme recognizes and binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cleave and inactivate the target RNA. Cleavage of a target RNA in such a manner will destroy its ability to direct synthesis of an encoded protein if the cleavage occurs in the coding sequence. After a ribozyme has bound and cleaved its RNA target, it can be released from that RNA to bind and cleave new targets repeatedly.

In some circumstances, the enzymatic nature of a ribozyme can be advantageous over other technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its transcription, translation or

association with another molecule) as the effective concentration of ribozyme necessary to effect a therapeutic treatment can be lower than that of an antisense oligonucleotide. This potential advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, a ribozyme is typically a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding, but also on the mechanism by which the molecule inhibits the expression of the RNA to which it binds. That is, the inhibition is caused by cleavage of the RNA target and so specificity is defined as the ratio of the rate of cleavage of the targeted RNA over the rate of cleavage of non-targeted RNA. This cleavage mechanism is dependent upon factors additional to those involved in base pairing. Thus, the specificity of action of a ribozyme can be greater than that of antisense oligonucleotide binding the same RNA site.

The ribozyme of the invention, e.g., an enzymatic ribozyme RNA molecule, can be formed in a hammerhead motif, a hairpin motif, as a hepatitis delta virus motif, a group I intron motif and/or an RNaseP-like RNA in association with an RNA guide sequence. Examples of hammerhead motifs are described by, e.g., Rossi (1992) Aids Research and Human Retroviruses 8:183; hairpin motifs by Hampel (1989) Biochemistry 28:4929, and Hampel (1990) Nuc. Acids Res. 18:299; the hepatitis delta virus motif by Perrotta (1992) Biochemistry 31:16; the RNaseP motif by Guerrier-Takada (1983) Cell 35:849; and the group I intron by Cech U.S. Pat. No. 4,987,071. The recitation of these specific motifs is not intended to be limiting. Those skilled in the art will recognize that a ribozyme of the invention, e.g., an enzymatic RNA molecule of this invention, can have a specific substrate binding site complementary to one or more of the target gene RNA regions. A ribozyme of the invention can have a nucleotide sequence within or surrounding that substrate binding site which imparts an RNA cleaving activity to the molecule.

RNA interference (RNAi)

In one aspect, the invention provides an RNA inhibitory molecule, a so-called "RNAi" molecule, comprising a xylanase sequence of the invention. The RNAi molecule comprises a double-stranded RNA (dsRNA) molecule. The RNAi can inhibit expression of a xylanase gene. In one aspect, the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length. While the invention is not limited by any particular mechanism of action, the RNAi can enter a cell and cause the degradation of a single-stranded RNA (ssRNA) of similar or identical sequences, including endogenous mRNAs.

When a cell is exposed to double-stranded RNA (dsRNA), mRNA from the homologous gene is selectively degraded by a process called RNA interference (RNAi). A possible basic mechanism behind RNAi is the breaking of a double-stranded RNA (dsRNA) matching a specific gene sequence into short pieces called short interfering RNA, which trigger the degradation of mRNA that matches its sequence. In one aspect, the RNAi's of the invention are used in gene-silencing therapeutics, see, e.g., Shuey (2002) Drug Discov. Today 7:1040-1046. In one aspect, the invention provides methods to selectively degrade RNA using the RNAi's of the invention. The process may be practiced *in vitro*, *ex vivo* or *in vivo*. In one aspect, the RNAi molecules of the invention can be used to generate a loss-of-function mutation in a cell, an organ or an animal. Methods for making and using RNAi molecules for selectively degrade RNA are well known in the art, see, e.g., U.S. Patent No. 6,506,559; 6,511,824; 6,515,109; 6,489,127.

Modification of Nucleic Acids

The invention provides methods of generating variants of the nucleic acids of the invention, e.g., those encoding a xylanase. These methods can be repeated or used in various combinations to generate xylanases having an altered or different activity or an altered or different stability from that of a xylanase encoded by the template nucleic acid. These methods also can be repeated or used in various combinations, e.g., to generate variations in gene/ message expression, message translation or message stability. In another aspect, the genetic composition of a cell is altered by, e.g., modification of a homologous gene ex vivo, followed by its reinsertion into the cell.

A nucleic acid of the invention can be altered by any means. For example, random or stochastic methods, or, non-stochastic, or "directed evolution," methods, see, e.g., U.S. Patent No. 6,361,974. Methods for random mutation of genes are well known in the art, see, e.g., U.S. Patent No. 5,830,696. For example, mutagens can be used to randomly mutate a gene. Mutagens include, e.g., ultraviolet light or gamma irradiation, or a chemical mutagen, e.g., mitomycin, nitrous acid, photoactivated psoralens, alone or in combination, to induce DNA breaks amenable to repair by recombination. Other chemical mutagens include, for example, sodium bisulfite, nitrous acid, hydroxylamine, hydrazine or formic acid. Other mutagens are analogues of nucleotide precursors, e.g., nitrosoguanidine, 5-bromouracil, 2-aminopurine, or acridine. These agents can be added to a PCR reaction in place of the nucleotide precursor thereby mutating the sequence. Intercalating agents such as proflavine, acriflavine, quinacrine and the like can also be used.

Any technique in molecular biology can be used, e.g., random PCR mutagenesis, see, e.g., Rice (1992) Proc. Natl. Acad. Sci. USA 89:5467-5471; or, combinatorial multiple cassette mutagenesis, see, e.g., Crameri (1995) Biotechniques 18:194-196. Alternatively, nucleic acids, e.g., genes, can be reassembled after random, or "stochastic," fragmentation, see, e.g., U.S. Patent Nos. 6,291,242; 6,287,862; 6,287,861; 5,955,358; 5,830,721; 5,824,514; 5,811,238; 5,605,793. In alternative aspects, modifications, additions or deletions are introduced by error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly (e.g., GeneReassembly™, see, e.g., U.S. Patent No. 6,537,776), gene site saturated mutagenesis (GSSM™), synthetic ligation reassembly (SLR), recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation, and/or a combination of these and other methods.

The following publications describe a variety of recursive recombination procedures and/or methods which can be incorporated into the methods of the invention: Stemmer (1999) "Molecular breeding of viruses for targeting and other clinical properties" Tumor Targeting 4:1-4; Ness (1999) Nature Biotechnology 17:893-896; Chang (1999) "Evolution of a cytokine using DNA family shuffling" Nature Biotechnology 17:793-797; Minshull (1999) "Protein evolution by molecular breeding" Current Opinion in Chemical Biology 3:284-290; Christians (1999) "Directed evolution of thymidine kinase for AZT phosphorylation using DNA family shuffling" Nature Biotechnology 17:259-264; Crameri (1998) "DNA shuffling of a family of genes from diverse species accelerates directed evolution" Nature 391:288-291; Crameri (1997) "Molecular evolution of an arsenate detoxification pathway by DNA shuffling," Nature Biotechnology 15:436-438; Zhang (1997) "Directed evolution of an effective fucosidase from a galactosidase by DNA shuffling and screening" Proc. Natl. Acad. Sci. USA 94:4504-4509; Patten et al. (1997) "Applications of DNA Shuffling to Pharmaceuticals and Vaccines" Current Opinion in Biotechnology 8:724-733; Crameri et al. (1996) "Construction and evolution of antibody-phage libraries by DNA shuffling" Nature Medicine 2:100-103; Gates et al. (1996) "Affinity selective isolation of ligands from peptide libraries through display on a lac repressor `headpiece dimer`" Journal

of Molecular Biology 255:373-386; Stemmer (1996) "Sexual PCR and Assembly PCR" In: The Encyclopedia of Molecular Biology. VCH Publishers, New York. pp.447-457; Crameri and Stemmer (1995) "Combinatorial multiple cassette mutagenesis creates all the permutations of mutant and wildtype cassettes" BioTechniques 18:194-195; Stemmer et al. (1995) "Single-step assembly of a gene and entire plasmid form large numbers of oligodeoxyribonucleotides" Gene, 164:49-53; Stemmer (1995) "The Evolution of Molecular Computation" Science 270: 1510; Stemmer (1995) "Searching Sequence Space" Bio/Technology 13:549-553; Stemmer (1994) "Rapid evolution of a protein in vitro by DNA shuffling" Nature 370:389-391; and Stemmer (1994) "DNA shuffling by random fragmentation and reassembly: In vitro recombination for molecular evolution." Proc. Natl. Acad. Sci. USA 91:10747-10751.

Mutational methods of generating diversity include, for example, site-directed mutagenesis (Ling et al. (1997) "Approaches to DNA mutagenesis: an overview" Anal Biochem. 254(2): 157-178; Dale et al. (1996) "Oligonucleotide-directed random mutagenesis using the phosphorothioate method" Methods Mol. Biol. 57:369-374; Smith (1985) "In vitro mutagenesis" Ann. Rev. Genet. 19:423-462; Botstein & Shortle (1985) "Strategies and applications of in vitro mutagenesis" Science 229:1193-1201; Carter (1986) "Site-directed mutagenesis" Biochem. J. 237:1-7; and Kunkel (1987) "The efficiency of oligonucleotide directed mutagenesis" in Nucleic Acids & Molecular Biology (Eckstein, F. and Lilley, D. M. J. eds., Springer Verlag, Berlin)); mutagenesis using uracil containing templates (Kunkel (1985) "Rapid and efficient site-specific mutagenesis without phenotypic selection" Proc. Natl. Acad. Sci. USA 82:488-492; Kunkel et al. (1987) "Rapid and efficient site-specific mutagenesis without phenotypic selection" Methods in Enzymol. 154, 367-382; and Bass et al. (1988) "Mutant Trp repressors with new DNA-binding specificities" Science 242:240-245); oligonucleotide-directed mutagenesis (Methods in Enzymol. 100: 468-500 (1983); Methods in Enzymol. 154: 329-350 (1987); Zoller (1982) "Oligonucleotide-directed mutagenesis using M13-derived vectors: an efficient and general procedure for the production of point mutations in any DNA fragment" Nucleic Acids Res. 10:6487-6500; Zoller & Smith (1983) "Oligonucleotide-directed mutagenesis of DNA fragments cloned into M13 vectors" Methods in Enzymol. 100:468-500; and Zoller (1987) Oligonucleotide-directed mutagenesis: a simple method using two oligonucleotide primers and a single-stranded DNA template" Methods in Enzymol. 154:329-350); phosphorothioate-modified DNA mutagenesis (Taylor (1985) "The use of phosphorothioate-modified DNA in restriction enzyme reactions to prepare nicked DNA" Nucl. Acids Res. 13: 8749-8764; Taylor (1985) "The rapid

generation of oligonucleotide-directed mutations at high frequency using phosphorothioate-modified DNA" Nucl. Acids Res. 13: 8765-8787 (1985); Nakamaye (1986) "Inhibition of restriction endonuclease Nci I cleavage by phosphorothioate groups and its application to oligonucleotide-directed mutagenesis" Nucl. Acids Res. 14: 9679-9698; Sayers (1988) "Y-T Exonucleases in phosphorothioate-based oligonucleotide-directed mutagenesis" Nucl. Acids Res. 16:791-802; and Sayers et al. (1988) "Strand specific cleavage of phosphorothioate-containing DNA by reaction with restriction endonucleases in the presence of ethidium bromide" Nucl. Acids Res. 16: 803-814); mutagenesis using gapped duplex DNA (Kramer et al. (1984) "The gapped duplex DNA approach to oligonucleotide-directed mutation construction" Nucl. Acids Res. 12: 9441-9456; Kramer & Fritz (1987) Methods in Enzymol. "Oligonucleotide-directed construction of mutations via gapped duplex DNA" 154:350-367; Kramer (1988) "Improved enzymatic in vitro reactions in the gapped duplex DNA approach to oligonucleotide-directed construction of mutations" Nucl. Acids Res. 16: 7207; and Fritz (1988) "Oligonucleotide-directed construction of mutations: a gapped duplex DNA procedure without enzymatic reactions *in vitro*" Nucl. Acids Res. 16: 6987-6999).

Additional protocols that can be used to practice the invention include point mismatch repair (Kramer (1984) "Point Mismatch Repair" Cell 38:879-887), mutagenesis using repair-deficient host strains (Carter et al. (1985) "Improved oligonucleotide site-directed mutagenesis using M13 vectors" Nucl. Acids Res. 13: 4431-4443; and Carter (1987) "Improved oligonucleotide-directed mutagenesis using M13 vectors" Methods in Enzymol. 154: 382-403), deletion mutagenesis (Eghtedarzadeh (1986) "Use of oligonucleotides to generate large deletions" Nucl. Acids Res. 14: 5115), restriction-selection and restriction-selection and restriction-purification (Wells et al. (1986) "Importance of hydrogen-bond formation in stabilizing the transition state of subtilisin" Phil. Trans. R. Soc. Lond. A 317: 415-423), mutagenesis by total gene synthesis (Nambiar et al. (1984) "Total synthesis and cloning of a gene coding for the ribonuclease S protein" Science 223: 1299-1301; Sakamar and Khorana (1988) "Total synthesis and expression of a gene for the a-subunit of bovine rod outer segment guanine nucleotide-binding protein (transducin)" Nucl. Acids Res. 14: 6361-6372; Wells et al. (1985) "Cassette mutagenesis: an efficient method for generation of multiple mutations at defined sites" Gene 34:315-323; and Grundstrom et al. (1985) "Oligonucleotide-directed mutagenesis by microscale `shot-gun` gene synthesis" Nucl. Acids Res. 13: 3305-3316), double-strand break repair (Mandecki (1986); Arnold (1993) "Protein engineering for unusual environments" Current Opinion in Biotechnology 4:450-455. "Oligonucleotide-directed double-strand break repair in plasmids of Escherichia coli: a

method for site-specific mutagenesis" Proc. Natl. Acad. Sci. USA, 83:7177-7181). Additional details on many of the above methods can be found in Methods in Enzymology Volume 154, which also describes useful controls for trouble-shooting problems with various mutagenesis methods.

Protocols that can be used to practice the invention are described, e.g., in U.S. Patent Nos. 5,605,793 to Stemmer (Feb. 25, 1997), "Methods for In Vitro Recombination;" U.S. Pat. No. 5,811,238 to Stemmer et al. (Sep. 22, 1998) "Methods for Generating Polynucleotides having Desired Characteristics by Iterative Selection and Recombination;" U.S. Pat. No. 5,830,721 to Stemmer et al. (Nov. 3, 1998), "DNA Mutagenesis by Random Fragmentation and Reassembly;" U.S. Pat. No. 5,834,252 to Stemmer, et al. (Nov. 10, 1998) "End-Complementary Polymerase Reaction;" U.S. Pat. No. 5,837,458 to Minshull, et al. (Nov. 17, 1998), "Methods and Compositions for Cellular and Metabolic Engineering;" WO 95/22625, Stemmer and Crameri, "Mutagenesis by Random Fragmentation and Reassembly;" WO 96/33207 by Stemmer and Lipschutz "End Complementary Polymerase Chain Reaction;" WO 97/20078 by Stemmer and Crameri "Methods for Generating Polynucleotides having Desired Characteristics by Iterative Selection and Recombination;" WO 97/35966 by Minshull and Stemmer, "Methods and Compositions for Cellular and Metabolic Engineering;" WO 99/41402 by Punnonen et al. "Targeting of Genetic Vaccine Vectors;" WO 99/41383 by Punnonen et al. "Antigen Library Immunization;" WO 99/41369 by Punnonen et al. "Genetic Vaccine Vector Engineering;" WO 99/41368 by Punnonen et al. "Optimization of Immunomodulatory Properties of Genetic Vaccines;" EP 752008 by Stemmer and Crameri, "DNA Mutagenesis by Random Fragmentation and Reassembly;" EP 0932670 by Stemmer "Evolving Cellular DNA Uptake by Recursive Sequence Recombination;" WO 99/23107 by Stemmer et al., "Modification of Virus Tropism and Host Range by Viral Genome Shuffling;" WO 99/21979 by Apt et al., "Human Papillomavirus Vectors;" WO 98/31837 by del Cardayre et al. "Evolution of Whole Cells and Organisms by Recursive Sequence Recombination;" WO 98/27230 by Patten and Stemmer, "Methods and Compositions for Polypeptide Engineering;" WO 98/27230 by Stemmer et al., "Methods for Optimization of Gene Therapy by Recursive Sequence Shuffling and Selection," WO 00/00632, "Methods for Generating Highly Diverse Libraries," WO 00/09679, "Methods for Obtaining in Vitro Recombined Polynucleotide Sequence Banks and Resulting Sequences," WO 98/42832 by Arnold et al., "Recombination of Polynucleotide Sequences Using Random or Defined Primers," WO 99/29902 by Arnold et al., "Method for Creating Polynucleotide and Polypeptide Sequences," WO 98/41653 by Vind, "An in Vitro Method for Construction

of a DNA Library," WO 98/41622 by Borchert et al., "Method for Constructing a Library Using DNA Shuffling," and WO 98/42727 by Pati and Zarling, "Sequence Alterations using Homologous Recombination."

Protocols that can be used to practice the invention (providing details regarding various diversity generating methods) are described, e.g., in U.S. Patent application serial no. (USSN) 09/407,800, "SHUFFLING OF CODON ALTERED GENES" by Patten et al. filed Sep. 28, 1999; "EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE SEQUENCE RECOMBINATION" by del Cardayre et al., United States Patent No. 6,379,964; "OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION" by Crameri et al., United States Patent Nos. 6,319,714; 6,368,861; 6,376,246; 6,423,542; 6,426,224 and PCT/US00/01203; "USE OF CODON-VARIED OLIGONUCLEOTIDE SYNTHESIS FOR SYNTHETIC SHUFFLING" by Welch et al., United States Patent No. 6,436,675; "METHODS FOR MAKING CHARACTER STRINGS, POLYNUCLEOTIDES & POLYPEPTIDES HAVING DESIRED CHARACTERISTICS" by Selifonov et al., filed Jan. 18, 2000, (PCT/US00/01202) and, e.g. "METHODS FOR MAKING CHARACTER STRINGS, POLYNUCLEOTIDES & POLYPEPTIDES HAVING DESIRED CHARACTERISTICS" by Selifonov et al., filed Jul. 18, 2000 (U.S. Ser. No. 09/618,579); "METHODS OF POPULATING DATA STRUCTURES FOR USE IN EVOLUTIONARY SIMULATIONS" by Selifonov and Stemmer, filed Jan. 18, 2000 (PCT/US00/01138); and "SINGLE-STRANDED NUCLEIC ACID TEMPLATE-MEDIATED RECOMBINATION AND NUCLEIC ACID FRAGMENT ISOLATION" by Affholter, filed Sep. 6, 2000 (U.S. Ser. No. 09/656,549); and United States Patent Nos. 6,177,263; 6,153,410.

Non-stochastic, or "directed evolution," methods include, e.g., saturation mutagenesis (GSSM™), synthetic ligation reassembly (SLR), or a combination thereof are used to modify the nucleic acids of the invention to generate xylanases with new or altered properties (e.g., activity under highly acidic or alkaline conditions, high or low temperatures, and the like). Polypeptides encoded by the modified nucleic acids can be screened for an activity before testing for xylan hydrolysis or other activity. Any testing modality or protocol can be used, e.g., using a capillary array platform. See, e.g., U.S. Patent Nos. 6,361,974; 6,280,926; 5,939,250.

Saturation mutagenesis, or, GSSM™

In one aspect, codon primers containing a degenerate N,N,G/T sequence are used to introduce point mutations into a polynucleotide, e.g., a xylanase or an antibody of the invention, so as to generate a set of progeny polypeptides in which a full range of single amino acid substitutions is represented at each amino acid position, e.g., an amino acid residue in an enzyme active site or ligand binding site targeted to be modified. These oligonucleotides can comprise a contiguous first homologous sequence, a degenerate N,N,G/T sequence, and, optionally, a second homologous sequence. The downstream progeny translational products from the use of such oligonucleotides include all possible amino acid changes at each amino acid site along the polypeptide, because the degeneracy of the N,N,G/T sequence includes codons for all 20 amino acids. In one aspect, one such degenerate oligonucleotide (comprised of, e.g., one degenerate N,N,G/T cassette) is used for subjecting each original codon in a parental polynucleotide template to a full range of codon substitutions. In another aspect, at least two degenerate cassettes are used – either in the same oligonucleotide or not, for subjecting at least two original codons in a parental polynucleotide template to a full range of codon substitutions. For example, more than one N,N,G/T sequence can be contained in one oligonucleotide to introduce amino acid mutations at more than one site. This plurality of N,N,G/T sequences can be directly contiguous, or separated by one or more additional nucleotide sequence(s). In another aspect, oligonucleotides serviceable for introducing additions and deletions can be used either alone or in combination with the codons containing an N,N,G/T sequence, to introduce any combination or permutation of amino acid additions, deletions, and/or substitutions.

In one aspect, simultaneous mutagenesis of two or more contiguous amino acid positions is done using an oligonucleotide that contains contiguous N,N,G/T triplets, i.e. a degenerate (N,N,G/T)n sequence. In another aspect, degenerate cassettes having less degeneracy than the N,N,G/T sequence are used. For example, it may be desirable in some instances to use (e.g. in an oligonucleotide) a degenerate triplet sequence comprised of only one N, where said N can be in the first second or third position of the triplet. Any other bases including any combinations and permutations thereof can be used in the remaining two positions of the triplet. Alternatively, it may be desirable in some instances to use (e.g. in an oligo) a degenerate N,N,N triplet sequence.

In one aspect, use of degenerate triplets (e.g., N,N,G/T triplets) allows for systematic and easy generation of a full range of possible natural amino acids (for a total of 20 amino acids) into each and every amino acid position in a polypeptide (in alternative

aspects, the methods also include generation of less than all possible substitutions per amino acid residue, or codon, position). For example, for a 100 amino acid polypeptide, 2000 distinct species (i.e. 20 possible amino acids per position X 100 amino acid positions) can be generated. Through the use of an oligonucleotide or set of oligonucleotides containing a degenerate N,N,G/T triplet, 32 individual sequences can code for all 20 possible natural amino acids. Thus, in a reaction vessel in which a parental polynucleotide sequence is subjected to saturation mutagenesis using at least one such oligonucleotide, there are generated 32 distinct progeny polynucleotides encoding 20 distinct polypeptides. In contrast, the use of a non-degenerate oligonucleotide in site-directed mutagenesis leads to only one progeny polypeptide product per reaction vessel. Nondegenerate oligonucleotides can optionally be used in combination with degenerate primers disclosed; for example, nondegenerate oligonucleotides can be used to generate specific point mutations in a working polynucleotide. This provides one means to generate specific silent point mutations, point mutations leading to corresponding amino acid changes, and point mutations that cause the generation of stop codons and the corresponding expression of polypeptide fragments.

In one aspect, each saturation mutagenesis reaction vessel contains polynucleotides encoding at least 20 progeny polypeptide (e.g., xylanases) molecules such that all 20 natural amino acids are represented at the one specific amino acid position corresponding to the codon position mutagenized in the parental polynucleotide (other aspects use less than all 20 natural combinations). The 32-fold degenerate progeny polypeptides generated from each saturation mutagenesis reaction vessel can be subjected to clonal amplification (e.g. cloned into a suitable host, e.g., *E. coli* host, using, e.g., an expression vector) and subjected to expression screening. When an individual progeny polypeptide is identified by screening to display a favorable change in property (when compared to the parental polypeptide, such as increased xylan hydrolysis activity under alkaline or acidic conditions), it can be sequenced to identify the correspondingly favorable amino acid substitution contained therein.

In one aspect, upon mutagenizing each and every amino acid position in a parental polypeptide using saturation mutagenesis as disclosed herein, favorable amino acid changes may be identified at more than one amino acid position. One or more new progeny molecules can be generated that contain a combination of all or part of these favorable amino acid substitutions. For example, if 2 specific favorable amino acid changes are identified in each of 3 amino acid positions in a polypeptide, the permutations include 3 possibilities at each position (no change from the original amino acid, and each of two favorable changes)

and 3 positions. Thus, there are 3 x 3 x 3 or 27 total possibilities, including 7 that were previously examined - 6 single point mutations (i.e. 2 at each of three positions) and no change at any position.

In yet another aspect, site-saturation mutagenesis can be used together with shuffling, chimerization, recombination and other mutagenizing processes, along with screening. This invention provides for the use of any mutagenizing process(es), including saturation mutagenesis, in an iterative manner. In one exemplification, the iterative use of any mutagenizing process(es) is used in combination with screening.

The invention also provides for the use of proprietary codon primers (containing a degenerate N,N,N sequence) to introduce point mutations into a polynucleotide, so as to generate a set of progeny polypeptides in which a full range of single amino acid substitutions is represented at each amino acid position (gene site saturated mutagenesis (GSSM™)). The oligos used are comprised contiguously of a first homologous sequence, a degenerate N,N,N sequence and preferably but not necessarily a second homologous sequence. The downstream progeny translational products from the use of such oligos include all possible amino acid changes at each amino acid site along the polypeptide, because the degeneracy of the N,N,N sequence includes codons for all 20 amino acids.

In one aspect, one such degenerate oligo (comprised of one degenerate N,N,N cassette) is used for subjecting each original codon in a parental polynucleotide template to a full range of codon substitutions. In another aspect, at least two degenerate N,N,N cassettes are used – either in the same oligo or not, for subjecting at least two original codons in a parental polynucleotide template to a full range of codon substitutions. Thus, more than one N,N,N sequence can be contained in one oligo to introduce amino acid mutations at more than one site. This plurality of N,N,N sequences can be directly contiguous, or separated by one or more additional nucleotide sequence(s). In another aspect, oligos serviceable for introducing additions and deletions can be used either alone or in combination with the codons containing an N,N,N sequence, to introduce any combination or permutation of amino acid additions, deletions and/or substitutions.

In a particular exemplification, it is possible to simultaneously mutagenize two or more contiguous amino acid positions using an oligo that contains contiguous N,N,N triplets, *i.e.* a degenerate $(N,N,N)_n$ sequence.

In another aspect, the present invention provides for the use of degenerate cassettes having less degeneracy than the N,N,N sequence. For example, it may be desirable in some instances to use (*e.g.* in an oligo) a degenerate triplet sequence comprised of only one

N, where the N can be in the first second or third position of the triplet. Any other bases including any combinations and permutations thereof can be used in the remaining two positions of the triplet. Alternatively, it may be desirable in some instances to use (*e.g.*, in an oligo) a degenerate N,N,N triplet sequence, N,N,G/T, or an N,N, G/C triplet sequence.

It is appreciated, however, that the use of a degenerate triplet (such as N,N,G/T or an N,N, G/C triplet sequence) as disclosed in the instant invention is advantageous for several reasons. In one aspect, this invention provides a means to systematically and fairly easily generate the substitution of the full range of possible amino acids (for a total of 20 amino acids) into each and every amino acid position in a polypeptide. Thus, for a 100 amino acid polypeptide, the invention provides a way to systematically and fairly easily generate 2000 distinct species (*i.e.*, 20 possible amino acids per position times 100 amino acid positions). It is appreciated that there is provided, through the use of an oligo containing a degenerate N,N,G/T or an N,N, G/C triplet sequence, 32 individual sequences that code for 20 possible amino acids. Thus, in a reaction vessel in which a parental polynucleotide sequence is subjected to saturation mutagenesis using one such oligo, there are generated 32 distinct progeny polynucleotides encoding 20 distinct polypeptides. In contrast, the use of a non-degenerate oligo in site-directed mutagenesis leads to only one progeny polypeptide product per reaction vessel.

This invention also provides for the use of nondegenerate oligos, which can optionally be used in combination with degenerate primers disclosed. It is appreciated that in some situations, it is advantageous to use nondegenerate oligos to generate specific point mutations in a working polynucleotide. This provides a means to generate specific silent point mutations, point mutations leading to corresponding amino acid changes and point mutations that cause the generation of stop codons and the corresponding expression of polypeptide fragments.

Thus, in one aspect of this invention, each saturation mutagenesis reaction vessel contains polynucleotides encoding at least 20 progeny polypeptide molecules such that all 20 amino acids are represented at the one specific amino acid position corresponding to the codon position mutagenized in the parental polynucleotide. The 32-fold degenerate progeny polypeptides generated from each saturation mutagenesis reaction vessel can be subjected to clonal amplification (*e.g.*, cloned into a suitable *E. coli* host using an expression vector) and subjected to expression screening. When an individual progeny polypeptide is identified by screening to display a favorable change in property (when compared to the

parental polypeptide), it can be sequenced to identify the correspondingly favorable amino acid substitution contained therein.

It is appreciated that upon mutagenizing each and every amino acid position in a parental polypeptide using saturation mutagenesis as disclosed herein, favorable amino acid changes may be identified at more than one amino acid position. One or more new progeny molecules can be generated that contain a combination of all or part of these favorable amino acid substitutions. For example, if 2 specific favorable amino acid changes are identified in each of 3 amino acid positions in a polypeptide, the permutations include 3 possibilities at each position (no change from the original amino acid and each of two favorable changes) and 3 positions. Thus, there are 3 x 3 x 3 or 27 total possibilities, including 7 that were previously examined - 6 single point mutations (*i.e.*, 2 at each of three positions) and no change at any position.

Thus, in a non-limiting exemplification, this invention provides for the use of saturation mutagenesis in combination with additional mutagenization processes, such as process where two or more related polynucleotides are introduced into a suitable host cell such that a hybrid polynucleotide is generated by recombination and reductive reassortment.

In addition to performing mutagenesis along the entire sequence of a gene, the instant invention provides that mutagenesis can be use to replace each of any number of bases in a polynucleotide sequence, wherein the number of bases to be mutagenized is preferably every integer from 15 to 100,000. Thus, instead of mutagenizing every position along a molecule, one can subject every or a discrete number of bases (preferably a subset totaling from 15 to 100,000) to mutagenesis. Preferably, a separate nucleotide is used for mutagenizing each position or group of positions along a polynucleotide sequence. A group of 3 positions to be mutagenized may be a codon. The mutations are preferably introduced using a mutagenic primer, containing a heterologous cassette, also referred to as a mutagenic cassette. Exemplary cassettes can have from 1 to 500 bases. Each nucleotide position in such heterologous cassettes be N, A, C, G, T, A/C, A/G, A/T, C/G, C/T, G/T, C/G/T, A/G/T, A/C/T, A/C/G, or E, where E is any base that is not A, C, G, or T (E can be referred to as a designer oligo).

In a general sense, saturation mutagenesis is comprised of mutagenizing a complete set of mutagenic cassettes (wherein each cassette is preferably about 1-500 bases in length) in defined polynucleotide sequence to be mutagenized (wherein the sequence to be mutagenized is preferably from about 15 to 100,000 bases in length). Thus, a group of mutations (ranging from 1 to 100 mutations) is introduced into each cassette to be

mutagenized. A grouping of mutations to be introduced into one cassette can be different or the same from a second grouping of mutations to be introduced into a second cassette during the application of one round of saturation mutagenesis. Such groupings are exemplified by deletions, additions, groupings of particular codons and groupings of particular nucleotide cassettes.

Defined sequences to be mutagenized include a whole gene, pathway, cDNA, an entire open reading frame (ORF) and entire promoter, enhancer, repressor/transactivator, origin of replication, intron, operator, or any polynucleotide functional group. Generally, a "defined sequences" for this purpose may be any polynucleotide that a 15 base-polynucleotide sequence and polynucleotide sequences of lengths between 15 bases and 15,000 bases (this invention specifically names every integer in between). Considerations in choosing groupings of codons include types of amino acids encoded by a degenerate mutagenic cassette.

In one exemplification a grouping of mutations that can be introduced into a mutagenic cassette, this invention specifically provides for degenerate codon substitutions (using degenerate oligos) that code for 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 and 20 amino acids at each position and a library of polypeptides encoded thereby.

Synthetic Ligation Reassembly (SLR)

The invention provides a non-stochastic gene modification system termed "synthetic ligation reassembly," or simply "SLR," a "directed evolution process," to generate polypeptides, e.g., xylanases or antibodies of the invention, with new or altered properties.

SLR is a method of ligating oligonucleotide fragments together non-stochastically. This method differs from stochastic oligonucleotide shuffling in that the nucleic acid building blocks are not shuffled, concatenated or chimerized randomly, but rather are assembled non-stochastically. See, e.g., U.S. Patent Application Serial No. (USSN) 09/332,835 entitled "Synthetic Ligation Reassembly in Directed Evolution" and filed on June 14, 1999 ("USSN 09/332,835"). In one aspect, SLR comprises the following steps: (a) providing a template polynucleotide, wherein the template polynucleotide comprises sequence encoding a homologous gene; (b) providing a plurality of building block polynucleotides, wherein the building block polynucleotides are designed to cross-over reassemble with the template polynucleotide at a predetermined sequence, and a building block polynucleotide comprises a sequence that is a variant of the homologous gene and a sequence homologous to the template polynucleotide flanking the variant sequence; (c)

combining a building block polynucleotide with a template polynucleotide such that the building block polynucleotide cross-over reassembles with the template polynucleotide to generate polynucleotides comprising homologous gene sequence variations.

SLR does not depend on the presence of high levels of homology between polynucleotides to be rearranged. Thus, this method can be used to non-stochastically generate libraries (or sets) of progeny molecules comprised of over 10^{100} different chimeras. SLR can be used to generate libraries comprised of over 10^{1000} different progeny chimeras. Thus, aspects of the present invention include non-stochastic methods of producing a set of finalized chimeric nucleic acid molecule shaving an overall assembly order that is chosen by design. This method includes the steps of generating by design a plurality of specific nucleic acid building blocks having serviceable mutually compatible ligatable ends, and assembling these nucleic acid building blocks, such that a designed overall assembly order is achieved.

The mutually compatible ligatable ends of the nucleic acid building blocks to be assembled are considered to be "serviceable" for this type of ordered assembly if they enable the building blocks to be coupled in predetermined orders. Thus, the overall assembly order in which the nucleic acid building blocks can be coupled is specified by the design of the ligatable ends. If more than one assembly step is to be used, then the overall assembly order in which the nucleic acid building blocks can be coupled is also specified by the sequential order of the assembly step(s). In one aspect, the annealed building pieces are treated with an enzyme, such as a ligase (e.g. T4 DNA ligase), to achieve covalent bonding of the building pieces.

In one aspect, the design of the oligonucleotide building blocks is obtained by analyzing a set of progenitor nucleic acid sequence templates that serve as a basis for producing a progeny set of finalized chimeric polynucleotides. These parental oligonucleotide templates thus serve as a source of sequence information that aids in the design of the nucleic acid building blocks that are to be mutagenized, e.g., chimerized or shuffled. In one aspect of this method, the sequences of a plurality of parental nucleic acid templates are aligned in order to select one or more demarcation points. The demarcation points can be located at an area of homology, and are comprised of one or more nucleotides. These demarcation points are preferably shared by at least two of the progenitor templates. The demarcation points can thereby be used to delineate the boundaries of oligonucleotide building blocks to be generated in order to rearrange the parental polynucleotides. The demarcation points identified and selected in the progenitor molecules serve as potential chimerization points in the assembly of the final chimeric progeny molecules. A demarcation

point can be an area of homology (comprised of at least one homologous nucleotide base) shared by at least two parental polynucleotide sequences. Alternatively, a demarcation point can be an area of homology that is shared by at least half of the parental polynucleotide sequences, or, it can be an area of homology that is shared by at least two thirds of the parental polynucleotide sequences. Even more preferably a serviceable demarcation points is an area of homology that is shared by at least three fourths of the parental polynucleotide sequences, or, it can be shared by at almost all of the parental polynucleotide sequences. In one aspect, a demarcation point is an area of homology that is shared by all of the parental polynucleotide sequences.

In one aspect, a ligation reassembly process is performed exhaustively in order to generate an exhaustive library of progeny chimeric polynucleotides. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same time, in another aspect, the assembly order (i.e. the order of assembly of each building block in the 5' to 3 sequence of each finalized chimeric nucleic acid) in each combination is by design (or non-stochastic) as described above. Because of the non-stochastic nature of this invention, the possibility of unwanted side products is greatly reduced.

In another aspect, the ligation reassembly method is performed systematically. For example, the method is performed in order to generate a systematically compartmentalized library of progeny molecules, with compartments that can be screened systematically, e.g. one by one. In other words this invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, a design can be achieved where specific sets of progeny products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, these methods allow a potentially very large number of progeny molecules to be examined systematically in smaller groups. Because of its ability to perform chimerizations in a manner that is highly flexible yet exhaustive and systematic as well, particularly when there is a low level of homology among the progenitor molecules, these methods provide for the generation of a library (or set) comprised of a large number of progeny molecules. Because of the non-stochastic nature of the instant ligation reassembly invention, the progeny molecules generated preferably comprise a library of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design. The saturation mutagenesis and optimized directed evolution methods also can be used to generate different progeny

molecular species. It is appreciated that the invention provides freedom of choice and control regarding the selection of demarcation points, the size and number of the nucleic acid building blocks, and the size and design of the couplings. It is appreciated, furthermore, that the requirement for intermolecular homology is highly relaxed for the operability of this invention. In fact, demarcation points can even be chosen in areas of little or no intermolecular homology. For example, because of codon wobble, i.e. the degeneracy of codons, nucleotide substitutions can be introduced into nucleic acid building blocks without altering the amino acid originally encoded in the corresponding progenitor template. Alternatively, a codon can be altered such that the coding for an originally amino acid is altered. This invention provides that such substitutions can be introduced into the nucleic acid building block in order to increase the incidence of intermolecular homologous demarcation points and thus to allow an increased number of couplings to be achieved among the building blocks, which in turn allows a greater number of progeny chimeric molecules to be generated.

Synthetic gene reassembly

In one aspect, the present invention provides a non-stochastic method termed synthetic gene reassembly (e.g., GeneReassembly™, see, e.g., U.S. Patent No. 6,537,776), which differs from stochastic shuffling in that the nucleic acid building blocks are not shuffled or concatenated or chimerized randomly, but rather are assembled non-stochastically.

The synthetic gene reassembly method does not depend on the presence of a high level of homology between polynucleotides to be shuffled. The invention can be used to non-stochastically generate libraries (or sets) of progeny molecules comprised of over 10^{100} different chimeras. Conceivably, synthetic gene reassembly can even be used to generate libraries comprised of over 10^{1000} different progeny chimeras.

Thus, in one aspect, the invention provides a non-stochastic method of producing a set of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design, which method is comprised of the steps of generating by design a plurality of specific nucleic acid building blocks having serviceable mutually compatible ligatable ends and assembling these nucleic acid building blocks, such that a designed overall assembly order is achieved.

In one aspect, synthetic gene reassembly comprises a method of: 1) preparing a progeny generation of molecule(s) (including a molecule comprising a polynucleotide

sequence, e.g., a molecule comprising a polypeptide coding sequence), that is mutagenized to achieve at least one point mutation, addition, deletion, &/or chimerization, from one or more ancestral or parental generation template(s); 2) screening the progeny generation molecule(s), e.g., using a high throughput method, for at least one property of interest (such as an improvement in an enzyme activity); 3) optionally obtaining &/or cataloguing structural &/or and functional information regarding the parental &/or progeny generation molecules; and 4) optionally repeating any of steps 1) to 3). In one aspect, there is generated (e.g., from a parent polynucleotide template), in what is termed "codon site-saturation mutagenesis," a progeny generation of polynucleotides, each having at least one set of up to three contiguous point mutations (i.e. different bases comprising a new codon), such that every codon (or every family of degenerate codons encoding the same amino acid) is represented at each codon position. Corresponding to, and encoded by, this progeny generation of polynucleotides, there is also generated a set of progeny polypeptides, each having at least one single amino acid point mutation. In a one aspect, there is generated, in what is termed "amino acid site-saturation mutagenesis", one such mutant polypeptide for each of the 19 naturally encoded polypeptide-forming alpha-amino acid substitutions at each and every amino acid position along the polypeptide. This yields, for each and every amino acid position along the parental polypeptide, a total of 20 distinct progeny polypeptides including the original amino acid, or potentially more than 21 distinct progeny polypeptides if additional amino acids are used either instead of or in addition to the 20 naturally encoded amino acids

Thus, in another aspect, this approach is also serviceable for generating mutants containing, in addition to &/or in combination with the 20 naturally encoded polypeptide-forming alpha-amino acids, other rare &/or not naturally-encoded amino acids and amino acid derivatives. In yet another aspect, this approach is also serviceable for generating mutants by the use of, in addition to &/or in combination with natural or unaltered codon recognition systems of suitable hosts, altered, mutagenized, &/or designer codon recognition systems (such as in a host cell with one or more altered tRNA molecules.

In yet another aspect, this invention relates to recombination and more specifically to a method for preparing polynucleotides encoding a polypeptide by a method of *in vivo* re-assortment of polynucleotide sequences containing regions of partial homology, assembling the polynucleotides to form at least one polynucleotide and screening the polynucleotides for the production of polypeptide(s) having a useful property.

In yet another aspect, this invention is serviceable for analyzing and cataloguing, with respect to any molecular property (e.g. an enzymatic activity) or combination of properties allowed by current technology, the effects of any mutational change achieved (including particularly saturation mutagenesis). Thus, a comprehensive method is provided for determining the effect of changing each amino acid in a parental polypeptide into each of at least 19 possible substitutions. This allows each amino acid in a parental polypeptide to be characterized and catalogued according to its spectrum of potential effects on a measurable property of the polypeptide.

In one aspect, an intron may be introduced into a chimeric progeny molecule by way of a nucleic acid building block. Introns often have consensus sequences at both termini in order to render them operational. In addition to enabling gene splicing, introns may serve an additional purpose by providing sites of homology to other nucleic acids to enable homologous recombination. For this purpose, and potentially others, it may be sometimes desirable to generate a large nucleic acid building block for introducing an intron. If the size is overly large easily generating by direct chemical synthesis of two single stranded oligos, such a specialized nucleic acid building block may also be generated by direct chemical synthesis of more than two single stranded oligos or by using a polymerase-based amplification reaction

The mutually compatible ligatable ends of the nucleic acid building blocks to be assembled are considered to be "serviceable" for this type of ordered assembly if they enable the building blocks to be coupled in predetermined orders. Thus, in one aspect, the overall assembly order in which the nucleic acid building blocks can be coupled is specified by the design of the ligatable ends and, if more than one assembly step is to be used, then the overall assembly order in which the nucleic acid building blocks can be coupled is also specified by the sequential order of the assembly step(s). In a one aspect of the invention, the annealed building pieces are treated with an enzyme, such as a ligase (*e.g.*, T4 DNA ligase) to achieve covalent bonding of the building pieces.

Coupling can occur in a manner that does not make use of every nucleotide in a participating overhang. The coupling is particularly lively to survive (e.g. in a transformed host) if the coupling reinforced by treatment with a ligase enzyme to form what may be referred to as a "gap ligation" or a "gapped ligation". This type of coupling can contribute to generation of unwanted background product(s), but it can also be used advantageously increase the diversity of the progeny library generated by the designed ligation reassembly. Certain overhangs are able to undergo self-coupling to form a palindromic coupling. A

coupling is strengthened substantially if it is reinforced by treatment with a ligase enzyme. Lack of 5' phosphates on these overhangs can be used advantageously to prevent this type of palindromic self-ligation. Accordingly, this invention provides that nucleic acid building blocks can be chemically made (or ordered) that lack a 5' phosphate group. Alternatively, they can be removed, e.g. by treatment with a phosphatase enzyme, such as a calf intestinal alkaline phosphatase (CIAP), in order to prevent palindromic self-ligations in ligation reassembly processes.

In a another aspect, the design of nucleic acid building blocks is obtained upon analysis of the sequences of a set of progenitor nucleic acid templates that serve as a basis for producing a progeny set of finalized chimeric nucleic acid molecules. These progenitor nucleic acid templates thus serve as a source of sequence information that aids in the design of the nucleic acid building blocks that are to be mutagenized, *i.e.* chimerized or shuffled.

In one exemplification, the invention provides for the chimerization of a family of related genes and their encoded family of related products. In a particular exemplification, the encoded products are enzymes. The xylanases of the present invention can be mutagenized in accordance with the methods described herein.

Thus according to one aspect of the invention, the sequences of a plurality of progenitor nucleic acid templates (*e.g.*, polynucleotides of Group A nucleic acid sequences) are aligned in order to select one or more demarcation points, which demarcation points can be located at an area of homology. The demarcation points can be used to delineate the boundaries of nucleic acid building blocks to be generated. Thus, the demarcation points identified and selected in the progenitor molecules serve as potential chimerization points in the assembly of the progeny molecules.

Typically a serviceable demarcation point is an area of homology (comprised of at least one homologous nucleotide base) shared by at least two progenitor templates, but the demarcation point can be an area of homology that is shared by at least half of the progenitor templates, at least two thirds of the progenitor templates, at least three fourths of the progenitor templates and preferably at almost all of the progenitor templates. Even more preferably still a serviceable demarcation point is an area of homology that is shared by all of the progenitor templates.

In a one aspect, the gene reassembly process is performed exhaustively in order to generate an exhaustive library. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same time, the assembly order (*i.e.* the order of assembly of each building

block in the 5' to 3 sequence of each finalized chimeric nucleic acid) in each combination is by design (or non-stochastic). Because of the non-stochastic nature of the method, the possibility of unwanted side products is greatly reduced.

In another aspect, the method provides that the gene reassembly process is performed systematically, for example to generate a systematically compartmentalized library, with compartments that can be screened systematically, *e.g.*, one by one. In other words the invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, an experimental design can be achieved where specific sets of progeny products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, it allows a potentially very large number of progeny molecules to be examined systematically in smaller groups.

Because of its ability to perform chimerizations in a manner that is highly flexible yet exhaustive and systematic as well, particularly when there is a low level of homology among the progenitor molecules, the instant invention provides for the generation of a library (or set) comprised of a large number of progeny molecules. Because of the non-stochastic nature of the instant gene reassembly invention, the progeny molecules generated preferably comprise a library of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design. In a particularly aspect, such a generated library is comprised of greater than 10^3 to greater than 10^{1000} different progeny molecular species.

In one aspect, a set of finalized chimeric nucleic acid molecules, produced as described is comprised of a polynucleotide encoding a polypeptide. According to one aspect, this polynucleotide is a gene, which may be a man-made gene. According to another aspect, this polynucleotide is a gene pathway, which may be a man-made gene pathway. The invention provides that one or more man-made genes generated by the invention may be incorporated into a man-made gene pathway, such as pathway operable in a eukaryotic organism (including a plant).

In another exemplification, the synthetic nature of the step in which the building blocks are generated allows the design and introduction of nucleotides (*e.g.*, one or more nucleotides, which may be, for example, codons or introns or regulatory sequences) that can later be optionally removed in an *in vitro* process (*e.g.*, by mutagenesis) or in an *in vivo* process (*e.g.*, by utilizing the gene splicing ability of a host organism). It is appreciated that in many instances the introduction of these nucleotides may also be desirable for many other reasons in addition to the potential benefit of creating a serviceable demarcation point.

Thus, according to another aspect, the invention provides that a nucleic acid building block can be used to introduce an intron. Thus, the invention provides that functional introns may be introduced into a man-made gene of the invention. The invention also provides that functional introns may be introduced into a man-made gene pathway of the invention. Accordingly, the invention provides for the generation of a chimeric polynucleotide that is a man-made gene containing one (or more) artificially introduced intron(s).

Accordingly, the invention also provides for the generation of a chimeric polynucleotide that is a man-made gene pathway containing one (or more) artificially introduced intron(s). Preferably, the artificially introduced intron(s) are functional in one or more host cells for gene splicing much in the way that naturally-occurring introns serve functionally in gene splicing. The invention provides a process of producing man-made intron-containing polynucleotides to be introduced into host organisms for recombination and/or splicing.

A man-made gene produced using the invention can also serve as a substrate for recombination with another nucleic acid. Likewise, a man-made gene pathway produced using the invention can also serve as a substrate for recombination with another nucleic acid. In a one aspect, the recombination is facilitated by, or occurs at, areas of homology between the man-made, intron-containing gene and a nucleic acid, which serves as a recombination partner. In one aspect, the recombination partner may also be a nucleic acid generated by the invention, including a man-made gene or a man-made gene pathway. Recombination may be facilitated by or may occur at areas of homology that exist at the one (or more) artificially introduced intron(s) in the man-made gene.

The synthetic gene reassembly method of the invention utilizes a plurality of nucleic acid building blocks, each of which preferably has two ligatable ends. The two ligatable ends on each nucleic acid building block may be two blunt ends (*i.e.* each having an overhang of zero nucleotides), or preferably one blunt end and one overhang, or more preferably still two overhangs.

A useful overhang for this purpose may be a 3' overhang or a 5' overhang. Thus, a nucleic acid building block may have a 3' overhang or alternatively a 5' overhang or alternatively two 3' overhangs or alternatively two 5' overhangs. The overall order in which the nucleic acid building blocks are assembled to form a finalized chimeric nucleic acid molecule is determined by purposeful experimental design and is not random.

In one aspect, a nucleic acid building block is generated by chemical synthesis of two single-stranded nucleic acids (also referred to as single-stranded oligos) and contacting them so as to allow them to anneal to form a double-stranded nucleic acid building block.

A double-stranded nucleic acid building block can be of variable size. The sizes of these building blocks can be small or large. Exemplary sizes for building block range from 1 base pair (not including any overhangs) to 100,000 base pairs (not including any overhangs). Other exemplary size ranges are also provided, which have lower limits of from 1 bp to 10,000 bp (including every integer value in between) and upper limits of from 2 bp to 100,000 bp (including every integer value in between).

Many methods exist by which a double-stranded nucleic acid building block can be generated that is serviceable for the invention; and these are known in the art and can be readily performed by the skilled artisan.

According to one aspect, a double-stranded nucleic acid building block is generated by first generating two single stranded nucleic acids and allowing them to anneal to form a double-stranded nucleic acid building block. The two strands of a double-stranded nucleic acid building block may be complementary at every nucleotide apart from any that form an overhang; thus containing no mismatches, apart from any overhang(s). According to another aspect, the two strands of a double-stranded nucleic acid building block are complementary at fewer than every nucleotide apart from any that form an overhang. Thus, according to this aspect, a double-stranded nucleic acid building block can be used to introduce codon degeneracy. Preferably the codon degeneracy is introduced using the site-saturation mutagenesis described herein, using one or more N,N,G/T cassettes or alternatively using one or more N,N,N cassettes.

The *in vivo* recombination method of the invention can be performed blindly on a pool of unknown hybrids or alleles of a specific polynucleotide or sequence. However, it is not necessary to know the actual DNA or RNA sequence of the specific polynucleotide.

The approach of using recombination within a mixed population of genes can be useful for the generation of any useful proteins, for example, interleukin I, antibodies, tPA and growth hormone. This approach may be used to generate proteins having altered specificity or activity. The approach may also be useful for the generation of hybrid nucleic acid sequences, for example, promoter regions, introns, exons, enhancer sequences, 31 untranslated regions or 51 untranslated regions of genes. Thus this approach may be used to generate genes having increased rates of expression. This approach may also be useful in the

study of repetitive DNA sequences. Finally, this approach may be useful to mutate ribozymes or aptamers.

In one aspect the invention described herein is directed to the use of repeated cycles of reductive reassortment, recombination and selection which allow for the directed molecular evolution of highly complex linear sequences, such as DNA, RNA or proteins thorough recombination.

Optimized Directed Evolution System

The invention provides a non-stochastic gene modification system termed "optimized directed evolution system" to generate polypeptides, e.g., xylanases or antibodies of the invention, with new or altered properties. Optimized directed evolution is directed to the use of repeated cycles of reductive reassortment, recombination and selection that allow for the directed molecular evolution of nucleic acids through recombination. Optimized directed evolution allows generation of a large population of evolved chimeric sequences, wherein the generated population is significantly enriched for sequences that have a predetermined number of crossover events.

A crossover event is a point in a chimeric sequence where a shift in sequence occurs from one parental variant to another parental variant. Such a point is normally at the juncture of where oligonucleotides from two parents are ligated together to form a single sequence. This method allows calculation of the correct concentrations of oligonucleotide sequences so that the final chimeric population of sequences is enriched for the chosen number of crossover events. This provides more control over choosing chimeric variants having a predetermined number of crossover events.

In addition, this method provides a convenient means for exploring a tremendous amount of the possible protein variant space in comparison to other systems. Previously, if one generated, for example, 10^{13} chimeric molecules during a reaction, it would be extremely difficult to test such a high number of chimeric variants for a particular activity. Moreover, a significant portion of the progeny population would have a very high number of crossover events which resulted in proteins that were less likely to have increased levels of a particular activity. By using these methods, the population of chimerics molecules can be enriched for those variants that have a particular number of crossover events. Thus, although one can still generate 10^{13} chimeric molecules during a reaction, each of the molecules chosen for further analysis most likely has, for example, only three crossover events. Because the resulting progeny population can be skewed to have a predetermined number of

crossover events, the boundaries on the functional variety between the chimeric molecules is reduced. This provides a more manageable number of variables when calculating which oligonucleotide from the original parental polynucleotides might be responsible for affecting a particular trait.

One method for creating a chimeric progeny polynucleotide sequence is to create oligonucleotides corresponding to fragments or portions of each parental sequence. Each oligonucleotide preferably includes a unique region of overlap so that mixing the oligonucleotides together results in a new variant that has each oligonucleotide fragment assembled in the correct order. Additional information can also be found, e.g., in USSN 09/332,835; U.S. Patent No. 6,361,974.

The number of oligonucleotides generated for each parental variant bears a relationship to the total number of resulting crossovers in the chimeric molecule that is ultimately created. For example, three parental nucleotide sequence variants might be provided to undergo a ligation reaction in order to find a chimeric variant having, for example, greater activity at high temperature. As one example, a set of 50 oligonucleotide sequences can be generated corresponding to each portions of each parental variant. Accordingly, during the ligation reassembly process there could be up to 50 crossover events within each of the chimeric sequences. The probability that each of the generated chimeric polynucleotides will contain oligonucleotides from each parental variant in alternating order is very low. If each oligonucleotide fragment is present in the ligation reaction in the same molar quantity it is likely that in some positions oligonucleotides from the same parental polynucleotide will ligate next to one another and thus not result in a crossover event. If the concentration of each oligonucleotide from each parent is kept constant during any ligation step in this example, there is a 1/3 chance (assuming 3 parents) that an oligonucleotide from the same parental variant will ligate within the chimeric sequence and produce no crossover.

Accordingly, a probability density function (PDF) can be determined to predict the population of crossover events that are likely to occur during each step in a ligation reaction given a set number of parental variants, a number of oligonucleotides corresponding to each variant, and the concentrations of each variant during each step in the ligation reaction. The statistics and mathematics behind determining the PDF is described below. By utilizing these methods, one can calculate such a probability density function, and thus enrich the chimeric progeny population for a predetermined number of crossover events resulting from a particular ligation reaction. Moreover, a target number of crossover events can be predetermined, and the system then programmed to calculate the starting quantities of

each parental oligonucleotide during each step in the ligation reaction to result in a probability density function that centers on the predetermined number of crossover events. These methods are directed to the use of repeated cycles of reductive reassortment, recombination and selection that allow for the directed molecular evolution of a nucleic acid encoding a polypeptide through recombination. This system allows generation of a large population of evolved chimeric sequences, wherein the generated population is significantly enriched for sequences that have a predetermined number of crossover events. A crossover event is a point in a chimeric sequence where a shift in sequence occurs from one parental variant to another parental variant. Such a point is normally at the juncture of where oligonucleotides from two parents are ligated together to form a single sequence. The method allows calculation of the correct concentrations of oligonucleotide sequences so that the final chimeric population of sequences is enriched for the chosen number of crossover events. This provides more control over choosing chimeric variants having a predetermined number of crossover events.

In addition, these methods provide a convenient means for exploring a tremendous amount of the possible protein variant space in comparison to other systems. By using the methods described herein, the population of chimerics molecules can be enriched for those variants that have a particular number of crossover events. Thus, although one can still generate 10^{13} chimeric molecules during a reaction, each of the molecules chosen for further analysis most likely has, for example, only three crossover events. Because the resulting progeny population can be skewed to have a predetermined number of crossover events, the boundaries on the functional variety between the chimeric molecules is reduced. This provides a more manageable number of variables when calculating which oligonucleotide from the original parental polynucleotides might be responsible for affecting a particular trait.

In one aspect, the method creates a chimeric progeny polynucleotide sequence by creating oligonucleotides corresponding to fragments or portions of each parental sequence. Each oligonucleotide preferably includes a unique region of overlap so that mixing the oligonucleotides together results in a new variant that has each oligonucleotide fragment assembled in the correct order. See also USSN 09/332,835.

Determining Crossover Events

Aspects of the invention include a system and software that receive a desired crossover probability density function (PDF), the number of parent genes to be reassembled,

and the number of fragments in the reassembly as inputs. The output of this program is a "fragment PDF" that can be used to determine a recipe for producing reassembled genes, and the estimated crossover PDF of those genes. The processing described herein is preferably performed in MATLAB™ (The Mathworks, Natick, Massachusetts) a programming language and development environment for technical computing.

Iterative Processes

In practicing the invention, these processes can be iteratively repeated. For example, a nucleic acid (or, the nucleic acid) responsible for an altered or new xylanase phenotype is identified, re-isolated, again modified, re-tested for activity. This process can be iteratively repeated until a desired phenotype is engineered. For example, an entire biochemical anabolic or catabolic pathway can be engineered into a cell, including, e.g., xylanase activity.

Similarly, if it is determined that a particular oligonucleotide has no affect at all on the desired trait (e.g., a new xylanase phenotype), it can be removed as a variable by synthesizing larger parental oligonucleotides that include the sequence to be removed. Since incorporating the sequence within a larger sequence prevents any crossover events, there will no longer be any variation of this sequence in the progeny polynucleotides. This iterative practice of determining which oligonucleotides are most related to the desired trait, and which are unrelated, allows more efficient exploration all of the possible protein variants that might be provide a particular trait or activity.

In vivo shuffling

In vivo shuffling of molecules is use in methods of the invention that provide variants of polypeptides of the invention, e.g., antibodies, xylanases, and the like. *In vivo* shuffling can be performed utilizing the natural property of cells to recombine multimers. While recombination *in vivo* has provided the major natural route to molecular diversity, genetic recombination remains a relatively complex process that involves 1) the recognition of homologies; 2) strand cleavage, strand invasion, and metabolic steps leading to the production of recombinant chiasma; and finally 3) the resolution of chiasma into discrete recombined molecules. The formation of the chiasma requires the recognition of homologous sequences.

In another aspect, the invention includes a method for producing a hybrid polynucleotide from at least a first polynucleotide and a second polynucleotide. The invention can be used to produce a hybrid polynucleotide by introducing at least a first

polynucleotide and a second polynucleotide which share at least one region of partial sequence homology (*e.g.*, SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45 , 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257 and combinations thereof) into a suitable host cell. The regions of partial sequence homology promote processes which result in sequence reorganization producing a hybrid polynucleotide. The term "hybrid polynucleotide", as used herein, is any nucleotide sequence which results from the method of the present invention and contains sequence from at least two original polynucleotide sequences. Such hybrid polynucleotides can result from intermolecular recombination events which promote sequence integration between DNA molecules. In addition, such hybrid polynucleotides can result from intramolecular reductive reassortment processes which utilize repeated sequences to alter a nucleotide sequence within a DNA molecule.

In *vivo* reassortment is focused on "inter-molecular" processes collectively referred to as "recombination" which in bacteria, is generally viewed as a "RecA-dependent" phenomenon. The invention can rely on recombination processes of a host cell to recombine and re-assort sequences, or the cells' ability to mediate reductive processes to decrease the complexity of quasi-repeated sequences in the cell by deletion. This process of "reductive reassortment" occurs by an "intra-molecular", RecA-independent process.

Therefore, in another aspect of the invention, novel polynucleotides can be generated by the process of reductive reassortment. The method involves the generation of constructs containing consecutive sequences (original encoding sequences), their insertion into an appropriate vector and their subsequent introduction into an appropriate host cell. The reassortment of the individual molecular identities occurs by combinatorial processes between the consecutive sequences in the construct possessing regions of homology, or between quasi-repeated units. The reassortment process recombines and/or reduces the complexity and extent of the repeated sequences and results in the production of novel molecular species. Various treatments may be applied to enhance the rate of reassortment. These could include treatment with ultra-violet light, or DNA damaging chemicals and/or the use of host cell lines displaying enhanced levels of "genetic instability". Thus the

reassortment process may involve homologous recombination or the natural property of quasi-repeated sequences to direct their own evolution.

Repeated or "quasi-repeated" sequences play a role in genetic instability. In the present invention, "quasi-repeats" are repeats that are not restricted to their original unit structure. Quasi-repeated units can be presented as an array of sequences in a construct; consecutive units of similar sequences. Once ligated, the junctions between the consecutive sequences become essentially invisible and the quasi-repetitive nature of the resulting construct is now continuous at the molecular level. The deletion process the cell performs to reduce the complexity of the resulting construct operates between the quasi-repeated sequences. The quasi-repeated units provide a practically limitless repertoire of templates upon which slippage events can occur. The constructs containing the quasi-repeats thus effectively provide sufficient molecular elasticity that deletion (and potentially insertion) events can occur virtually anywhere within the quasi-repetitive units.

When the quasi-repeated sequences are all ligated in the same orientation, for instance head to tail or vice versa, the cell cannot distinguish individual units. Consequently, the reductive process can occur throughout the sequences. In contrast, when for example, the units are presented head to head, rather than head to tail, the inversion delineates the endpoints of the adjacent unit so that deletion formation will favor the loss of discrete units. Thus, it is preferable with the present method that the sequences are in the same orientation. Random orientation of quasi-repeated sequences will result in the loss of reassortment efficiency, while consistent orientation of the sequences will offer the highest efficiency. However, while having fewer of the contiguous sequences in the same orientation decreases the efficiency, it may still provide sufficient elasticity for the effective recovery of novel molecules. Constructs can be made with the quasi-repeated sequences in the same orientation to allow higher efficiency.

Sequences can be assembled in a head to tail orientation using any of a variety of methods, including the following:

a) Primers that include a poly-A head and poly-T tail which when made single-stranded would provide orientation can be utilized. This is accomplished by having the first few bases of the primers made from RNA and hence easily removed RNAseH.

b) Primers that include unique restriction cleavage sites can be utilized. Multiple sites, a battery of unique sequences and repeated synthesis and ligation steps would be required.

c) The inner few bases of the primer could be thiolated and an exonuclease used to produce properly tailed molecules.

The recovery of the re-assorted sequences relies on the identification of cloning vectors with a reduced repetitive index (RI). The re-assorted encoding sequences can then be recovered by amplification. The products are re-cloned and expressed. The recovery of cloning vectors with reduced RI can be affected by:

1) The use of vectors only stably maintained when the construct is reduced in complexity.
2) The physical recovery of shortened vectors by physical procedures. In this case, the cloning vector would be recovered using standard plasmid isolation procedures and size fractionated on either an agarose gel, or column with a low molecular weight cut off utilizing standard procedures.
3) The recovery of vectors containing interrupted genes which can be selected when insert size decreases.
4) The use of direct selection techniques with an expression vector and the appropriate selection.

Encoding sequences (for example, genes) from related organisms may demonstrate a high degree of homology and encode quite diverse protein products. These types of sequences are particularly useful in the present invention as quasi-repeats. However, while the examples illustrated below demonstrate the reassortment of nearly identical original encoding sequences (quasi-repeats), this process is not limited to such nearly identical repeats.

The following example demonstrates a method of the invention. Encoding nucleic acid sequences (quasi-repeats) derived from three (3) unique species are described. Each sequence encodes a protein with a distinct set of properties. Each of the sequences differs by a single or a few base pairs at a unique position in the sequence. The quasi-repeated sequences are separately or collectively amplified and ligated into random assemblies such that all possible permutations and combinations are available in the population of ligated molecules. The number of quasi-repeat units can be controlled by the assembly conditions. The average number of quasi-repeated units in a construct is defined as the repetitive index (RI).

Once formed, the constructs may, or may not be size fractionated on an agarose gel according to published protocols, inserted into a cloning vector and transfected

into an appropriate host cell. The cells are then propagated and "reductive reassortment" is effected. The rate of the reductive reassortment process may be stimulated by the introduction of DNA damage if desired. Whether the reduction in RI is mediated by deletion formation between repeated sequences by an "intra-molecular" mechanism, or mediated by recombination-like events through "inter-molecular" mechanisms is immaterial. The end result is a reassortment of the molecules into all possible combinations.

Optionally, the method comprises the additional step of screening the library members of the shuffled pool to identify individual shuffled library members having the ability to bind or otherwise interact, or catalyze a particular reaction (*e.g.*, such as catalytic domain of an enzyme) with a predetermined macromolecule, such as for example a proteinaceous receptor, an oligosaccharide, virion, or other predetermined compound or structure.

The polypeptides that are identified from such libraries can be used for therapeutic, diagnostic, research and related purposes (*e.g.*, catalysts, solutes for increasing osmolarity of an aqueous solution and the like) and/or can be subjected to one or more additional cycles of shuffling and/or selection.

In another aspect, it is envisioned that prior to or during recombination or reassortment, polynucleotides generated by the method of the invention can be subjected to agents or processes which promote the introduction of mutations into the original polynucleotides. The introduction of such mutations would increase the diversity of resulting hybrid polynucleotides and polypeptides encoded therefrom. The agents or processes which promote mutagenesis can include, but are not limited to: (+)-CC-1065, or a synthetic analog such as (+)-CC-1065-(N3-Adenine (*See* Sun and Hurley, (1992); an N-acetylated or deacetylated 4'-fluro-4-aminobiphenyl adduct capable of inhibiting DNA synthesis (*See* , for example, van de Poll *et al.* (1992)); or a N-acetylated or deacetylated 4-aminobiphenyl adduct capable of inhibiting DNA synthesis (*See* also, van de Poll *et al.* (1992), pp. 751-758); trivalent chromium, a trivalent chromium salt, a polycyclic aromatic hydrocarbon (PAH) DNA adduct capable of inhibiting DNA replication, such as 7-bromomethyl-benz[*a*]anthracene ("BMA"), tris(2,3-dibromopropyl)phosphate ("Tris-BP"), 1,2-dibromo-3-chloropropane ("DBCP"), 2-bromoacrolein (2BA), benzo[*a*]pyrene-7,8-dihydrodiol-9-10-epoxide ("BPDE"), a platinum(II) halogen salt, N-hydroxy-2-amino-3-methylimidazo[4,5-*f*]-quinoline ("N-hydroxy-IQ") and N-hydroxy-2-amino-1-methyl-6-phenylimidazo[4,5-*f*]-pyridine ("N-hydroxy-PhIP"). Exemplary means for slowing or halting PCR amplification consist of UV light (+)-CC-1065 and (+)-CC-1065-(N3-Adenine). Particularly encompassed

means are DNA adducts or polynucleotides comprising the DNA adducts from the polynucleotides or polynucleotides pool, which can be released or removed by a process including heating the solution comprising the polynucleotides prior to further processing.

In another aspect the invention is directed to a method of producing recombinant proteins having biological activity by treating a sample comprising double-stranded template polynucleotides encoding a wild-type protein under conditions according to the invention which provide for the production of hybrid or re-assorted polynucleotides.

Producing sequence variants

The invention also provides additional methods for making sequence variants of the nucleic acid (e.g., xylanase) sequences of the invention. The invention also provides additional methods for isolating xylanases using the nucleic acids and polypeptides of the invention. In one aspect, the invention provides for variants of a xylanase coding sequence (e.g., a gene, cDNA or message) of the invention, which can be altered by any means, including, e.g., random or stochastic methods, or, non-stochastic, or "directed evolution," methods, as described above.

The isolated variants may be naturally occurring. Variant can also be created *in vitro*. Variants may be created using genetic engineering techniques such as site directed mutagenesis, random chemical mutagenesis, Exonuclease III deletion procedures, and standard cloning techniques. Alternatively, such variants, fragments, analogs, or derivatives may be created using chemical synthesis or modification procedures. Other methods of making variants are also familiar to those skilled in the art. These include procedures in which nucleic acid sequences obtained from natural isolates are modified to generate nucleic acids which encode polypeptides having characteristics which enhance their value in industrial or laboratory applications. In such procedures, a large number of variant sequences having one or more nucleotide differences with respect to the sequence obtained from the natural isolate are generated and characterized. These nucleotide differences can result in amino acid changes with respect to the polypeptides encoded by the nucleic acids from the natural isolates.

For example, variants may be created using error prone PCR. In error prone PCR, PCR is performed under conditions where the copying fidelity of the DNA polymerase is low, such that a high rate of point mutations is obtained along the entire length of the PCR product. Error prone PCR is described, e.g., in Leung, D.W., et al., Technique, 1:11-15, 1989) and Caldwell, R. C. & Joyce G.F., PCR Methods Applic., 2:28-33, 1992. Briefly, in

such procedures, nucleic acids to be mutagenized are mixed with PCR primers, reaction buffer, $MgCl_2$, $MnCl_2$, Taq polymerase and an appropriate concentration of dNTPs for achieving a high rate of point mutation along the entire length of the PCR product. For example, the reaction may be performed using 20 fmoles of nucleic acid to be mutagenized, 30 pmole of each PCR primer, a reaction buffer comprising 50mM KCl, 10mM Tris HCl (pH 8.3) and 0.01% gelatin, 7mM MgCl2, 0.5mM $MnCl_2$, 5 units of Taq polymerase, 0.2mM dGTP, 0.2mM dATP, 1mM dCTP, and 1mM dTTP. PCR may be performed for 30 cycles of 94°C for 1 min, 45°C for 1 min, and 72°C for 1 min. However, it will be appreciated that these parameters may be varied as appropriate. The mutagenized nucleic acids are cloned into an appropriate vector and the activities of the polypeptides encoded by the mutagenized nucleic acids are evaluated.

Variants may also be created using oligonucleotide directed mutagenesis to generate site-specific mutations in any cloned DNA of interest. Oligonucleotide mutagenesis is described, e.g., in Reidhaar-Olson (1988) Science 241:53-57. Briefly, in such procedures a plurality of double stranded oligonucleotides bearing one or more mutations to be introduced into the cloned DNA are synthesized and inserted into the cloned DNA to be mutagenized. Clones containing the mutagenized DNA are recovered and the activities of the polypeptides they encode are assessed.

Another method for generating variants is assembly PCR. Assembly PCR involves the assembly of a PCR product from a mixture of small DNA fragments. A large number of different PCR reactions occur in parallel in the same vial, with the products of one reaction priming the products of another reaction. Assembly PCR is described in, e.g., U.S. Patent No. 5,965,408.

Still another method of generating variants is sexual PCR mutagenesis. In sexual PCR mutagenesis, forced homologous recombination occurs between DNA molecules of different but highly related DNA sequence *in vitro*, as a result of random fragmentation of the DNA molecule based on sequence homology, followed by fixation of the crossover by primer extension in a PCR reaction. Sexual PCR mutagenesis is described, e.g., in Stemmer (1994) Proc. Natl. Acad. Sci. USA 91:10747-10751. Briefly, in such procedures a plurality of nucleic acids to be recombined are digested with DNase to generate fragments having an average size of 50-200 nucleotides. Fragments of the desired average size are purified and resuspended in a PCR mixture. PCR is conducted under conditions which facilitate recombination between the nucleic acid fragments. For example, PCR may be performed by resuspending the purified fragments at a concentration of 10-30ng/μl in a solution of 0.2mM

of each dNTP, 2.2mM $MgCl_2$, 50mM KCL, 10mM Tris HCl, pH 9.0, and 0.1% Triton X-100. 2.5 units of Taq polymerase per 100:l of reaction mixture is added and PCR is performed using the following regime: 94°C for 60 seconds, 94°C for 30 seconds, 50-55°C for 30 seconds, 72°C for 30 seconds (30-45 times) and 72°C for 5 minutes. However, it will be appreciated that these parameters may be varied as appropriate. In some aspects, oligonucleotides may be included in the PCR reactions. In other aspects, the Klenow fragment of DNA polymerase I may be used in a first set of PCR reactions and Taq polymerase may be used in a subsequent set of PCR reactions. Recombinant sequences are isolated and the activities of the polypeptides they encode are assessed.

Variants may also be created by *in vivo* mutagenesis. In some aspects, random mutations in a sequence of interest are generated by propagating the sequence of interest in a bacterial strain, such as an E. coli strain, which carries mutations in one or more of the DNA repair pathways. Such "mutator" strains have a higher random mutation rate than that of a wild-type parent. Propagating the DNA in one of these strains will eventually generate random mutations within the DNA. Mutator strains suitable for use for *in vivo* mutagenesis are described in PCT Publication No. WO 91/16427, published October 31, 1991, entitled "Methods for Phenotype Creation from Multiple Gene Populations".

Variants may also be generated using cassette mutagenesis. In cassette mutagenesis a small region of a double stranded DNA molecule is replaced with a synthetic oligonucleotide "cassette" that differs from the native sequence. The oligonucleotide often contains completely and/or partially randomized native sequence.

Recursive ensemble mutagenesis may also be used to generate variants. Recursive ensemble mutagenesis is an algorithm for protein engineering (protein mutagenesis) developed to produce diverse populations of phenotypically related mutants whose members differ in amino acid sequence. This method uses a feedback mechanism to control successive rounds of combinatorial cassette mutagenesis. Recursive ensemble mutagenesis is described in Arkin, A.P. and Youvan, D.C., PNAS, USA, 89:7811-7815, 1992.

In some aspects, variants are created using exponential ensemble mutagenesis. Exponential ensemble mutagenesis is a process for generating combinatorial libraries with a high percentage of unique and functional mutants, wherein small groups of residues are randomized in parallel to identify, at each altered position, amino acids which lead to functional proteins. Exponential ensemble mutagenesis is described in Delegrave, S. and Youvan, D.C., Biotechnology Research, 11:1548-1552, 1993. Random and site-directed

mutagenesis are described in Arnold, F.H., Current Opinion in Biotechnology, 4:450-455, 1993.

In some aspects, the variants are created using shuffling procedures wherein portions of a plurality of nucleic acids which encode distinct polypeptides are fused together to create chimeric nucleic acid sequences which encode chimeric polypeptides as described in U.S. Patent No. 5,965,408, filed July 9, 1996, entitled, "Method of DNA Reassembly by Interrupting Synthesis" and U.S. Patent No. 5,939,250, filed May 22, 1996, entitled, "Production of Enzymes Having Desired Activities by Mutagenesis.

The variants of the polypeptides of Group B amino acid sequences may be variants in which one or more of the amino acid residues of the polypeptides of the Group B amino acid sequences are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code.

Conservative substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the following replacements: replacements of an aliphatic amino acid such as Alanine, Valine, Leucine and Isoleucine with another aliphatic amino acid; replacement of a Serine with a Threonine or vice versa; replacement of an acidic residue such as Aspartic acid and Glutamic acid with another acidic residue; replacement of a residue bearing an amide group, such as Asparagine and Glutamine, with another residue bearing an amide group; exchange of a basic residue such as Lysine and Arginine with another basic residue; and replacement of an aromatic residue such as Phenylalanine, Tyrosine with another aromatic residue.

Other variants are those in which one or more of the amino acid residues of the polypeptides of the Group B amino acid sequences includes a substituent group.

Still other variants are those in which the polypeptide is associated with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol).

Additional variants are those in which additional amino acids are fused to the polypeptide, such as a leader sequence, a secretory sequence, a proprotein sequence or a sequence which facilitates purification, enrichment, or stabilization of the polypeptide.

In some aspects, the fragments, derivatives and analogs retain the same biological function or activity as the polypeptides of Group B amino acid sequences and sequences substantially identical thereto. In other aspects, the fragment, derivative, or analog

includes a proprotein, such that the fragment, derivative, or analog can be activated by cleavage of the proprotein portion to produce an active polypeptide.

Optimizing codons to achieve high levels of protein expression in host cells

The invention provides methods for modifying xylanase-encoding nucleic acids to modify codon usage. In one aspect, the invention provides methods for modifying codons in a nucleic acid encoding a xylanase to increase or decrease its expression in a host cell. The invention also provides nucleic acids encoding a xylanase modified to increase its expression in a host cell, xylanase so modified, and methods of making the modified xylanases. The method comprises identifying a "non-preferred" or a "less preferred" codon in xylanase-encoding nucleic acid and replacing one or more of these non-preferred or less preferred codons with a "preferred codon" encoding the same amino acid as the replaced codon and at least one non-preferred or less preferred codon in the nucleic acid has been replaced by a preferred codon encoding the same amino acid. A preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell.

Host cells for expressing the nucleic acids, expression cassettes and vectors of the invention include bacteria, yeast, fungi, plant cells, insect cells and mammalian cells. Thus, the invention provides methods for optimizing codon usage in all of these cells, codon-altered nucleic acids and polypeptides made by the codon-altered nucleic acids. Exemplary host cells include gram negative bacteria, such as *Escherichia coli* and *Pseudomonas* fluorescens; gram positive bacteria, such as *Streptomyces diversa*, *Lactobacillus gasseri*, *Lactococcus lactis*, *Lactococcus cremoris*, *Bacillus subtilis*. Exemplary host cells also include eukaryotic organisms, e.g., various yeast, such as *Saccharomyces* sp., including *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, and *Kluyveromyces lactis*, *Hansenula polymorpha*, *Aspergillus niger*, and mammalian cells and cell lines and insect cells and cell lines. Thus, the invention also includes nucleic acids and polypeptides optimized for expression in these organisms and species.

For example, the codons of a nucleic acid encoding a xylanase isolated from a bacterial cell are modified such that the nucleic acid is optimally expressed in a bacterial cell different from the bacteria from which the xylanase was derived, a yeast, a fungi, a plant cell, an insect cell or a mammalian cell. Methods for optimizing codons are well known in the art, see, e.g., U.S. Patent No. 5,795,737; Baca (2000) Int. J. Parasitol. 30:113-118; Hale (1998) Protein Expr. Purif. 12:185-188; Narum (2001) Infect. Immun. 69:7250-7253. See also

Narum (2001) Infect. Immun. 69:7250-7253, describing optimizing codons in mouse systems; Outchkourov (2002) Protein Expr. Purif. 24:18-24, describing optimizing codons in yeast; Feng (2000) Biochemistry 39:15399-15409, describing optimizing codons in *E. coli*; Humphreys (2000) Protein Expr. Purif. 20:252-264, describing optimizing codon usage that affects secretion in *E. coli*.

Transgenic non-human animals

The invention provides transgenic non-human animals comprising a nucleic acid, a polypeptide (e.g., a xylanase), an expression cassette or vector or a transfected or transformed cell of the invention. The invention also provides methods of making and using these transgenic non-human animals.

The transgenic non-human animals can be, e.g., goats, rabbits, sheep, pigs, cows, rats and mice, comprising the nucleic acids of the invention. These animals can be used, e.g., as *in vivo* models to study xylanase activity, or, as models to screen for agents that change the xylanase activity *in vivo*. The coding sequences for the polypeptides to be expressed in the transgenic non-human animals can be designed to be constitutive, or, under the control of tissue-specific, developmental-specific or inducible transcriptional regulatory factors. Transgenic non-human animals can be designed and generated using any method known in the art; see, e.g., U.S. Patent Nos. 6,211,428; 6,187,992; 6,156,952; 6,118,044; 6,111,166; 6,107,541; 5,959,171; 5,922,854; 5,892,070; 5,880,327; 5,891,698; 5,639,940; 5,573,933; 5,387,742; 5,087,571, describing making and using transformed cells and eggs and transgenic mice, rats, rabbits, sheep, pigs and cows. See also, e.g., Pollock (1999) J. Immunol. Methods 231:147-157, describing the production of recombinant proteins in the milk of transgenic dairy animals; Baguisi (1999) Nat. Biotechnol. 17:456-461, demonstrating the production of transgenic goats. U.S. Patent No. 6,211,428, describes making and using transgenic non-human mammals which express in their brains a nucleic acid construct comprising a DNA sequence. U.S. Patent No. 5,387,742, describes injecting cloned recombinant or synthetic DNA sequences into fertilized mouse eggs, implanting the injected eggs in pseudo-pregnant females, and growing to term transgenic mice whose cells express proteins related to the pathology of Alzheimer's disease. U.S. Patent No. 6,187,992, describes making and using a transgenic mouse whose genome comprises a disruption of the gene encoding amyloid precursor protein (APP).

"Knockout animals" can also be used to practice the methods of the invention. For example, in one aspect, the transgenic or modified animals of the invention comprise a "knockout animal," e.g., a "knockout mouse," engineered not to express an endogenous gene,

which is replaced with a gene expressing a xylanase of the invention, or, a fusion protein comprising a xylanase of the invention.

Transgenic Plants and Seeds

The invention provides transgenic plants and seeds comprising a nucleic acid, a polypeptide (e.g., a xylanase), an expression cassette or vector or a transfected or transformed cell of the invention. The invention also provides plant products, e.g., oils, seeds, leaves, extracts and the like, comprising a nucleic acid and/or a polypeptide (e.g., a xylanase) of the invention. The transgenic plant can be dicotyledonous (a dicot) or monocotyledonous (a monocot). The invention also provides methods of making and using these transgenic plants and seeds. The transgenic plant or plant cell expressing a polypeptide of the present invention may be constructed in accordance with any method known in the art. See, for example, U.S. Patent No. 6,309,872.

Nucleic acids and expression constructs of the invention can be introduced into a plant cell by any means. For example, nucleic acids or expression constructs can be introduced into the genome of a desired plant host, or, the nucleic acids or expression constructs can be episomes. Introduction into the genome of a desired plant can be such that the host's xylanase production is regulated by endogenous transcriptional or translational control elements. The invention also provides "knockout plants" where insertion of gene sequence by, e.g., homologous recombination, has disrupted the expression of the endogenous gene. Means to generate "knockout" plants are well-known in the art, see, e.g., Strepp (1998) Proc Natl. Acad. Sci. USA 95:4368-4373; Miao (1995) Plant J 7:359-365. See discussion on transgenic plants, below.

The nucleic acids of the invention can be used to confer desired traits on essentially any plant, e.g., on starch-producing plants, such as potato, wheat, rice, barley, and the like. Nucleic acids of the invention can be used to manipulate metabolic pathways of a plant in order to optimize or alter host's expression of xylanase. The can change xylanase activity in a plant. Alternatively, a xylanase of the invention can be used in production of a transgenic plant to produce a compound not naturally produced by that plant. This can lower production costs or create a novel product.

In one aspect, the first step in production of a transgenic plant involves making an expression construct for expression in a plant cell. These techniques are well known in the art. They can include selecting and cloning a promoter, a coding sequence for facilitating efficient binding of ribosomes to mRNA and selecting the appropriate gene terminator sequences. One exemplary constitutive promoter is CaMV35S, from the cauliflower mosaic

virus, which generally results in a high degree of expression in plants. Other promoters are more specific and respond to cues in the plant's internal or external environment. An exemplary light-inducible promoter is the promoter from the cab gene, encoding the major chlorophyll a/b binding protein.

In one aspect, the nucleic acid is modified to achieve greater expression in a plant cell. For example, a sequence of the invention is likely to have a higher percentage of A-T nucleotide pairs compared to that seen in a plant, some of which prefer G-C nucleotide pairs. Therefore, A-T nucleotides in the coding sequence can be substituted with G-C nucleotides without significantly changing the amino acid sequence to enhance production of the gene product in plant cells.

Selectable marker gene can be added to the gene construct in order to identify plant cells or tissues that have successfully integrated the transgene. This may be necessary because achieving incorporation and expression of genes in plant cells is a rare event, occurring in just a few percent of the targeted tissues or cells. Selectable marker genes encode proteins that provide resistance to agents that are normally toxic to plants, such as antibiotics or herbicides. Only plant cells that have integrated the selectable marker gene will survive when grown on a medium containing the appropriate antibiotic or herbicide. As for other inserted genes, marker genes also require promoter and termination sequences for proper function.

In one aspect, making transgenic plants or seeds comprises incorporating sequences of the invention and, optionally, marker genes into a target expression construct (e.g., a plasmid), along with positioning of the promoter and the terminator sequences. This can involve transferring the modified gene into the plant through a suitable method. For example, a construct may be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation and microinjection of plant cell protoplasts, or the constructs can be introduced directly to plant tissue using ballistic methods, such as DNA particle bombardment. For example, see, e.g., Christou (1997) Plant Mol. Biol. 35:197-203; Pawlowski (1996) Mol. Biotechnol. 6:17-30; Klein (1987) Nature 327:70-73; Takumi (1997) Genes Genet. Syst. 72:63-69, discussing use of particle bombardment to introduce transgenes into wheat; and Adam (1997) supra, for use of particle bombardment to introduce YACs into plant cells. For example, Rinehart (1997) supra, used particle bombardment to generate transgenic cotton plants. Apparatus for accelerating particles is described U.S. Pat. No. 5,015,580; and, the commercially available BioRad (Biolistics) PDS-2000 particle

acceleration instrument; see also, John, U.S. Patent No. 5,608,148; and Ellis, U.S. Patent No. 5, 681,730, describing particle-mediated transformation of gymnosperms.

In one aspect, protoplasts can be immobilized and injected with a nucleic acids, e.g., an expression construct. Although plant regeneration from protoplasts is not easy with cereals, plant regeneration is possible in legumes using somatic embryogenesis from protoplast derived callus. Organized tissues can be transformed with naked DNA using gene gun technique, where DNA is coated on tungsten microprojectiles, shot 1/100th the size of cells, which carry the DNA deep into cells and organelles. Transformed tissue is then induced to regenerate, usually by somatic embryogenesis. This technique has been successful in several cereal species including maize and rice.

Nucleic acids, e.g., expression constructs, can also be introduced in to plant cells using recombinant viruses. Plant cells can be transformed using viral vectors, such as, e.g., tobacco mosaic virus derived vectors (Rouwendal (1997) Plant Mol. Biol. 33:989-999), see Porta (1996) "Use of viral replicons for the expression of genes in plants," Mol. Biotechnol. 5:209-221.

Alternatively, nucleic acids, e.g., an expression construct, can be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. *Agrobacterium tumefaciens*-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, e.g., Horsch (1984) *Science* 233:496-498; Fraley (1983) *Proc. Natl. Acad. Sci. USA* 80:4803 (1983); *Gene Transfer to Plants*, Potrykus, ed. (Springer-Verlag, Berlin 1995). The DNA in an A. *tumefaciens* cell is contained in the bacterial chromosome as well as in another structure known as a Ti (tumor-inducing) plasmid. The Ti plasmid contains a stretch of DNA termed T-DNA (~20 kb long) that is transferred to the plant cell in the infection process and a series of vir (virulence) genes that direct the infection process. *A. tumefaciens* can only infect a plant through wounds: when a plant root or stem is wounded it gives off certain chemical signals, in response to which, the vir genes of *A. tumefaciens* become activated and direct a series of events necessary for the transfer of the T-DNA from the Ti plasmid to the plant's chromosome. The T-DNA then enters the plant cell through the wound. One speculation is that the T-DNA waits until the plant DNA is being replicated or transcribed, then inserts itself into the exposed plant DNA. In order to use *A. tumefaciens* as a transgene vector, the tumor-inducing section of T-DNA have to be removed, while retaining the T-DNA border regions

and the vir genes. The transgene is then inserted between the T-DNA border regions, where it is transferred to the plant cell and becomes integrated into the plant's chromosomes.

The invention provides for the transformation of monocotyledonous plants using the nucleic acids of the invention, including important cereals, see Hiei (1997) Plant Mol. Biol. 35:205-218. See also, *e.g.*, Horsch, Science (1984) 233:496; Fraley (1983) Proc. Natl. Acad. Sci USA 80:4803; Thykjaer (1997) supra; Park (1996) Plant Mol. Biol. 32:1135-1148, discussing T-DNA integration into genomic DNA. See also D'Halluin, U.S. Patent No. 5,712,135, describing a process for the stable integration of a DNA comprising a gene that is functional in a cell of a cereal, or other monocotyledonous plant.

In one aspect, the third step can involve selection and regeneration of whole plants capable of transmitting the incorporated target gene to the next generation. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker that has been introduced together with the desired nucleotide sequences. Plant regeneration from cultured protoplasts is described in Evans et al., *Protoplasts Isolation and Culture, Handbook of Plant Cell Culture*, pp. 124-176, MacMillilan Publishing Company, New York, 1983; and Binding, *Regeneration of Plants, Plant Protoplasts*, pp. 21-73, CRC Press, Boca Raton, 1985. Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee (1987) Ann. Rev. of Plant Phys. 38:467-486. To obtain whole plants from transgenic tissues such as immature embryos, they can be grown under controlled environmental conditions in a series of media containing nutrients and hormones, a process known as tissue culture. Once whole plants are generated and produce seed, evaluation of the progeny begins.

After the expression cassette is stably incorporated in transgenic plants, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. Since transgenic expression of the nucleic acids of the invention leads to phenotypic changes, plants comprising the recombinant nucleic acids of the invention can be sexually crossed with a second plant to obtain a final product. Thus, the seed of the invention can be derived from a cross between two transgenic plants of the invention, or a cross between a plant of the invention and another plant. The desired effects (e.g., expression of the polypeptides of the invention to produce a plant in which flowering behavior is altered) can be enhanced when both parental plants express the polypeptides (e.g., a xylanase) of the invention. The desired effects can be passed to future plant generations by standard propagation means.

The nucleic acids and polypeptides of the invention are expressed in or inserted in any plant or seed. Transgenic plants of the invention can be dicotyledonous or monocotyledonous. Examples of monocot transgenic plants of the invention are grasses, such as meadow grass (blue grass, *Poa*), forage grass such as festuca, lolium, temperate grass, such as *Agrostis*, and cereals, e.g., wheat, oats, rye, barley, rice, sorghum, and maize (corn). Examples of dicot transgenic plants of the invention are tobacco, legumes, such as lupins, potato, sugar beet, pea, bean and soybean, and cruciferous plants (family *Brassicaceae*), such as cauliflower, rape seed, and the closely related model organism *Arabidopsis thaliana*. Thus, the transgenic plants and seeds of the invention include a broad range of plants, including, but not limited to, species from the genera *Anacardium, Arachis, Asparagus, Atropa, Avena, Brassica, Citrus, Citrullus, Capsicum, Carthamus, Cocos, Coffea, Cucumis, Cucurbita, Daucus, Elaeis, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Lactuca, Linum, Lolium, Lupinus, Lycopersicon, Malus, Manihot, Majorana, Medicago, Nicotiana, Olea, Oryza, Panieum, Pannisetum, Persea, Phaseolus, Pistachia, Pisum, Pyrus, Prunus, Raphanus, Ricinus, Secale, Senecio, Sinapis, Solanum, Sorghum, Theobromus, Trigonella, Triticum, Vicia, Vitis, Vigna*, and *Zea*.

In alternative embodiments, the nucleic acids of the invention are expressed in plants which contain fiber cells, including, *e.g.*, cotton, silk cotton tree (Kapok, Ceiba pentandra), desert willow, creosote bush, winterfat, balsa, ramie, kenaf, hemp, roselle, jute, sisal abaca and flax. In alternative embodiments, the transgenic plants of the invention can be members of the genus *Gossypium*, including members of any *Gossypium* species, such as *G. arboreum*;. *G. herbaceum*, *G. barbadense*, and *G. hirsutum*.

The invention also provides for transgenic plants to be used for producing large amounts of the polypeptides (e.g., a xylanase or antibody) of the invention. For example, see Palmgren (1997) Trends Genet. 13:348; Chong (1997) Transgenic Res. 6:289-296 (producing human milk protein beta-casein in transgenic potato plants using an auxin-inducible, bidirectional mannopine synthase (mas1',2') promoter with *Agrobacterium tumefaciens*-mediated leaf disc transformation methods).

Using known procedures, one of skill can screen for plants of the invention by detecting the increase or decrease of transgene mRNA or protein in transgenic plants. Means for detecting and quantitation of mRNAs or proteins are well known in the art.

Polypeptides and peptides

In one aspect, the invention provides isolated or recombinant polypeptides having a sequence identity (e.g., at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity) to an exemplary sequence of the invention, e.g., proteins having a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278,

SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380. In one aspect, the polypeptide has a xylanase activity, e.g., can hydrolyze a glycosidic bond in a polysaccharide, e.g., a xylan. In one aspect, the polypeptide has a xylanase activity comprising catalyzing hydrolysis of internal β-1,4-xylosidic linkages. In one aspect, the xylanase activity comprises an endo-1,4-beta-xylanase activity. In one aspect, the xylanase activity comprises hydrolyzing a xylan to produce a smaller molecular weight xylose and xylo-oligomer. In one aspect, the xylan comprises an arabinoxylan, such as a water soluble arabinoxylan.

The polypeptides of the invention include xylanases in an active or inactive form. For example, the polypeptides of the invention include proproteins before "maturation" or processing of prepro sequences, e.g., by a proprotein-processing enzyme, such as a proprotein convertase to generate an "active" mature protein. The polypeptides of the invention include xylanases inactive for other reasons, e.g., before "activation" by a post-translational processing event, e.g., an endo- or exo-peptidase or proteinase action, a phosphorylation event, an amidation, a glycosylation or a sulfation, a dimerization event, and the like. The polypeptides of the invention include all active forms, including active subsequences, e.g., catalytic domains or active sites, of the xylanase.

Methods for identifying "prepro" domain sequences and signal sequences are well known in the art, see, e.g., Van de Ven (1993) Crit. Rev. Oncog. 4(2):115-136. For example, to identify a prepro sequence, the protein is purified from the extracellular space and the N-terminal protein sequence is determined and compared to the unprocessed form.

The invention includes polypeptides with or without a signal sequence and/or a prepro sequence. The invention includes polypeptides with heterologous signal sequences and/or prepro sequences. The prepro sequence (including a sequence of the invention used as a heterologous prepro domain) can be located on the amino terminal or the carboxy terminal

end of the protein. The invention also includes isolated or recombinant signal sequences, prepro sequences and catalytic domains (e.g., "active sites") comprising sequences of the invention.

The percent sequence identity can be over the full length of the polypeptide, or, the identity can be over a region of at least about 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700 or more residues. Polypeptides of the invention can also be shorter than the full length of exemplary polypeptides. In alternative aspects, the invention provides polypeptides (peptides, fragments) ranging in size between about 5 and the full length of a polypeptide, e.g., an enzyme, such as a xylanase; exemplary sizes being of about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, or more residues, e.g., contiguous residues of an exemplary xylanase of the invention.

Peptides of the invention (e.g., a subsequence of an exemplary polypeptide of the invention) can be useful as, e.g., labeling probes, antigens, toleragens, motifs, xylanase active sites (e.g., "catalytic domains"), signal sequences and/or prepro domains.

Polypeptides and peptides of the invention can be isolated from natural sources, be synthetic, or be recombinantly generated polypeptides. Peptides and proteins can be recombinantly expressed *in vitro* or *in vivo*. The peptides and polypeptides of the invention can be made and isolated using any method known in the art. Polypeptide and peptides of the invention can also be synthesized, whole or in part, using chemical methods well known in the art. See e.g., Caruthers (1980) Nucleic Acids Res. Symp. Ser. 215-223; Horn (1980) Nucleic Acids Res. Symp. Ser. 225-232; Banga, A.K., Therapeutic Peptides and Proteins, Formulation, Processing and Delivery Systems (1995) Technomic Publishing Co., Lancaster, PA. For example, peptide synthesis can be performed using various solid-phase techniques (see e.g., Roberge (1995) Science 269:202; Merrifield (1997) Methods Enzymol. 289:3-13) and automated synthesis may be achieved, e.g., using the ABI 431A Peptide Synthesizer (Perkin Elmer) in accordance with the instructions provided by the manufacturer.

The peptides and polypeptides of the invention can also be glycosylated. The glycosylation can be added post-translationally either chemically or by cellular biosynthetic mechanisms, wherein the later incorporates the use of known glycosylation motifs, which can be native to the sequence or can be added as a peptide or added in the nucleic acid coding sequence. The glycosylation can be O-linked or N-linked.

The peptides and polypeptides of the invention, as defined above, include all "mimetic" and "peptidomimetic" forms. The terms "mimetic" and "peptidomimetic" refer to

a synthetic chemical compound which has substantially the same structural and/or functional characteristics of the polypeptides of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogues of amino acids, or, is a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity. As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the invention, i.e., that its structure and/or function is not substantially altered. Thus, in one aspect, a mimetic composition is within the scope of the invention if it has a xylanase activity.

Polypeptide mimetic compositions of the invention can contain any combination of non-natural structural components. In alternative aspect, mimetic compositions of the invention include one or all of the following three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, i.e., to induce or stabilize a secondary structure, e.g., a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. For example, a polypeptide of the invention can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, e.g., glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, e.g., ketomethylene (e.g., $-C(=O)-CH_2-$ for $-C(=O)-NH-$), aminomethylene (CH_2-NH), ethylene, olefin ($CH=CH$), ether (CH_2-O), thioether (CH_2-S), tetrazole (CN_4-), thiazole, retroamide, thioamide, or ester (see, e.g., Spatola (1983) in Chemistry and Biochemistry of Amino Acids, Peptides and Proteins, Vol. 7, pp 267-357, "Peptide Backbone Modifications," Marcell Dekker, NY).

A polypeptide of the invention can also be characterized as a mimetic by containing all or some non-natural residues in place of naturally occurring amino acid residues. Non-natural residues are well described in the scientific and patent literature; a few exemplary non-natural compositions useful as mimetics of natural amino acid residues and guidelines are described below. Mimetics of aromatic amino acids can be generated by replacing by, e.g., D- or L- naphylalanine; D- or L- phenylglycine; D- or L-2 thieneylalanine;

D- or L-1, -2, 3-, or 4- pyreneylalanine; D- or L-3 thieneylalanine; D- or L-(2-pyridinyl)-alanine; D- or L-(3-pyridinyl)-alanine; D- or L-(2-pyrazinyl)-alanine; D- or L-(4-isopropyl)-phenylglycine; D-(trifluoromethyl)-phenylglycine; D-(trifluoromethyl)-phenylalanine; D-p-fluoro-phenylalanine; D- or L-p-biphenylphenylalanine; D- or L-p-methoxy-biphenylphenylalanine; D- or L-2-indole(alkyl)alanines; and, D- or L-alkylainines, where alkyl can be substituted or unsubstituted methyl, ethyl, propyl, hexyl, butyl, pentyl, isopropyl, iso-butyl, sec-isotyl, iso-pentyl, or a non-acidic amino acids. Aromatic rings of a non-natural amino acid include, e.g., thiazolyl, thiophenyl, pyrazolyl, benzimidazolyl, naphthyl, furanyl, pyrrolyl, and pyridyl aromatic rings.

Mimetics of acidic amino acids can be generated by substitution by, e.g., non-carboxylate amino acids while maintaining a negative charge; (phosphono)alanine; sulfated threonine. Carboxyl side groups (e.g., aspartyl or glutamyl) can also be selectively modified by reaction with carbodiimides (R'-N-C-N-R') such as, e.g., 1-cyclohexyl-3(2-morpholinyl-(4-ethyl) carbodiimide or 1-ethyl-3(4-azonia- 4,4- dimetholpentyl) carbodiimide. Aspartyl or glutamyl can also be converted to asparaginyl and glutaminyl residues by reaction with ammonium ions. Mimetics of basic amino acids can be generated by substitution with, e.g., (in addition to lysine and arginine) the amino acids ornithine, citrulline, or (guanidino)-acetic acid, or (guanidino)alkyl-acetic acid, where alkyl is defined above. Nitrile derivative (e.g., containing the CN-moiety in place of COOH) can be substituted for asparagine or glutamine. Asparaginyl and glutaminyl residues can be deaminated to the corresponding aspartyl or glutamyl residues. Arginine residue mimetics can be generated by reacting arginyl with, e.g., one or more conventional reagents, including, e.g., phenylglyoxal, 2,3-butanedione, 1,2-cyclo-hexanedione, or ninhydrin, preferably under alkaline conditions. Tyrosine residue mimetics can be generated by reacting tyrosyl with, e.g., aromatic diazonium compounds or tetranitromethane. N-acetylimidizol and tetranitromethane can be used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Cysteine residue mimetics can be generated by reacting cysteinyl residues with, e.g., alpha-haloacetates such as 2-chloroacetic acid or chloroacetamide and corresponding amines; to give carboxymethyl or carboxyamidomethyl derivatives. Cysteine residue mimetics can also be generated by reacting cysteinyl residues with, e.g., bromo-trifluoroacetone, alpha-bromo-beta-(5-imidozoyl) propionic acid; chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide; methyl 2-pyridyl disulfide; p-chloromercuribenzoate; 2-chloromercuri-4 nitrophenol; or, chloro-7-nitrobenzo-oxa-1,3-diazole. Lysine mimetics can be generated (and amino terminal residues can be altered) by reacting lysinyl with, e.g., succinic or other

carboxylic acid anhydrides. Lysine and other alpha-amino-containing residue mimetics can also be generated by reaction with imidoesters, such as methyl picolinimidate, pyridoxal phosphate, pyridoxal, chloroborohydride, trinitro-benzenesulfonic acid, O-methylisourea, 2,4, pentanedione, and transamidase-catalyzed reactions with glyoxylate. Mimetics of methionine can be generated by reaction with, e.g., methionine sulfoxide. Mimetics of proline include, e.g., pipecolic acid, thiazolidine carboxylic acid, 3- or 4- hydroxy proline, dehydroproline, 3- or 4-methylproline, or 3,3,-dimethylproline. Histidine residue mimetics can be generated by reacting histidyl with, e.g., diethylprocarbonate or para-bromophenacyl bromide. Other mimetics include, e.g., those generated by hydroxylation of proline and lysine; phosphorylation of the hydroxyl groups of seryl or threonyl residues; methylation of the alpha-amino groups of lysine, arginine and histidine; acetylation of the N-terminal amine; methylation of main chain amide residues or substitution with N-methyl amino acids; or amidation of C-terminal carboxyl groups.

A residue, e.g., an amino acid, of a polypeptide of the invention can also be replaced by an amino acid (or peptidomimetic residue) of the opposite chirality. Thus, any amino acid naturally occurring in the L-configuration (which can also be referred to as the R or S, depending upon the structure of the chemical entity) can be replaced with the amino acid of the same chemical structural type or a peptidomimetic, but of the opposite chirality, referred to as the D- amino acid, but also can be referred to as the R- or S- form.

The invention also provides methods for modifying the polypeptides of the invention by either natural processes, such as post-translational processing (e.g., phosphorylation, acylation, etc), or by chemical modification techniques, and the resulting modified polypeptides. Modifications can occur anywhere in the polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also a given polypeptide may have many types of modifications. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of a phosphatidylinositol, cross-linking cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristolyation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, and transfer-

RNA mediated addition of amino acids to protein such as arginylation. See, e.g., Creighton, T.E., Proteins – Structure and Molecular Properties 2nd Ed., W.H. Freeman and Company, New York (1993); Posttranslational Covalent Modification of Proteins, B.C. Johnson, Ed., Academic Press, New York, pp. 1-12 (1983).

Solid-phase chemical peptide synthesis methods can also be used to synthesize the polypeptide or fragments of the invention. Such method have been known in the art since the early 1960's (Merrifield, R. B., J. Am. Chem. Soc., 85:2149-2154, 1963) (See also Stewart, J. M. and Young, J. D., Solid Phase Peptide Synthesis, 2nd Ed., Pierce Chemical Co., Rockford, Ill., pp. 11-12)) and have recently been employed in commercially available laboratory peptide design and synthesis kits (Cambridge Research Biochemicals). Such commercially available laboratory kits have generally utilized the teachings of H. M. Geysen et al, Proc. Natl. Acad. Sci., USA, 81:3998 (1984) and provide for synthesizing peptides upon the tips of a multitude of "rods" or "pins" all of which are connected to a single plate. When such a system is utilized, a plate of rods or pins is inverted and inserted into a second plate of corresponding wells or reservoirs, which contain solutions for attaching or anchoring an appropriate amino acid to the pin's or rod's tips. By repeating such a process step, i.e., inverting and inserting the rod's and pin's tips into appropriate solutions, amino acids are built into desired peptides. In addition, a number of available FMOC peptide synthesis systems are available. For example, assembly of a polypeptide or fragment can be carried out on a solid support using an Applied Biosystems, Inc. Model 431A™ automated peptide synthesizer. Such equipment provides ready access to the peptides of the invention, either by direct synthesis or by synthesis of a series of fragments that can be coupled using other known techniques.

The invention includes xylanases of the invention with and without signal. The polypeptide comprising a signal sequence of the invention can be a xylanase of the invention or another xylanase or another enzyme or other polypeptide.

The invention includes immobilized xylanases, anti-xylanase antibodies and fragments thereof. The invention provides methods for inhibiting xylanase activity, e.g., using dominant negative mutants or anti-xylanase antibodies of the invention. The invention includes heterocomplexes, e.g., fusion proteins, heterodimers, etc., comprising the xylanases of the invention.

Polypeptides of the invention can have a xylanase activity under various conditions, e.g., extremes in pH and/or temperature, oxidizing agents, and the like. The invention provides methods leading to alternative xylanase preparations with different

catalytic efficiencies and stabilities, e.g., towards temperature, oxidizing agents and changing wash conditions. In one aspect, xylanase variants can be produced using techniques of site-directed mutagenesis and/or random mutagenesis. In one aspect, directed evolution can be used to produce a great variety of xylanase variants with alternative specificities and stability.

The proteins of the invention are also useful as research reagents to identify xylanase modulators, e.g., activators or inhibitors of xylanase activity. Briefly, test samples (compounds, broths, extracts, and the like) are added to xylanase assays to determine their ability to inhibit substrate cleavage. Inhibitors identified in this way can be used in industry and research to reduce or prevent undesired proteolysis. As with xylanases, inhibitors can be combined to increase the spectrum of activity.

The enzymes of the invention are also useful as research reagents to digest proteins or in protein sequencing. For example, the xylanases may be used to break polypeptides into smaller fragments for sequencing using, e.g. an automated sequencer.

The invention also provides methods of discovering new xylanases using the nucleic acids, polypeptides and antibodies of the invention. In one aspect, phagemid libraries are screened for expression-based discovery of xylanases. In another aspect, lambda phage libraries are screened for expression-based discovery of xylanases. Screening of the phage or phagemid libraries can allow the detection of toxic clones; improved access to substrate; reduced need for engineering a host, by-passing the potential for any bias resulting from mass excision of the library; and, faster growth at low clone densities. Screening of phage or phagemid libraries can be in liquid phase or in solid phase. In one aspect, the invention provides screening in liquid phase. This gives a greater flexibility in assay conditions; additional substrate flexibility; higher sensitivity for weak clones; and ease of automation over solid phase screening.

The invention provides screening methods using the proteins and nucleic acids of the invention and robotic automation to enable the execution of many thousands of biocatalytic reactions and screening assays in a short period of time, e.g., per day, as well as ensuring a high level of accuracy and reproducibility (see discussion of arrays, below). As a result, a library of derivative compounds can be produced in a matter of weeks. For further teachings on modification of molecules, including small molecules, see PCT/US94/09174.

Another aspect of the invention is an isolated or purified polypeptide comprising the sequence of one of Group A nucleic acid sequences and sequences substantially identical thereto, or fragments comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof. As discussed above, such

polypeptides may be obtained by inserting a nucleic acid encoding the polypeptide into a vector such that the coding sequence is operably linked to a sequence capable of driving the expression of the encoded polypeptide in a suitable host cell. For example, the expression vector may comprise a promoter, a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

Another aspect of the invention is polypeptides or fragments thereof which have at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, or more than about 95% homology to one of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, or a fragment comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof. Homology may be determined using any of the programs described above which aligns the polypeptides or fragments being compared and determines the extent of amino acid identity or similarity between them. It will be appreciated that amino acid "homology" includes conservative amino acid substitutions such as those described above.

The polypeptides or fragments having homology to one of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, or a fragment comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof may be obtained by isolating the nucleic acids encoding them using the techniques described above.

Alternatively, the homologous polypeptides or fragments may be obtained through biochemical enrichment or purification procedures. The sequence of potentially homologous polypeptides or fragments may be determined by xylan hydrolase digestion, gel electrophoresis and/or microsequencing. The sequence of the prospective homologous polypeptide or fragment can be compared to one of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, or a fragment comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof using any of the programs described above.

Another aspect of the invention is an assay for identifying fragments or variants of Group B amino acid sequences and sequences substantially identical thereto, which retain the enzymatic function of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto. For example the fragments or variants of said polypeptides, may be used to catalyze biochemical reactions, which indicate that the fragment

or variant retains the enzymatic activity of the polypeptides in the Group B amino acid sequences.

The assay for determining if fragments of variants retain the enzymatic activity of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto includes the steps of: contacting the polypeptide fragment or variant with a substrate molecule under conditions which allow the polypeptide fragment or variant to function and detecting either a decrease in the level of substrate or an increase in the level of the specific reaction product of the reaction between the polypeptide and substrate.

The polypeptides of Group B amino acid sequences and sequences substantially identical thereto or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof may be used in a variety of applications. For example, the polypeptides or fragments thereof may be used to catalyze biochemical reactions. In accordance with one aspect of the invention, there is provided a process for utilizing the polypeptides of Group B amino acid sequences and sequences substantially identical thereto or polynucleotides encoding such polypeptides for hydrolyzing glycosidic linkages. In such procedures, a substance containing a glycosidic linkage (*e.g.*, a starch) is contacted with one of the polypeptides of Group B amino acid sequences, or sequences substantially identical thereto under conditions which facilitate the hydrolysis of the glycosidic linkage.

The present invention exploits the unique catalytic properties of enzymes. Whereas the use of biocatalysts (i.e., purified or crude enzymes, non-living or living cells) in chemical transformations normally requires the identification of a particular biocatalyst that reacts with a specific starting compound, the present invention uses selected biocatalysts and reaction conditions that are specific for functional groups that are present in many starting compounds, such as small molecules. Each biocatalyst is specific for one functional group, or several related functional groups and can react with many starting compounds containing this functional group.

The biocatalytic reactions produce a population of derivatives from a single starting compound. These derivatives can be subjected to another round of biocatalytic reactions to produce a second population of derivative compounds. Thousands of variations of the original small molecule or compound can be produced with each iteration of biocatalytic derivatization.

Enzymes react at specific sites of a starting compound without affecting the rest of the molecule, a process which is very difficult to achieve using traditional chemical

methods. This high degree of biocatalytic specificity provides the means to identify a single active compound within the library. The library is characterized by the series of biocatalytic reactions used to produce it, a so called "biosynthetic history". Screening the library for biological activities and tracing the biosynthetic history identifies the specific reaction sequence producing the active compound. The reaction sequence is repeated and the structure of the synthesized compound determined. This mode of identification, unlike other synthesis and screening approaches, does not require immobilization technologies and compounds can be synthesized and tested free in solution using virtually any type of screening assay. It is important to note, that the high degree of specificity of enzyme reactions on functional groups allows for the "tracking" of specific enzymatic reactions that make up the biocatalytically produced library.

Many of the procedural steps are performed using robotic automation enabling the execution of many thousands of biocatalytic reactions and screening assays per day as well as ensuring a high level of accuracy and reproducibility. As a result, a library of derivative compounds can be produced in a matter of weeks which would take years to produce using current chemical methods.

In a particular aspect, the invention provides a method for modifying small molecules, comprising contacting a polypeptide encoded by a polynucleotide described herein or enzymatically active fragments thereof with a small molecule to produce a modified small molecule. A library of modified small molecules is tested to determine if a modified small molecule is present within the library which exhibits a desired activity. A specific biocatalytic reaction which produces the modified small molecule of desired activity is identified by systematically eliminating each of the biocatalytic reactions used to produce a portion of the library and then testing the small molecules produced in the portion of the library for the presence or absence of the modified small molecule with the desired activity. The specific biocatalytic reactions which produce the modified small molecule of desired activity is optionally repeated. The biocatalytic reactions are conducted with a group of biocatalysts that react with distinct structural moieties found within the structure of a small molecule, each biocatalyst is specific for one structural moiety or a group of related structural moieties; and each biocatalyst reacts with many different small molecules which contain the distinct structural moiety.

Xylanase signal sequences, prepro and catalytic domains

The invention provides xylanase signal sequences (e.g., signal peptides (SPs)), prepro domains and catalytic domains (CDs). The SPs, prepro domains and/or CDs of the invention can be isolated or recombinant peptides or can be part of a fusion protein, e.g., as a heterologous domain in a chimeric protein. The invention provides nucleic acids encoding these catalytic domains (CDs), prepro domains and signal sequences (SPs, e.g., a peptide having a sequence comprising/ consisting of amino terminal residues of a polypeptide of the invention). In one aspect, the invention provides a signal sequence comprising a peptide comprising/ consisting of a sequence as set forth in residues 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 39, 1 to 40, 1 to 41, 1 to 42, 1 to 43, 1 to 44 of a polypeptide of the invention.

In one aspect, the invention provides a signal sequence comprising a peptide comprising/ consisting of a sequence as set forth in Table 4 below. For example, in reading Table 4, the invention provides a signal sequence comprising/ consisting of residues 1 to 23 of SEQ ID NO:102 (encoded by SEQ ID NO:101), a signal sequence comprising/ consisting of residues 1 to 41 of SEQ ID NO:104 (encoded by SEQ ID NO:103), etc.

Table 4: exemplary signal sequences of the invention

SEQ ID NO:	Signal sequence (amino acid positions)
101, 102	1-23
103, 104	1-41
105, 106	1-22
109, 110	1-26
11, 12	1-28
113, 114	1-28
119, 120	1-33
121, 122	1-20
123, 124	1-20
131, 132	1-26
135, 136	1-25
139, 140	1-24
141, 142	1-25
143, 144	1-32
147, 148	1-28
149, 150	1-18
15, 16	1-20
151, 152	1-21
153, 154	1-16
155, 156	1-21

157, 158	1-29
159, 160	1-23
161, 162	1-32
163, 164	1-26
165, 166	1-23
167, 168	1-36
169, 170	1-24
17, 18	1-31
171, 172	1-29
173, 174	1-22
175, 176	1-27
177, 178	1-26
179, 180	1-19
181, 182	1-25
183, 184	1-32
185, 186	1-27
187, 188	1-28
19, 20	1-29
191, 192	1-27
193, 194	1-21
195, 196	1-23
197, 198	1-28
199, 200	1-30
203, 204	1-30
205, 206	1-29
207, 208	1-27
209, 210	1-25
21, 22	1-28
211, 212	1-29
215, 216	1-31
217, 218	1-29
219, 220	1-23
221, 222	1-24
223, 224	1-28
225, 226	1-25
227, 228	1-39
229, 230	1-28
23, 24	1-29
231, 232	1-41
233, 234	1-26
235, 236	1-28
237, 238	1-32
239, 240	1-30
241, 242	1-28
243, 244	1-33
245, 246	1-32
249, 250	1-33
253, 254	1-24
255, 256	1-51
259, 260	1-24
261, 262	1-26
263, 264	1-29

267, 268	1-30
27, 28	1-27
271, 272	1-22
273, 274	1-74
277, 278	1-19
279, 280	1-22
283, 284	1-28
287, 288	1-23
289, 290	1-22
295, 296	1-26
299, 300	1-24
301, 302	1-28
303, 304	1-74
305, 306	1-32
309, 310	1-20
311, 312	1-33
313, 314	1-22
315, 316	1-28
319, 320	1-27
325, 326	1-27
327, 328	1-29
329, 330	1-35
33, 34	1-23
331, 332	1-28
333, 334	1-30
335, 336	1-50
339, 340	1-23
341, 342	1-45
347, 348	1-20
349, 350	1-20
351, 352	1-73
353, 354	1-18
355, 356	1-21
357, 358	1-25
359, 360	1-31
361, 362	1-26
365, 366	1-65
367, 368	1-23
369, 370	1-27
39, 40	1-24
41, 42	1-37
45, 46	1-25
47, 48	1-26
5, 6	1-47
51, 52	1-30
53, 54	1-37
55, 56	1-24
57, 58	1-22
59, 60	1-21
63, 64	1-20
65, 66	1-22
67, 68	1-28

69, 70	1-25
7, 8	1-57
73, 74	1-21
75, 76	1-22
77, 78	1-27
79, 80	1-36
83, 84	1-30
87, 88	1-29
89, 90	1-40
9, 10	1-36
95, 96	1-24
99, 100	1-33

The xylanase signal sequences (SPs) and/or prepro sequences of the invention can be isolated peptides, or, sequences joined to another xylanase or a non-xylanase polypeptide, e.g., as a fusion (chimeric) protein. In one aspect, the invention provides polypeptides comprising xylanase signal sequences of the invention. In one aspect, polypeptides comprising xylanase signal sequences SPs and/or prepro of the invention comprise sequences heterologous to a xylanase of the invention (e.g., a fusion protein comprising an SP and/or prepro of the invention and sequences from another xylanase or a non-xylanase protein). In one aspect, the invention provides xylanases of the invention with heterologous SPs and/or prepro sequences, e.g., sequences with a yeast signal sequence. A xylanase of the invention can comprise a heterologous SP and/or prepro in a vector, e.g., a pPIC series vector (Invitrogen, Carlsbad, CA).

In one aspect, SPs and/or prepro sequences of the invention are identified following identification of novel xylanase polypeptides. The pathways by which proteins are sorted and transported to their proper cellular location are often referred to as protein targeting pathways. One of the most important elements in all of these targeting systems is a short amino acid sequence at the amino terminus of a newly synthesized polypeptide called the signal sequence. This signal sequence directs a protein to its appropriate location in the cell and is removed during transport or when the protein reaches its final destination. Most lysosomal, membrane, or secreted proteins have an amino-terminal signal sequence that marks them for translocation into the lumen of the endoplasmic reticulum. More than 100 signal sequences for proteins in this group have been determined. The signal sequences can vary in length from 13 to 36 amino acid residues. Various methods of recognition of signal sequences are known to those of skill in the art. For example, in one aspect, novel xylanase signal peptides are identified by a method referred to as SignalP. SignalP uses a combined neural network which recognizes both signal peptides and their cleavage sites. (Nielsen, et

al., "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites." Protein Engineering, vol. 10, no. 1, p. 1-6 (1997).

It should be understood that in some aspects xylanases of the invention may not have SPs and/or prepro sequences, or "domains." In one aspect, the invention provides the xylanases of the invention lacking all or part of an SP and/or a prepro domain. In one aspect, the invention provides a nucleic acid sequence encoding a signal sequence (SP) and/or prepro from one xylanase operably linked to a nucleic acid sequence of a different xylanase or, optionally, a signal sequence (SPs) and/or prepro domain from a non-xylanase protein may be desired.

The invention also provides isolated or recombinant polypeptides comprising signal sequences (SPs), prepro domain and/or catalytic domains (CDs) of the invention and heterologous sequences. The heterologous sequences are sequences not naturally associated (e.g., to a xylanase) with an SP, prepro domain and/or CD. The sequence to which the SP, prepro domain and/or CD are not naturally associated can be on the SP's, prepro domain and/or CD's amino terminal end, carboxy terminal end, and/or on both ends of the SP and/or CD. In one aspect, the invention provides an isolated or recombinant polypeptide comprising (or consisting of) a polypeptide comprising a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention with the proviso that it is not associated with any sequence to which it is naturally associated (e.g., a xylanase sequence). Similarly in one aspect, the invention provides isolated or recombinant nucleic acids encoding these polypeptides. Thus, in one aspect, the isolated or recombinant nucleic acid of the invention comprises coding sequence for a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention and a heterologous sequence (i.e., a sequence not naturally associated with the a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention). The heterologous sequence can be on the 3' terminal end, 5' terminal end, and/or on both ends of the SP, prepro domain and/or CD coding sequence.

Hybrid (chimeric) xylanases and peptide libraries

In one aspect, the invention provides hybrid xylanases and fusion proteins, including peptide libraries, comprising sequences of the invention. The peptide libraries of the invention can be used to isolate peptide modulators (e.g., activators or inhibitors) of targets, such as xylanase substrates, receptors, enzymes. The peptide libraries of the invention can be used to identify formal binding partners of targets, such as ligands, e.g., cytokines, hormones and the like. In one aspect, the invention provides chimeric proteins

comprising a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention or a combination thereof and a heterologous sequence (see above).

In one aspect, the fusion proteins of the invention (e.g., the peptide moiety) are conformationally stabilized (relative to linear peptides) to allow a higher binding affinity for targets. The invention provides fusions of xylanases of the invention and other peptides, including known and random peptides. They can be fused in such a manner that the structure of the xylanases is not significantly perturbed and the peptide is metabolically or structurally conformationally stabilized. This allows the creation of a peptide library that is easily monitored both for its presence within cells and its quantity.

Amino acid sequence variants of the invention can be characterized by a predetermined nature of the variation, a feature that sets them apart from a naturally occurring form, e.g., an allelic or interspecies variation of a xylanase sequence. In one aspect, the variants of the invention exhibit the same qualitative biological activity as the naturally occurring analogue. Alternatively, the variants can be selected for having modified characteristics. In one aspect, while the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed xylanase variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, as discussed herein for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants can be done using, e.g., assays of xylan hydrolysis. In alternative aspects, amino acid substitutions can be single residues; insertions can be on the order of from about 1 to 20 amino acids, although considerably larger insertions can be done. Deletions can range from about 1 to about 20, 30, 40, 50, 60, 70 residues or more. To obtain a final derivative with the optimal properties, substitutions, deletions, insertions or any combination thereof may be used. Generally, these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances.

The invention provides xylanases where the structure of the polypeptide backbone, the secondary or the tertiary structure, e.g., an alpha-helical or beta-sheet structure, has been modified. In one aspect, the charge or hydrophobicity has been modified. In one aspect, the bulk of a side chain has been modified. Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative. For example, substitutions can be made which more significantly affect: the structure of the

polypeptide backbone in the area of the alteration, for example a alpha-helical or a beta-sheet structure; a charge or a hydrophobic site of the molecule, which can be at an active site; or a side chain. The invention provides substitutions in polypeptide of the invention where (a) a hydrophilic residues, e.g. seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine. The variants can exhibit the same qualitative biological activity (i.e. xylanase activity) although variants can be selected to modify the characteristics of the xylanases as needed.

In one aspect, xylanases of the invention comprise epitopes or purification tags, signal sequences or other fusion sequences, etc. In one aspect, the xylanases of the invention can be fused to a random peptide to form a fusion polypeptide. By "fused" or "operably linked" herein is meant that the random peptide and the xylanase are linked together, in such a manner as to minimize the disruption to the stability of the xylanase structure, e.g., it retains xylanase activity. The fusion polypeptide (or fusion polynucleotide encoding the fusion polypeptide) can comprise further components as well, including multiple peptides at multiple loops.

In one aspect, the peptides and nucleic acids encoding them are randomized, either fully randomized or they are biased in their randomization, e.g. in nucleotide/residue frequency generally or per position. "Randomized" means that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. In one aspect, the nucleic acids which give rise to the peptides can be chemically synthesized, and thus may incorporate any nucleotide at any position. Thus, when the nucleic acids are expressed to form peptides, any amino acid residue may be incorporated at any position. The synthetic process can be designed to generate randomized nucleic acids, to allow the formation of all or most of the possible combinations over the length of the nucleic acid, thus forming a library of randomized nucleic acids. The library can provide a sufficiently structurally diverse population of randomized expression products to affect a probabilistically sufficient range of cellular responses to provide one or more cells exhibiting a desired response. Thus, the invention provides an interaction library large enough so that at least one of its members will have a structure that gives it affinity for some molecule, protein, or other factor.

Xylanases are multidomain enzymes that consist optionally of a signal peptide, a carbohydrate binding module, a xylanase catalytic domain, a linker and/or another catalytic domain.

The invention provides a means for generating chimeric polypeptides which may encode biologically active hybrid polypeptides (*e.g.*, hybrid xylanases). In one aspect, the original polynucleotides encode biologically active polypeptides. The method of the invention produces new hybrid polypeptides by utilizing cellular processes which integrate the sequence of the original polynucleotides such that the resulting hybrid polynucleotide encodes a polypeptide demonstrating activities derived from the original biologically active polypeptides. For example, the original polynucleotides may encode a particular enzyme from different microorganisms. An enzyme encoded by a first polynucleotide from one organism or variant may, for example, function effectively under a particular environmental condition, *e.g.* high salinity. An enzyme encoded by a second polynucleotide from a different organism or variant may function effectively under a different environmental condition, such as extremely high temperatures. A hybrid polynucleotide containing sequences from the first and second original polynucleotides may encode an enzyme which exhibits characteristics of both enzymes encoded by the original polynucleotides. Thus, the enzyme encoded by the hybrid polynucleotide may function effectively under environmental conditions shared by each of the enzymes encoded by the first and second polynucleotides, *e.g.*, high salinity and extreme temperatures.

Enzymes encoded by the polynucleotides of the invention include, but are not limited to, hydrolases, such as xylanases. Glycosidase hydrolases were first classified into families in 1991, see, e.g., Henrissat (1991) Biochem. J. 280:309-316. Since then, the classifications have been continually updated, see, e.g., Henrissat (1993) Biochem. J. 293:781-788; Henrissat (1996) Biochem. J. 316:695-696; Henrissat (2000) Plant Physiology 124:1515-1519. There are 87 identified families of glycosidase hydrolases. In one aspect, the xylanases of the invention may be categorized in families 8, 10, 11, 26 and 30. In one aspect, the invention also provides xylanase-encoding nucleic acids with a common novelty in that they are derived from a common family, e.g., family 5, 6, 8, 10, 11, 26 or 30, as set forth in Table 5, below.

Table 5

SEQ ID	FAMILY
9, 10	8
1, 2	8

5, 6	8
7, 8	8
99, 100	10
11, 12	10
127, 128	10
27, 28	10
97, 98	10
45, 46	10
141, 142	10
107, 108	10
129, 130	10
93, 94	10
63, 64	10
25, 26	10
49, 50	10
67, 68	10
85, 86	10
29, 30	10
51, 52	10
35, 36	10
147, 148	10
119, 120	10
123, 124	10
249, 250	10
149, 150	10
83, 84	10
43, 44	10
133, 134	10
113, 114	10
105, 106	10
75, 76	10
111, 112	10
117, 118	10
115, 116	10
125, 126	10
137, 138	10
135, 136	10
69, 70	10
89, 90	10
31, 32	10
13, 14	10
65, 66	10
57, 58	10
77, 78	10
73, 74	10
109, 110	10
59, 60	10
71, 72	10
139, 140	10
55, 56	10
15, 16	10

131, 132	10
95, 96	10
101, 102	10
39, 40	10
143, 144	10
103, 104	10
17, 18	10
53, 54	10
21, 22	10
151, 152	10
23, 24	10
121, 122	10
41, 42	10
47, 48	10
247, 248	10
33, 34	10
19, 20	10
87, 88	10
81, 82	10
91, 92	10
61, 62	10
37, 38	10
79, 80	10
231, 232	11
157, 158	11
189, 190	11
167, 168	11
207, 208	11
251, 252	11
213, 214	11
177, 178	11
187, 188	11
205, 206	11
211, 212	11
197, 198	11
209, 210	11
185, 186	11
229, 230	11
223, 224	11
179, 180	11
193, 194	11
173, 174	11
217, 218	11
153, 154	11
219, 220	11
183, 184	11
253, 254	11
199, 200	11
255, 256	11
155, 156	11
169, 170	11

195, 196	11
215, 216	11
191, 192	11
175, 176	11
161, 162	11
221, 222	11
225, 226	11
163, 164	11
159, 160	11
233, 234	11
171, 172	11
203, 204	11
181, 182	11
227, 228	11
165, 166	11
257, 258	26
237, 238	30
241, 242	30
239, 240	30
245, 246	30
235, 236	30
313, 314	30
345, 346	10
321, 322	10
323, 324	10
315, 316	10
201, 202	10
265, 266	10
145, 146	10
287, 288	10
293, 294	10
351, 352	10
311, 312	10
279, 280	10
289, 290	10
283, 284	10
373, 374	10
337, 338	10
371, 372	10
291, 292	10
3, 4	10
307, 308	10
343, 344	10
349, 350	10
329, 330	10
355, 356	10
339, 340	10
295, 296	10
333, 334	10
281, 282	10
361, 362	10

347, 348	10
319, 320	10
357, 358	10
365, 366	10
273, 274	10
277, 278	10
271, 272	10
285, 286	10
259, 260	10
325, 326	10
331, 332	10
359, 360	10
303, 304	10
363, 364	10
305, 306	10
341, 342	10
375, 376	11
377, 378	11
379, 380	11
301, 302	11
309, 310	11
263, 264	11
269, 270	11
353, 354	11
299, 300	11
367, 368	11
261, 262	11
369, 370	11
267, 268	11
317, 318	11
297, 298	11
327, 328	5
275, 276	6

A hybrid polypeptide resulting from the method of the invention may exhibit specialized enzyme activity not displayed in the original enzymes. For example, following recombination and/or reductive reassortment of polynucleotides encoding hydrolase activities, the resulting hybrid polypeptide encoded by a hybrid polynucleotide can be screened for specialized hydrolase activities obtained from each of the original enzymes, i.e. the type of bond on which the hydrolase acts and the temperature at which the hydrolase functions. Thus, for example, the hydrolase may be screened to ascertain those chemical functionalities which distinguish the hybrid hydrolase from the original hydrolases, such as: (a) amide (peptide bonds), i.e., xylanases; (b) ester bonds, i.e., esterases and lipases; (c) acetals, i.e., glycosidases and, for example, the temperature, pH or salt concentration at which the hybrid polypeptide functions.

Sources of the original polynucleotides may be isolated from individual organisms ("isolates"), collections of organisms that have been grown in defined media ("enrichment cultures"), or, uncultivated organisms ("environmental samples"). The use of a culture-independent approach to derive polynucleotides encoding novel bioactivities from environmental samples is most preferable since it allows one to access untapped resources of biodiversity.

"Environmental libraries" are generated from environmental samples and represent the collective genomes of naturally occurring organisms archived in cloning vectors that can be propagated in suitable prokaryotic hosts. Because the cloned DNA is initially extracted directly from environmental samples, the libraries are not limited to the small fraction of prokaryotes that can be grown in pure culture. Additionally, a normalization of the environmental DNA present in these samples could allow more equal representation of the DNA from all of the species present in the original sample. This can dramatically increase the efficiency of finding interesting genes from minor constituents of the sample which may be under-represented by several orders of magnitude compared to the dominant species.

For example, gene libraries generated from one or more uncultivated microorganisms are screened for an activity of interest. Potential pathways encoding bioactive molecules of interest are first captured in prokaryotic cells in the form of gene expression libraries. Polynucleotides encoding activities of interest are isolated from such libraries and introduced into a host cell. The host cell is grown under conditions which promote recombination and/or reductive reassortment creating potentially active biomolecules with novel or enhanced activities.

Additionally, subcloning may be performed to further isolate sequences of interest. In subcloning, a portion of DNA is amplified, digested, generally by restriction enzymes, to cut out the desired sequence, the desired sequence is ligated into a recipient vector and is amplified. At each step in subcloning, the portion is examined for the activity of interest, in order to ensure that DNA that encodes the structural protein has not been excluded. The insert may be purified at any step of the subcloning, for example, by gel electrophoresis prior to ligation into a vector or where cells containing the recipient vector and cells not containing the recipient vector are placed on selective media containing, for example, an antibiotic, which will kill the cells not containing the recipient vector. Specific methods of subcloning cDNA inserts into vectors are well-known in the art (Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press

(1989)). In another aspect, the enzymes of the invention are subclones. Such subclones may differ from the parent clone by, for example, length, a mutation, a tag or a label.

In one aspect, the signal sequences of the invention are identified following identification of novel xylanase polypeptides. The pathways by which proteins are sorted and transported to their proper cellular location are often referred to as protein targeting pathways. One of the most important elements in all of these targeting systems is a short amino acid sequence at the amino terminus of a newly synthesized polypeptide called the signal sequence. This signal sequence directs a protein to its appropriate location in the cell and is removed during transport or when the protein reaches its final destination. Most lysosomal, membrane, or secreted proteins have an amino-terminal signal sequence that marks them for translocation into the lumen of the endoplasmic reticulum. More than 100 signal sequences for proteins in this group have been determined. The sequences vary in length from 13 to 36 amino acid residues. Various methods of recognition of signal sequences are known to those of skill in the art. In one aspect, the peptides are identified by a method referred to as SignalP. SignalP uses a combined neural network which recognizes both signal peptides and their cleavage sites. See, e.g., Nielsen (1997) "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites." Protein Engineering, vol. 10, no. 1, p. 1-6. It should be understood that some of the xylanases of the invention may or may not contain signal sequences. It may be desirable to include a nucleic acid sequence encoding a signal sequence from one xylanase operably linked to a nucleic acid sequence of a different xylanase or, optionally, a signal sequence from a non-xylanase protein may be desired.

The microorganisms from which the polynucleotide may be prepared include prokaryotic microorganisms, such as *Eubacteria* and *Archaebacteria* and lower eukaryotic microorganisms such as fungi, some algae and protozoa. Polynucleotides may be isolated from environmental samples in which case the nucleic acid may be recovered without culturing of an organism or recovered from one or more cultured organisms. In one aspect, such microorganisms may be extremophiles, such as hyperthermophiles, psychrophiles, psychrotrophs, halophiles, barophiles and acidophiles. Polynucleotides encoding enzymes isolated from extremophilic microorganisms can be used. Such enzymes may function at temperatures above 100°C in terrestrial hot springs and deep sea thermal vents, at temperatures below 0°C in arctic waters, in the saturated salt environment of the Dead Sea, at pH values around 0 in coal deposits and geothermal sulfur-rich springs, or at pH values greater than 11 in sewage sludge. For example, several esterases and lipases cloned and

expressed from extremophilic organisms show high activity throughout a wide range of temperatures and pHs.

Polynucleotides selected and isolated as hereinabove described are introduced into a suitable host cell. A suitable host cell is any cell which is capable of promoting recombination and/or reductive reassortment. The selected polynucleotides are preferably already in a vector which includes appropriate control sequences. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or preferably, the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (Davis *et al.*, 1986).

As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Streptomyces*, *Salmonella typhimurium*; fungal cells, such as yeast; insect cells such as *Drosophila S2* and *Spodoptera Sf9*; animal cells such as CHO, COS or Bowes melanoma; adenoviruses; and plant cells. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

With particular references to various mammalian cell culture systems that can be employed to express recombinant protein, examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described in "SV40-transformed simian cells support the replication of early SV40 mutants" (Gluzman, 1981) and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

In another aspect, it is envisioned the method of the present invention can be used to generate novel polynucleotides encoding biochemical pathways from one or more operons or gene clusters or portions thereof. For example, bacteria and many eukaryotes have a coordinated mechanism for regulating genes whose products are involved in related processes. The genes are clustered, in structures referred to as "gene clusters," on a single chromosome and are transcribed together under the control of a single regulatory sequence, including a single promoter which initiates transcription of the entire cluster. Thus, a gene cluster is a group of adjacent genes that are either identical or related, usually as to their function. An example of a biochemical pathway encoded by gene clusters are polyketides.

Gene cluster DNA can be isolated from different organisms and ligated into vectors, particularly vectors containing expression regulatory sequences which can control and regulate the production of a detectable protein or protein-related array activity from the ligated gene clusters. Use of vectors which have an exceptionally large capacity for exogenous DNA introduction are particularly appropriate for use with such gene clusters and are described by way of example herein to include the f-factor (or fertility factor) of *E. coli*. This f-factor of *E. coli* is a plasmid which affects high-frequency transfer of itself during conjugation and is ideal to achieve and stably propagate large DNA fragments, such as gene clusters from mixed microbial samples. One aspect of the invention is to use cloning vectors, referred to as "fosmids" or bacterial artificial chromosome (BAC) vectors. These are derived from *E. coli* f-factor which is able to stably integrate large segments of genomic DNA. When integrated with DNA from a mixed uncultured environmental sample, this makes it possible to achieve large genomic fragments in the form of a stable "environmental DNA library." Another type of vector for use in the present invention is a cosmid vector. Cosmid vectors were originally designed to clone and propagate large segments of genomic DNA. Cloning into cosmid vectors is described in detail in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press (1989). Once ligated into an appropriate vector, two or more vectors containing different polyketide synthase gene clusters can be introduced into a suitable host cell. Regions of partial sequence homology shared by the gene clusters will promote processes which result in sequence reorganization resulting in a hybrid gene cluster. The novel hybrid gene cluster can then be screened for enhanced activities not found in the original gene clusters.

Therefore, in a one aspect, the invention relates to a method for producing a biologically active hybrid polypeptide and screening such a polypeptide for enhanced activity by:

1) introducing at least a first polynucleotide in operable linkage and a second polynucleotide in operable linkage, the at least first polynucleotide and second polynucleotide sharing at least one region of partial sequence homology, into a suitable host cell;
2) growing the host cell under conditions which promote sequence reorganization resulting in a hybrid polynucleotide in operable linkage;
3) expressing a hybrid polypeptide encoded by the hybrid polynucleotide;
4) screening the hybrid polypeptide under conditions which promote identification of enhanced biological activity; and

5) isolating the a polynucleotide encoding the hybrid polypeptide.

Methods for screening for various enzyme activities are known to those of skill in the art and are discussed throughout the present specification. Such methods may be employed when isolating the polypeptides and polynucleotides of the invention.

Screening Methodologies and "On-line" Monitoring Devices

In practicing the methods of the invention, a variety of apparatus and methodologies can be used to in conjunction with the polypeptides and nucleic acids of the invention, e.g., to screen polypeptides for xylanase activity (e.g., assays such as hydrolysis of casein in zymograms, the release of fluorescence from gelatin, or the release of p-nitroanalide from various small peptide substrates), to screen compounds as potential modulators, e.g., activators or inhibitors, of a xylanase activity, for antibodies that bind to a polypeptide of the invention, for nucleic acids that hybridize to a nucleic acid of the invention, to screen for cells expressing a polypeptide of the invention and the like. In addition to the array formats described in detail below for screening samples, alternative formats can also be used to practice the methods of the invention. Such formats include, for example, mass spectrometers, chromatographs, e.g., high-throughput HPLC and other forms of liquid chromatography, and smaller formats, such as 1536-well plates, 384-well plates and so on. High throughput screening apparatus can be adapted and used to practice the methods of the invention, see, e.g., U.S. Patent Application No. 20020001809.

Capillary Arrays

Nucleic acids or polypeptides of the invention can be immobilized to or applied to an array. Arrays can be used to screen for or monitor libraries of compositions (e.g., small molecules, antibodies, nucleic acids, etc.) for their ability to bind to or modulate the activity of a nucleic acid or a polypeptide of the invention. Capillary arrays, such as the GIGAMATRIX™, Diversa Corporation, San Diego, CA; and arrays described in, e.g., U.S. Patent Application No. 20020080350 A1; WO 0231203 A; WO 0244336 A, provide an alternative apparatus for holding and screening samples. In one aspect, the capillary array includes a plurality of capillaries formed into an array of adjacent capillaries, wherein each capillary comprises at least one wall defining a lumen for retaining a sample. The lumen may be cylindrical, square, hexagonal or any other geometric shape so long as the walls form a lumen for retention of a liquid or sample. The capillaries of the capillary array can be held together in close proximity to form a planar structure. The capillaries can be bound together, by being fused (e.g., where the capillaries are made of glass), glued, bonded, or clamped side-

by-side. Additionally, the capillary array can include interstitial material disposed between adjacent capillaries in the array, thereby forming a solid planar device containing a plurality of through-holes.

A capillary array can be formed of any number of individual capillaries, for example, a range from 100 to 4,000,000 capillaries. Further, a capillary array having about 100,000 or more individual capillaries can be formed into the standard size and shape of a Microtiter® plate for fitment into standard laboratory equipment. The lumens are filled manually or automatically using either capillary action or microinjection using a thin needle. Samples of interest may subsequently be removed from individual capillaries for further analysis or characterization. For example, a thin, needle-like probe is positioned in fluid communication with a selected capillary to either add or withdraw material from the lumen.

In a single-pot screening assay, the assay components are mixed yielding a solution of interest, prior to insertion into the capillary array. The lumen is filled by capillary action when at least a portion of the array is immersed into a solution of interest. Chemical or biological reactions and/or activity in each capillary are monitored for detectable events. A detectable event is often referred to as a "hit", which can usually be distinguished from "non-hit" producing capillaries by optical detection. Thus, capillary arrays allow for massively parallel detection of "hits".

In a multi-pot screening assay, a polypeptide or nucleic acid, e.g., a ligand, can be introduced into a first component, which is introduced into at least a portion of a capillary of a capillary array. An air bubble can then be introduced into the capillary behind the first component. A second component can then be introduced into the capillary, wherein the second component is separated from the first component by the air bubble. The first and second components can then be mixed by applying hydrostatic pressure to both sides of the capillary array to collapse the bubble. The capillary array is then monitored for a detectable event resulting from reaction or non-reaction of the two components.

In a binding screening assay, a sample of interest can be introduced as a first liquid labeled with a detectable particle into a capillary of a capillary array, wherein the lumen of the capillary is coated with a binding material for binding the detectable particle to the lumen. The first liquid may then be removed from the capillary tube, wherein the bound detectable particle is maintained within the capillary, and a second liquid may be introduced into the capillary tube. The capillary is then monitored for a detectable event resulting from reaction or non-reaction of the particle with the second liquid.

Arrays, or "Biochips"

Nucleic acids or polypeptides of the invention can be immobilized to or applied to an array. Arrays can be used to screen for or monitor libraries of compositions (e.g., small molecules, antibodies, nucleic acids, etc.) for their ability to bind to or modulate the activity of a nucleic acid or a polypeptide of the invention. For example, in one aspect of the invention, a monitored parameter is transcript expression of a xylanase gene. One or more, or, all the transcripts of a cell can be measured by hybridization of a sample comprising transcripts of the cell, or, nucleic acids representative of or complementary to transcripts of a cell, by hybridization to immobilized nucleic acids on an array, or "biochip." By using an "array" of nucleic acids on a microchip, some or all of the transcripts of a cell can be simultaneously quantified. Alternatively, arrays comprising genomic nucleic acid can also be used to determine the genotype of a newly engineered strain made by the methods of the invention. Polypeptide arrays" can also be used to simultaneously quantify a plurality of proteins. The present invention can be practiced with any known "array," also referred to as a "microarray" or "nucleic acid array" or "polypeptide array" or "antibody array" or "biochip," or variation thereof. Arrays are generically a plurality of "spots" or "target elements," each target element comprising a defined amount of one or more biological molecules, e.g., oligonucleotides, immobilized onto a defined area of a substrate surface for specific binding to a sample molecule, e.g., mRNA transcripts.

In practicing the methods of the invention, any known array and/or method of making and using arrays can be incorporated in whole or in part, or variations thereof, as described, for example, in U.S. Patent Nos. 6,277,628; 6,277,489; 6,261,776; 6,258,606; 6,054,270; 6,048,695; 6,045,996; 6,022,963; 6,013,440; 5,965,452; 5,959,098; 5,856,174; 5,830,645; 5,770,456; 5,632,957; 5,556,752; 5,143,854; 5,807,522; 5,800,992; 5,744,305; 5,700,637; 5,556,752; 5,434,049; see also, e.g., WO 99/51773; WO 99/09217; WO 97/46313; WO 96/17958; see also, e.g., Johnston (1998) Curr. Biol. 8:R171-R174; Schummer (1997) Biotechniques 23:1087-1092; Kern (1997) Biotechniques 23:120-124; Solinas-Toldo (1997) Genes, Chromosomes & Cancer 20:399-407; Bowtell (1999) Nature Genetics Supp. 21:25-32. See also published U.S. patent applications Nos. 20010018642; 20010019827; 20010016322; 20010014449; 20010014448; 20010012537; 20010008765.

<u>Antibodies and Antibody-based screening methods</u>

The invention provides isolated or recombinant antibodies that specifically bind to a xylanase of the invention. These antibodies can be used to isolate, identify or

quantify the xylanases of the invention or related polypeptides. These antibodies can be used to isolate other polypeptides within the scope the invention or other related xylanases. The antibodies can be designed to bind to an active site of a xylanase. Thus, the invention provides methods of inhibiting xylanases using the antibodies of the invention (see discussion above regarding applications for anti-xylanase compositions of the invention).

The invention provides fragments of the enzymes of the invention, including immunogenic fragments of a polypeptide of the invention. The invention provides compositions comprising a polypeptide or peptide of the invention and adjuvants or carriers and the like.

The antibodies can be used in immunoprecipitation, staining, immunoaffinity columns, and the like. If desired, nucleic acid sequences encoding for specific antigens can be generated by immunization followed by isolation of polypeptide or nucleic acid, amplification or cloning and immobilization of polypeptide onto an array of the invention. Alternatively, the methods of the invention can be used to modify the structure of an antibody produced by a cell to be modified, e.g., an antibody's affinity can be increased or decreased. Furthermore, the ability to make or modify antibodies can be a phenotype engineered into a cell by the methods of the invention.

Methods of immunization, producing and isolating antibodies (polyclonal and monoclonal) are known to those of skill in the art and described in the scientific and patent literature, see, e.g., Coligan, CURRENT PROTOCOLS IN IMMUNOLOGY, Wiley/Greene, NY (1991); Stites (eds.) BASIC AND CLINICAL IMMUNOLOGY (7th ed.) Lange Medical Publications, Los Altos, CA ("Stites"); Goding, MONOCLONAL ANTIBODIES: PRINCIPLES AND PRACTICE (2d ed.) Academic Press, New York, NY (1986); Kohler (1975) Nature 256:495; Harlow (1988) ANTIBODIES, A LABORATORY MANUAL, Cold Spring Harbor Publications, New York. Antibodies also can be generated *in vitro*, e.g., using recombinant antibody binding site expressing phage display libraries, in addition to the traditional in vivo methods using animals. See, e.g., Hoogenboom (1997) Trends Biotechnol. 15:62-70; Katz (1997) Annu. Rev. Biophys. Biomol. Struct. 26:27-45.

The polypeptides of Group B amino acid sequences and sequences substantially identical thereto or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof, may also be used to generate antibodies which bind specifically to the polypeptides or fragments. The resulting antibodies may be used in immunoaffinity chromatography procedures to isolate or purify the polypeptide or to determine whether the polypeptide is present in a biological sample. In such procedures, a

protein preparation, such as an extract, or a biological sample is contacted with an antibody capable of specifically binding to one of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof.

In immunoaffinity procedures, the antibody is attached to a solid support, such as a bead or other column matrix. The protein preparation is placed in contact with the antibody under conditions in which the antibody specifically binds to one of the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, or fragment thereof. After a wash to remove non-specifically bound proteins, the specifically bound polypeptides are eluted.

The ability of proteins in a biological sample to bind to the antibody may be determined using any of a variety of procedures familiar to those skilled in the art. For example, binding may be determined by labeling the antibody with a detectable label such as a fluorescent agent, an enzymatic label, or a radioisotope. Alternatively, binding of the antibody to the sample may be detected using a secondary antibody having such a detectable label thereon. Particular assays include ELISA assays, sandwich assays, radioimmunoassays and Western Blots.

Polyclonal antibodies generated against the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, for example, a nonhuman. The antibody so obtained will then bind the polypeptide itself. In this manner, even a sequence encoding only a fragment of the polypeptide can be used to generate antibodies which may bind to the whole native polypeptide. Such antibodies can then be used to isolate the polypeptide from cells expressing that polypeptide.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, Nature, 256:495-497, 1975), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, Immunology Today 4:72, 1983) and the EBV-hybridoma technique (Cole, *et al.*, 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96).

Techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to the polypeptides

of Group B amino acid sequences and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof. Alternatively, transgenic mice may be used to express humanized antibodies to these polypeptides or fragments thereof.

Antibodies generated against the polypeptides of Group B amino acid sequences and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof may be used in screening for similar polypeptides from other organisms and samples. In such techniques, polypeptides from the organism are contacted with the antibody and those polypeptides which specifically bind the antibody are detected. Any of the procedures described above may be used to detect antibody binding. One such screening assay is described in "Methods for Measuring Cellulase Activities", *Methods in Enzymology*, Vol 160, pp. 87-116.

<u>Kits</u>

The invention provides kits comprising the compositions, e.g., nucleic acids, expression cassettes, vectors, cells, transgenic seeds or plants or plant parts, polypeptides (e.g., xylanases) and/or antibodies of the invention. The kits also can contain instructional material teaching the methodologies and industrial uses of the invention, as described herein.

<u>Whole cell engineering and measuring metabolic parameters</u>

The methods of the invention provide whole cell evolution, or whole cell engineering, of a cell to develop a new cell strain having a new phenotype, e.g., a new or modified xylanase activity, by modifying the genetic composition of the cell. The genetic composition can be modified by addition to the cell of a nucleic acid of the invention, e.g., a coding sequence for an enzyme of the invention. See, e.g., WO0229032; WO0196551.

To detect the new phenotype, at least one metabolic parameter of a modified cell is monitored in the cell in a "real time" or "on-line" time frame. In one aspect, a plurality of cells, such as a cell culture, is monitored in "real time" or "on-line." In one aspect, a plurality of metabolic parameters is monitored in "real time" or "on-line." Metabolic parameters can be monitored using the xylanases of the invention.

Metabolic flux analysis (MFA) is based on a known biochemistry framework. A linearly independent metabolic matrix is constructed based on the law of mass conservation and on the pseudo-steady state hypothesis (PSSH) on the intracellular metabolites. In practicing the methods of the invention, metabolic networks are established, including the:

• identity of all pathway substrates, products and intermediary metabolites

• identity of all the chemical reactions interconverting the pathway metabolites, the stoichiometry of the pathway reactions,

• identity of all the enzymes catalyzing the reactions, the enzyme reaction kinetics,

• the regulatory interactions between pathway components, e.g. allosteric interactions, enzyme-enzyme interactions etc,

• intracellular compartmentalization of enzymes or any other supramolecular organization of the enzymes, and,

• the presence of any concentration gradients of metabolites, enzymes or effector molecules or diffusion barriers to their movement.

Once the metabolic network for a given strain is built, mathematic presentation by matrix notion can be introduced to estimate the intracellular metabolic fluxes if the on-line metabolome data is available. Metabolic phenotype relies on the changes of the whole metabolic network within a cell. Metabolic phenotype relies on the change of pathway utilization with respect to environmental conditions, genetic regulation, developmental state and the genotype, etc. In one aspect of the methods of the invention, after the on-line MFA calculation, the dynamic behavior of the cells, their phenotype and other properties are analyzed by investigating the pathway utilization. For example, if the glucose supply is increased and the oxygen decreased during the yeast fermentation, the utilization of respiratory pathways will be reduced and/or stopped, and the utilization of the fermentative pathways will dominate. Control of physiological state of cell cultures will become possible after the pathway analysis. The methods of the invention can help determine how to manipulate the fermentation by determining how to change the substrate supply, temperature, use of inducers, etc. to control the physiological state of cells to move along desirable direction. In practicing the methods of the invention, the MFA results can also be compared with transcriptome and proteome data to design experiments and protocols for metabolic engineering or gene shuffling, etc.

In practicing the methods of the invention, any modified or new phenotype can be conferred and detected, including new or improved characteristics in the cell. Any aspect of metabolism or growth can be monitored.

Monitoring expression of an mRNA transcript

In one aspect of the invention, the engineered phenotype comprises increasing or decreasing the expression of an mRNA transcript (e.g., a xylanase message) or generating

new (e.g., xylanase) transcripts in a cell. This increased or decreased expression can be traced by testing for the presence of a xylanase of the invention or by xylanase activity assays. mRNA transcripts, or messages, also can be detected and quantified by any method known in the art, including, e.g., Northern blots, quantitative amplification reactions, hybridization to arrays, and the like. Quantitative amplification reactions include, e.g., quantitative PCR, including, e.g., quantitative reverse transcription polymerase chain reaction, or RT-PCR; quantitative real time RT-PCR, or "real-time kinetic RT-PCR" (see, e.g., Kreuzer (2001) Br. J. Haematol. 114:313-318; Xia (2001) Transplantation 72:907-914).

In one aspect of the invention, the engineered phenotype is generated by knocking out expression of a homologous gene. The gene's coding sequence or one or more transcriptional control elements can be knocked out, e.g., promoters or enhancers. Thus, the expression of a transcript can be completely ablated or only decreased.

In one aspect of the invention, the engineered phenotype comprises increasing the expression of a homologous gene. This can be effected by knocking out of a negative control element, including a transcriptional regulatory element acting in cis- or trans- , or, mutagenizing a positive control element. One or more, or, all the transcripts of a cell can be measured by hybridization of a sample comprising transcripts of the cell, or, nucleic acids representative of or complementary to transcripts of a cell, by hybridization to immobilized nucleic acids on an array.

Monitoring expression of a polypeptides, peptides and amino acids

In one aspect of the invention, the engineered phenotype comprises increasing or decreasing the expression of a polypeptide (e.g., a xylanase) or generating new polypeptides in a cell. This increased or decreased expression can be traced by determining the amount of xylanase present or by xylanase activity assays. Polypeptides, peptides and amino acids also can be detected and quantified by any method known in the art, including, e.g., nuclear magnetic resonance (NMR), spectrophotometry, radiography (protein radiolabeling), electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, various immunological methods, e.g. immunoprecipitation, immunodiffusion, immuno-electrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, gel electrophoresis (e.g., SDS-PAGE), staining with antibodies, fluorescent activated cell sorter (FACS), pyrolysis mass spectrometry, Fourier-Transform Infrared Spectrometry, Raman spectrometry, GC-MS, and LC-Electrospray and

cap-LC-tandem-electrospray mass spectrometries, and the like. Novel bioactivities can also be screened using methods, or variations thereof, described in U.S. Patent No. 6,057,103. Furthermore, as discussed below in detail, one or more, or, all the polypeptides of a cell can be measured using a protein array.

Industrial Applications

The xylanase enzymes of the invention can be highly selective catalysts. They can catalyze reactions with exquisite stereo-, regio- and chemo- selectivities that are unparalleled in conventional synthetic chemistry. Moreover, enzymes are remarkably versatile. The xylanase enzymes of the invention can be tailored to function in organic solvents, operate at extreme pHs (for example, high pHs and low pHs) extreme temperatures (for example, high temperatures and low temperatures), extreme salinity levels (for example, high salinity and low salinity) and catalyze reactions with compounds that are structurally unrelated to their natural, physiological substrates.

Detergent Compositions

The invention provides detergent compositions comprising one or more polypeptides (e.g., xylanases) of the invention, and methods of making and using these compositions. The invention incorporates all methods of making and using detergent compositions, see, e.g., U.S. Patent No. 6,413,928; 6,399,561; 6,365,561; 6,380,147. The detergent compositions can be a one and two part aqueous composition, a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel and/or a paste and a slurry form. The xylanases of the invention can also be used as a detergent additive product in a solid or a liquid form. Such additive products are intended to supplement or boost the performance of conventional detergent compositions and can be added at any stage of the cleaning process.

The actual active enzyme content depends upon the method of manufacture of a detergent composition and is not critical, assuming the detergent solution has the desired enzymatic activity. In one aspect, the amount of xylanase present in the final solution ranges from about 0.001 mg to 0.5 mg per gram of the detergent composition. The particular enzyme chosen for use in the process and products of this invention depends upon the conditions of final utility, including the physical product form, use pH, use temperature, and soil types to be degraded or altered. The enzyme can be chosen to provide optimum activity and stability for any given set of utility conditions. In one aspect, the xylanases of the present invention are active in the pH ranges of from about 4 to about 12 and in the temperature

range of from about 20°C to about 95°C. The detergents of the invention can comprise cationic, semi-polar nonionic or zwitterionic surfactants; or, mixtures thereof.

Xylanases of the invention can be formulated into powdered and liquid detergents having pH between 4.0 and 12.0 at levels of about 0.01 to about 5% (preferably 0.1% to 0.5%) by weight. These detergent compositions can also include other enzymes such as xylanases, cellulases, lipases or endoglycosidases, endo-beta.-1,4-glucanases, beta-glucanases, endo-beta-1,3(4)-glucanases, cutinases, peroxidases, laccases, amylases, glucoamylases, pectinases, reductases, oxidases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xyloglucanases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, pectin methylesterases, cellobiohydrolases and/or transglutaminases. These detergent compositions can also include builders and stabilizers.

The addition of xylanases of the invention to conventional cleaning compositions does not create any special use limitation. In other words, any temperature and pH suitable for the detergent is also suitable for the compositions of the invention as long as the enzyme is active at or tolerant of the pH and/or temperature of the intended use. In addition, the xylanases of the invention can be used in a cleaning composition without detergents, again either alone or in combination with builders and stabilizers.

The present invention provides cleaning compositions including detergent compositions for cleaning hard surfaces, detergent compositions for cleaning fabrics, dishwashing compositions, oral cleaning compositions, denture cleaning compositions, and contact lens cleaning solutions.

In one aspect, the invention provides a method for washing an object comprising contacting the object with a polypeptide of the invention under conditions sufficient for washing. A xylanase of the invention may be included as a detergent additive. The detergent composition of the invention may, for example, be formulated as a hand or machine laundry detergent composition comprising a polypeptide of the invention. A laundry additive suitable for pre-treatment of stained fabrics can comprise a polypeptide of the invention. A fabric softener composition can comprise a xylanase of the invention. Alternatively, a xylanase of the invention can be formulated as a detergent composition for use in general household hard surface cleaning operations. In alternative aspects, detergent additives and detergent compositions of the invention may comprise one or more other enzymes such as a xylanase, a lipase, a cutinase, another xylanase, a carbohydrase, a cellulase, a pectinase, a mannanase, an arabinase, a galactanase, a xylanase, an oxidase, e.g.,

a lactase, and/or a peroxidase (see also, above). The properties of the enzyme(s) of the invention are chosen to be compatible with the selected detergent (i.e. pH-optimum, compatibility with other enzymatic and non-enzymatic ingredients, etc.) and the enzyme(s) is present in effective amounts. In one aspect, xylanase enzymes of the invention are used to remove malodorous materials from fabrics. Various detergent compositions and methods for making them that can be used in practicing the invention are described in, e.g., U.S. Patent Nos. 6,333,301; 6,329,333; 6,326,341; 6,297,038; 6,309,871; 6,204,232; 6,197,070; 5,856,164.

When formulated as compositions suitable for use in a laundry machine washing method, the xylanases of the invention can comprise both a surfactant and a builder compound. They can additionally comprise one or more detergent components, e.g., organic polymeric compounds, bleaching agents, additional enzymes, suds suppressors, dispersants, lime-soap dispersants, soil suspension and anti-redeposition agents and corrosion inhibitors. Laundry compositions of the invention can also contain softening agents, as additional detergent components. Such compositions containing carbohydrase can provide fabric cleaning, stain removal, whiteness maintenance, softening, color appearance, dye transfer inhibition and sanitization when formulated as laundry detergent compositions.

The density of the laundry detergent compositions of the invention can range from about 200 to 1500 g/liter, or, about 400 to 1200 g/liter, or, about 500 to 950 g/liter, or, 600 to 800 g/liter, of composition; this can be measured at about 20°C.

The "compact" form of laundry detergent compositions of the invention is best reflected by density and, in terms of composition, by the amount of inorganic filler salt. Inorganic filler salts are conventional ingredients of detergent compositions in powder form. In conventional detergent compositions, the filler salts are present in substantial amounts, typically 17% to 35% by weight of the total composition. In one aspect of the compact compositions, the filler salt is present in amounts not exceeding 15% of the total composition, or, not exceeding 10%, or, not exceeding 5% by weight of the composition. The inorganic filler salts can be selected from the alkali and alkaline-earth-metal salts of sulphates and chlorides, e.g., sodium sulphate.

Liquid detergent compositions of the invention can also be in a "concentrated form." In one aspect, the liquid detergent compositions can contain a lower amount of water, compared to conventional liquid detergents. In alternative aspects, the water content of the concentrated liquid detergent is less than 40%, or, less than 30%, or, less than 20% by weight

of the detergent composition. Detergent compounds of the invention can comprise formulations as described in WO 97/01629.

Xylanases of the invention can be useful in formulating various cleaning compositions. A number of known compounds are suitable surfactants including nonionic, anionic, cationic, or zwitterionic detergents, can be used, e.g., as disclosed in U.S. Patent Nos. 4,404,128; 4,261,868; 5,204,015. In addition, xylanases can be used, for example, in bar or liquid soap applications, dish care formulations, contact lens cleaning solutions or products, peptide hydrolysis, waste treatment, textile applications, as fusion-cleavage enzymes in protein production, and the like. Xylanases may provide enhanced performance in a detergent composition as compared to another detergent xylanase, that is, the enzyme group may increase cleaning of certain enzyme sensitive stains such as grass or blood, as determined by usual evaluation after a standard wash cycle. Xylanases can be formulated into known powdered and liquid detergents having pH between 6.5 and 12.0 at levels of about 0.01 to about 5% (for example, about 0.1% to 0.5%) by weight. These detergent cleaning compositions can also include other enzymes such as known xylanases, xylanases, amylases, cellulases, lipases or endoglycosidases, as well as builders and stabilizers.

In one aspect, the invention provides detergent compositions having xylanase activity (a xylanase of the invention) for use with fruit, vegetables and/or mud and clay compounds (see, for example, U.S. Pat. No. 5,786,316).

Treating fibers and textiles

The invention provides methods of treating fibers and fabrics using one or more xylanases of the invention. The xylanases can be used in any fiber- or fabric-treating method, which are well known in the art, see, e.g., U.S. Patent No. 6,261,828; 6,077,316; 6,024,766; 6,021,536; 6,017,751; 5,980,581; US Patent Publication No. 20020142438 A1. For example, xylanases of the invention can be used in fiber and/or fabric desizing. In one aspect, the feel and appearance of a fabric is improved by a method comprising contacting the fabric with a xylanase of the invention in a solution. In one aspect, the fabric is treated with the solution under pressure. For example, xylanases of the invention can be used in the removal of stains.

The xylanases of the invention can be used to treat any cellulosic material, including fibers (e.g., fibers from cotton, hemp, flax or linen), sewn and unsewn fabrics, e.g., knits, wovens, denims, yarns, and toweling, made from cotton, cotton blends or natural or manmade cellulosics (e.g. originating from xylan-containing cellulose fibers such as from

wood pulp) or blends thereof. Examples of blends are blends of cotton or rayon/viscose with one or more companion material such as wool, synthetic fibers (e.g. polyamide fibers, acrylic fibers, polyester fibers, polyvinyl alcohol fibers, polyvinyl chloride fibers, polyvinylidene chloride fibers, polyurethane fibers, polyurea fibers, aramid fibers), and cellulose-containing fibers (e.g. rayon/viscose, ramie, hemp, flax/linen, jute, cellulose acetate fibers, lyocell).

The textile treating processes of the invention (using xylanases of the invention) can be used in conjunction with other textile treatments, e.g., scouring and bleaching. Scouring is the removal of non-cellulosic material from the cotton fiber, e.g., the cuticle (mainly consisting of waxes) and primary cell wall (mainly consisting of pectin, protein and xyloglucan). A proper wax removal is necessary for obtaining a high wettability. This is needed for dyeing. Removal of the primary cell walls by the processes of the invention improves wax removal and ensures a more even dyeing. Treating textiles with the processes of the invention can improve whiteness in the bleaching process. The main chemical used in scouring is sodium, hydroxide in high concentrations and at high temperatures. Bleaching comprises oxidizing the textile. Bleaching typically involves use of hydrogen peroxide as the oxidizing agent in order to obtain either a fully bleached (white) fabric or to ensure a clean shade of the dye.

The invention also provides alkaline xylanases (xylanases active under alkaline conditions). These have wide-ranging applications in textile processing, degumming of plant fibers (e.g., plant bast fibers), treatment of pectic wastewaters, paper-making, and coffee and tea fermentations. See, e.g., Hoondal (2002) Applied Microbiology and Biotechnology 59:409-418.

Treating foods and food processing

The xylanases of the invention have numerous applications in food processing industry. For example, in one aspect, the xylanases of the invention are used to improve the extraction of oil from oil-rich plant material, e.g., oil-rich seeds, for example, soybean oil from soybeans, olive oil from olives, rapeseed oil from rapeseed and/or sunflower oil from sunflower seeds.

The xylanases of the invention can be used for separation of components of plant cell materials. For example, xylanases of the invention can be used in the separation of xylan-rich material (e.g., plant cells) into components. In one aspect, xylanases of the invention can be used to separate xylan-rich or oil-rich crops into valuable protein and oil and hull fractions. The separation process may be performed by use of methods known in the art.

The xylanases of the invention can be used in the preparation of fruit or vegetable juices, syrups, extracts and the like to increase yield. The xylanases of the invention can be used in the enzymatic treatment (e.g., hydrolysis of xylan-comprising plant materials) of various plant cell wall-derived materials or waste materials, e.g. from cereals, grains, wine or juice production, or agricultural residues such as vegetable hulls, bean hulls, sugar beet pulp, olive pulp, potato pulp, and the like. The xylanases of the invention can be used to modify the consistency and appearance of processed fruit or vegetables. The xylanases of the invention can be used to treat plant material to facilitate processing of plant material, including foods, facilitate purification or extraction of plant components. The xylanases of the invention can be used to improve feed value, decrease the water binding capacity, improve the degradability in waste water plants and/or improve the conversion of plant material to ensilage, and the like.

In one aspect, xylanases of the invention are used in baking applications, e.g., cookies and crackers, to hydrolyze arabinoxylans and create non-sticky doughs that are not difficult to machine and to reduce biscuit size. Use xylanases of the invention to hydrolyze arabinoxylans is used to prevent rapid rehydration of the baked product resulting in loss of crispiness and reduced shelf-life. In one aspect, xylanases of the invention are used as additives in dough processing. In one aspect, xylanases of the invention are used in dough conditioning, wherein in one aspect the xylanases possess high activity over a temperature range of about 25-35°C and at near neutral pH (7.0 – 7.5). In one aspect, dough conditioning enzymes can be inactivated at the extreme temperatures of baking (>500°F).

In one aspect, xylanases of the invention are used as additives in dough processing to perform optimally under dough pH and temperature conditions. In one aspect, an enzyme of the invention is used for dough conditioning. In one aspect, a xylanase of the invention possesses high activity over a temperature range of 25-35°C and at near neutral pH (7.0 – 7.5). In one aspect, the enzyme is inactivated at the extreme temperatures of baking, for example, >500°F.

Paper or pulp treatment

The xylanases of the invention can be in paper or pulp treatment or paper deinking. For example, in one aspect, the invention provides a paper treatment process using a xylanase of the invention. In one aspect, the xylanase of the invention is applicable both in reduction of the need for a chemical bleaching agent, such as chlorine dioxide, and in high alkaline and high temperature environments. In one aspect, the xylanase of the invention is a

thermostable alkaline endoxylanase which can effect a greater than 25% reduction in the chlorine dioxide requirement of kraft pulp with a less than 0.5% pulp yield loss. In one aspect, boundary parameters are pH 10, 65-85°C and treatment time of less than 60 minutes at an enzyme loading of less than 0.001 wt%. A pool of xylanases may be tested for the ability to hydrolyze dye-labeled xylan at, for example, pH 10 and 60°C. The enzymes that test positive under these conditions may then be evaluated at, for example pH 10 and 70°C. Alternatively, enzymes may be tested at pH 8 and pH 10 at 70°C. In discovery of xylanases desirable in the pulp and paper industry libraries from high temperature or highly alkaline environments were targeted. Specifically, these libraries were screened for enzymes functioning at alkaline pH and a temperature of approximately 45°C. In another aspect, the xylanases of the invention are useful in the pulp and paper industry in degradation of a lignin hemicellulose linkage, in order to release the lignin.

Animal feeds and food or feed additives

The invention provides methods for treating animal feeds and foods and food or feed additives using xylanases of the invention, animals including mammals (e.g., humans), birds, fish and the like. The invention provides animal feeds, foods, and additives comprising xylanases of the invention. In one aspect, treating animal feeds, foods and additives using xylanases of the invention can help in the availability of nutrients, e.g., starch, protein, and the like, in the animal feed or additive. By breaking down difficult to digest proteins or indirectly or directly unmasking starch (or other nutrients), the xylanase makes nutrients more accessible to other endogenous or exogenous enzymes. The xylanase can also simply cause the release of readily digestible and easily absorbed nutrients and sugars.

When added to animal feed, xylanases of the invention improve the *in vivo* break-down of plant cell wall material partly due to a reduction of the intestinal viscosity (see, e.g., Bedford et al., Proceedings of the 1st Symposium on Enzymes in Animal Nutrition, 1993, pp. 73-77), whereby a better utilization of the plant nutrients by the animal is achieved. Thus, by using xylanases of the invention in feeds the growth rate and/or feed conversion ratio (i.e. the weight of ingested feed relative to weight gain) of the animal is improved.

The animal feed additive of the invention may be a granulated enzyme product which may readily be-mixed with feed components. Alternatively, feed additives of the invention can form a component of a pre-mix. The granulated enzyme product of the invention may be coated or uncoated. The particle size of the enzyme granulates can be compatible with that of feed and pre-mix components. This provides a safe and convenient

mean of incorporating enzymes into feeds. Alternatively, the animal feed additive of the invention may be a stabilized liquid composition. This may be an aqueous or oil-based slurry. See, e.g., U.S. Patent No. 6,245,546.

Xylanases of the present invention, in the modification of animal feed or a food, can process the food or feed either *in vitro* (by modifying components of the feed or food) or *in vivo*. Xylanases can be added to animal feed or food compositions containing high amounts of xylans, e.g. feed or food containing plant material from cereals, grains and the like. When added to the feed or food the xylanase significantly improves the *in vivo* break-down of xylan-containing material, e.g., plant cell walls, whereby a better utilization of the plant nutrients by the animal (e.g., human) is achieved. In one aspect, the growth rate and/or feed conversion ratio (i.e. the weight of ingested feed relative to weight gain) of the animal is improved. For example a partially or indigestible xylan-comprising protein is fully or partially degraded by a xylanase of the invention, e.g. in combination with another enzyme, e.g., beta-galactosidase, to peptides and galactose and/or galactooligomers. These enzyme digestion products are more digestible by the animal. Thus, xylanases of the invention can contribute to the available energy of the feed or food. Also, by contributing to the degradation of xylan-comprising proteins, a xylanase of the invention can improve the digestibility and uptake of carbohydrate and non-carbohydrate feed or food constituents such as protein, fat and minerals.

In another aspect, xylanase of the invention can be supplied by expressing the enzymes directly in transgenic feed crops (as, e.g., transgenic plants, seeds and the like), such as grains, cereals, corn, soy bean, rape seed, lupin and the like. As discussed above, the invention provides transgenic plants, plant parts and plant cells comprising a nucleic acid sequence encoding a polypeptide of the invention. In one aspect, the nucleic acid is expressed such that the xylanase of the invention is produced in recoverable quantities. The xylanase can be recovered from any plant or plant part. Alternatively, the plant or plant part containing the recombinant polypeptide can be used as such for improving the quality of a food or feed, e.g., improving nutritional value, palatability, and rheological properties, or to destroy an antinutritive factor.

In one aspect, the invention provides methods for removing oligosaccharides from feed prior to consumption by an animal subject using a xylanase of the invention. In this process a feed is formed having an increased metabolizable energy value. In addition to xylanases of the invention, galactosidases, cellulases and combinations thereof can be used. In one aspect, the enzyme is added in an amount equal to between about 0.1% and 1% by

weight of the feed material. In one aspect, the feed is a cereal, a wheat, a grain, a soybean (e.g., a ground soybean) material. See, e.g., U.S. Patent No. 6,399,123.

In another aspect, the invention provides methods for utilizing xylanase as a nutritional supplement in the diets of animals by preparing a nutritional supplement containing a recombinant xylanase enzyme comprising at least thirty contiguous amino acids of an amino acid of Group B amino acid sequences, and administering the nutritional supplement to an animal to increase the utilization of xylan contained in food ingested by the animal.

In yet another aspect, the invention provides an edible pelletized enzyme delivery matrix and method of use for delivery of xylanase to an animal, for example as a nutritional supplement. The enzyme delivery matrix readily releases a xylanase enzyme, such as one having an amino acid sequence of group B amino acid sequences, or at least 30 contiguous amino acids thereof, in aqueous media, such as, for example, the digestive fluid of an animal. The invention enzyme delivery matrix is prepared from a granulate edible carrier selected from such components as grain germ that is spent of oil, hay, alfalfa, timothy, soy hull, sunflower seed meal, wheat midd, and the like, that readily disperse the recombinant enzyme contained therein into aqueous media. In use, the edible pelletized enzyme delivery matrix is administered to an animal to delivery of xylanase to the animal. Suitable grain-based substrates may comprise or be derived from any suitable edible grain, such as wheat, corn, soy, sorghum, alfalfa, barley, and the like. An exemplary grain-based substrate is a corn-based substrate. The substrate may be derived from any suitable part of the grain, but is preferably a grain germ approved for animal feed use, such as corn germ that is obtained in a wet or dry milling process. The grain germ preferably comprises spent germ, which is grain germ from which oil has been expelled, such as by pressing or hexane or other solvent extraction. Alternatively, the grain germ is expeller extracted, that is, the oil has been removed by pressing.

The enzyme delivery matrix of the invention is in the form of discrete plural particles, pellets or granules. By "granules" is meant particles that are compressed or compacted, such as by a pelletizing, extrusion, or similar compacting to remove water from the matrix. Such compression or compacting of the particles also promotes intraparticle cohesion of the particles. For example, the granules can be prepared by pelletizing the grain-based substrate in a pellet mill. The pellets prepared thereby are ground or crumbled to a granule size suitable for use as an adjuvant in animal feed. Since the matrix is itself approved for use in animal feed, it can be used as a diluent for delivery of enzymes in animal feed.

Preferably, the enzyme delivery matrix is in the form of granules having a granule size ranging from about 4 to about 400 mesh (USS); more preferably, about 8 to about 80 mesh; and most preferably about 14 to about 20 mesh. If the grain germ is spent via solvent extraction, use of a lubricity agent such as corn oil may be necessary in the pelletizer, but such a lubricity agent ordinarily is not necessary if the germ is expeller extracted. In other aspects of the invention, the matrix is prepared by other compacting or compressing processes such as, for example, by extrusion of the grain-based substrate through a die and grinding of the extrudate to a suitable granule size.

The enzyme delivery matrix may further include a polysaccharide component as a cohesiveness agent to enhance the cohesiveness of the matrix granules. The cohesiveness agent is believed to provide additional hydroxyl groups, which enhance the bonding between grain proteins within the matrix granule. It is further believed that the additional hydroxyl groups so function by enhancing the hydrogen bonding of proteins to starch and to other proteins. The cohesiveness agent may be present in any amount suitable to enhance the cohesiveness of the granules of the enzyme delivery matrix. Suitable cohesiveness agents include one or more of dextrins, maltodextrins, starches, such as corn starch, flours, cellulosics, hemicellulosics, and the like. For example, the percentage of grain germ and cohesiveness agent in the matrix (not including the enzyme) is 78% corn germ meal and 20% by weight of corn starch.

Because the enzyme-releasing matrix of the invention is made from biodegradable materials, the matrix may be subject to spoilage, such as by molding. To prevent or inhibit such molding, the matrix may include a mold inhibitor, such as a propionate salt, which may be present in any amount sufficient to inhibit the molding of the enzyme-releasing matrix, thus providing a delivery matrix in a stable formulation that does not require refrigeration.

The xylanase enzyme contained in the invention enzyme delivery matrix and methods is preferably a thermostable xylanase, as described herein, so as to resist inactivation of the xylanase during manufacture where elevated temperatures and/or steam may be employed to prepare the palletized enzyme delivery matrix. During digestion of feed containing the invention enzyme delivery matrix, aqueous digestive fluids will cause release of the active enzyme. Other types of thermostable enzymes and nutritional supplements that are thermostable can also be incorporated in the delivery matrix for release under any type of aqueous conditions.

A coating can be applied to the invention enzyme matrix particles for many different purposes, such as to add a flavor or nutrition supplement to animal feed, to delay release of animal feed supplements and enzymes in gastric conditions, and the like. Or, the coating may be applied to achieve a functional goal, for example, whenever it is desirable to slow release of the enzyme from the matrix particles or to control the conditions under which the enzyme will be released. The composition of the coating material can be such that it is selectively broken down by an agent to which it is susceptible (such as heat, acid or base, enzymes or other chemicals). Alternatively, two or more coatings susceptible to different such breakdown agents may be consecutively applied to the matrix particles.

The invention is also directed towards a process for preparing an enzyme-releasing matrix. In accordance with the invention, the process comprises providing discrete plural particles of a grain-based substrate in a particle size suitable for use as an enzyme-releasing matrix, wherein the particles comprise a xylanase enzyme encoded by an amino acid sequence of Group B amino acid sequences or at least 30 consecutive amino acids thereof. Preferably, the process includes compacting or compressing the particles of enzyme-releasing matrix into granules, which most preferably is accomplished by pelletizing. The mold inhibitor and cohesiveness agent, when used, can be added at any suitable time, and preferably are mixed with the grain-based substrate in the desired proportions prior to pelletizing of the grain-based substrate. Moisture content in the pellet mill feed preferably is in the ranges set forth above with respect to the moisture content in the finished product, and preferably is about 14-15%. Preferably, moisture is added to the feedstock in the form of an aqueous preparation of the enzyme to bring the feedstock to this moisture content. The temperature in the pellet mill preferably is brought to about 82°C with steam. The pellet mill may be operated under any conditions that impart sufficient work to the feedstock to provide pellets. The pelleting process itself is a cost-effective process for removing water from the enzyme-containing composition.

In one aspect, the pellet mill is operated with a 1/8 in. by 2 in. die at 100 lb./min. pressure at 82°C. to provide pellets, which then are crumbled in a pellet mill crumbler to provide discrete plural particles having a particle size capable of passing through an 8 mesh screen but being retained on a 20 mesh screen.

The thermostable xylanases of the invention can be used in the pellets of the invention. They can have high optimum temperatures and high heat resistance such that an enzyme reaction at a temperature not hitherto carried out can be achieved. The gene encoding the xylanase according to the present invention (e.g. as set forth in any of the

sequences in Group A nucleic acid sequences) can be used in preparation of xylanases (e.g. using GSSM™ as described herein) having characteristics different from those of the xylanases of Group B amino acid sequences (in terms of optimum pH, optimum temperature, heat resistance, stability to solvents, specific activity, affinity to substrate, secretion ability, translation rate, transcription control and the like). Furthermore, a polynucleotide of Group A nucleic acid sequences may be employed for screening of variant xylanases prepared by the methods described herein to determine those having a desired activity, such as improved or modified thermostability or thermotolerance. For example, U.S. Patent No. 5,830,732, describes a screening assay for determining thermotolerance of a xylanase.

Waste treatment

The xylanases of the invention can be used in a variety of other industrial applications, e.g., in waste treatment. For example, in one aspect, the invention provides a solid waste digestion process using xylanases of the invention. The methods can comprise reducing the mass and volume of substantially untreated solid waste. Solid waste can be treated with an enzymatic digestive process in the presence of an enzymatic solution (including xylanases of the invention) at a controlled temperature. This results in a reaction without appreciable bacterial fermentation from added microorganisms. The solid waste is converted into a liquefied waste and any residual solid waste. The resulting liquefied waste can be separated from said any residual solidified waste. See e.g., U.S. Patent No. 5,709,796.

Oral care products

The invention provides oral care product comprising xylanases of the invention. Exemplary oral care products include toothpastes, dental creams, gels or tooth powders, odontics, mouth washes, pre- or post brushing rinse formulations, chewing gums, lozenges, or candy. See, e.g., U.S. Patent No. 6,264,925.

Brewing and fermenting

The invention provides methods of brewing (e.g., fermenting) beer comprising xylanases of the invention. In one exemplary process, starch-containing raw materials are disintegrated and processed to form a malt. A xylanase of the invention is used at any point in the fermentation process. For example, xylanases of the invention can be used in the processing of barley malt. The major raw material of beer brewing is barley malt. This can be a three stage process. First, the barley grain can be steeped to increase water content, e.g., to around about 40%. Second, the grain can be germinated by incubation at 15 to 25°C for 3 to 6 days when enzyme synthesis is stimulated under the control of gibberellins. In one

aspect, xylanases of the invention are added at this (or any other) stage of the process. Xylanases of the invention can be used in any beer or alcoholic beverage producing process, as described, e.g., in U.S. Patent No. 5,762,991; 5,536,650; 5,405,624; 5,021,246; 4,788,066.

In one aspect, an enzyme of the invention is used to improve filterability and wort viscosity and to obtain a more complete hydrolysis of endosperm components. Use of an enzyme of the invention would also increase extract yield. The process of brewing involves germination of the barley grain (malting) followed by the extraction and the breakdown of the stored carbohydrates to yield simple sugars that are used by yeast for alcoholic fermentation. Efficient breakdown of the carbohydrate reserves present in the barley endosperm and brewing adjuncts requires the activity of several different enzymes.

In one aspect, an enzyme of the invention has activity in slightly acidic pH (e.g., 5.5-6.0) in, e.g., the 40°C to 70°C temperature range; and, in one aspect, with inactivation at 95°C. Activity under such conditions would be optimal, but are not an essential requirement for efficacy. In one aspect, an enzyme of the invention has activity between 40-75° C, and pH 5.5-6.0; stable at 70° for at least 50 minutes, and, in one aspect, is inactivated at 96-100 °C. Enzymes of the invention can be used with other enzymes, e.g., beta-1,4-endoglucanases and amylases.

Medical and research applications

Xylanases of the invention can be used as antimicrobial agents due to their bacteriolytic properties. Xylanases of the invention can be used to eliminating or protecting animals from salmonellae, as described in e.g., PCT Application Nos. WO0049890 and WO9903497.

Other industrial applications

Xylanases of the invention can be used, including Group B amino acid sequences are used in a wide variety of food, animal feed and beverage applications. New xylanases are discovered by screening existing libraries and DNA libraries constructed from diverse mesophilic and moderately thermophilic locations as well as from targeted sources including digestive flora, microorganisms in animal waste, soil bacteria and highly alkaline habitats. Biotrap and primary enrichment strategies using arabinoxylan substrates and/or non-soluble polysaccharide fractions of animal feed material are also useful.

Two screening formats (activity-based and sequence-based) are used in the discovery of novel xylanases. The activity-based approach is direct screening for xylanase activity in agar plates using a substrate such as AZO-xylan (Megazyme). Alternatively a

sequence-based approach may be used, which relies on bioinformatics and molecular biology to design probes for hybridization and biopanning. See, for example, U.S. Patents No. 6,054,267, 6,030,779, 6,368,798, 6,344,328. Hits from the screening are purified, sequenced, characterized (for example, determination of specificity, temperature and pH optima), analyzed using bioinformatics, subcloned and expressed for basic biochemical characterization. These methods may be used in screening for xylanases useful in a myriad of applications, including dough conditioning and as animal feed additive enzymes.

In characterizing enzymes obtained from screening, the exemplary utility in dough processing and baking applications may be assessed. Characterization may include, for example, measurement of substrate specificity (xylan, arabinoxylan, CMC, BBG), temperature and pH stability and specific activity. A commercial enzyme may be used as a benchmark. In one aspect, the enzymes of the invention have significant activity at pH ≥ 7 and 25-35° C, are inactive on insoluble xylan, are stable and active in 50-67% sucrose.

In another aspect, utility as feed additives may be assessed from characterization of candidate enzymes. Characterization may include, for example, measurement of substrate specificity (xylan, arabinoxylan, CMC, BβG), temperature and pH stability, specific activity and gastric stability. In one aspect the feed is designed for a monogastric animal and in another aspect the feed is designed for a ruminant animal. In one aspect, the enzymes of the invention have significant activity at pH 2-4 and 35-40°C, a half-life greater than 30 minutes in gastric fluid, formulation (in buffer or cells) half-life greater than 5 minutes at 85°C and are used as a monogastric animal feed additive. In another aspect, the enzymes of the invention have one or more of the following characteristics: significant activity at pH 6.5-7.0 and 35-40°C, a half-life greater than 30 minutes in rumen fluid, formulation stability as stable as dry powder and are used as a ruminant animal feed additive.

Enzymes are reactive toward a wide range of natural and unnatural substrates, thus enabling the modification of virtually any organic lead compound. Moreover, unlike traditional chemical catalysts, enzymes are highly enantio- and regio-selective. The high degree of functional group specificity exhibited by enzymes enables one to keep track of each reaction in a synthetic sequence leading to a new active compound. Enzymes are also capable of catalyzing many diverse reactions unrelated to their physiological function in nature. For example, peroxidases catalyze the oxidation of phenols by hydrogen peroxide. Peroxidases can also catalyze hydroxylation reactions that are not related to the native function of the

enzyme. Other examples are xylanases which catalyze the breakdown of polypeptides. In organic solution some xylanases can also acylate sugars, a function unrelated to the native function of these enzymes.

The present invention exploits the unique catalytic properties of enzymes. Whereas the use of biocatalysts (i.e., purified or crude enzymes, non-living or living cells) in chemical transformations normally requires the identification of a particular biocatalyst that reacts with a specific starting compound, the present invention uses selected biocatalysts and reaction conditions that are specific for functional groups that are present in many starting compounds. Each biocatalyst is specific for one functional group, or several related functional groups and can react with many starting compounds containing this functional group. The biocatalytic reactions produce a population of derivatives from a single starting compound. These derivatives can be subjected to another round of biocatalytic reactions to produce a second population of derivative compounds. Thousands of variations of the original compound can be produced with each iteration of biocatalytic derivatization.

Enzymes react at specific sites of a starting compound without affecting the rest of the molecule, a process which is very difficult to achieve using traditional chemical methods. This high degree of biocatalytic specificity provides the means to identify a single active compound within the library. The library is characterized by the series of biocatalytic reactions used to produce it, a so-called "biosynthetic history". Screening the library for biological activities and tracing the biosynthetic history identifies the specific reaction sequence producing the active compound. The reaction sequence is repeated and the structure of the synthesized compound determined. This mode of identification, unlike other synthesis and screening approaches, does not require immobilization technologies and compounds can be synthesized and tested free in solution using virtually any type of screening assay. It is important to note, that the high degree of specificity of enzyme reactions on functional groups allows for the "tracking" of specific enzymatic reactions that make up the biocatalytically produced library.

Many of the procedural steps are performed using robotic automation enabling the execution of many thousands of biocatalytic reactions and screening assays per day as well as ensuring a high level of accuracy and reproducibility. As a result, a library of derivative compounds can be produced in a matter of weeks which would take years to produce using current chemical methods. (For further teachings on modification of molecules, including small molecules, see PCT/US94/09174).

The invention will be further described with reference to the following examples; however, it is to be understood that the invention is not limited to such examples.

EXAMPLES

EXAMPLE 1: PLATE BASED ENDOGLYCOSIDASE ENZYME DISCOVERY: EXPRESSION SCREENING

Titer determination of Lambda Library: Add 1.0 µL of Lambda Zap Express amplified library stock to 600µL *E. coli* MRF' cells (OD_{600}=1.0). Dilute MRF' stock with 10mM $MgSO_4$. Incubate mixture at 37°C for 15 minutes, then transfer suspension to 5-6mL of NZY top agar at 50 °C and gently mix. Immediately pour agar solution onto large (150mm) NZY media plate and allow top agar to solidify completely (approximately 30 minutes). Invert the plate. Incubate the plate at 39°C for 8-12 hours. (The number of plaques is approximated. Phage titer determined to give 50,000 pfu/plate. Dilute an aliquot of Library phage with SM buffer if needed.)

Substrate screening: Add Lambda Zap Express (50,000 pfu) from amplified library to 600µL of *E. coli* MRF' cells (OD_{600}=1.0) and incubate at 37°C for 15 minutes. While phage/cell suspension is incubating, add 1.0mL of desired polysaccharide dye-labeled substrate (usually 1-2% w/v) to 5.0mL NZY top agar at 50°C and mix thoroughly. (Solution kept at 50°C until needed.) Transfer the cell suspension to substrate/top agar solution and gently mix. Immediately pour solution onto large (150mm) NZY media plate. Allow top agar to solidify completely (approximately 30 minutes), then invert plate. Incubate plate at 39°C for 8-12 hours. Observe plate for clearing zones (halos) around plaques. Core plaques with halos out of agar and transfer to a sterile micro tube. (A large bore 200µL pipette tip works well to remove (core) the agar plug containing the desired plaque.) Resuspend phage in 500µL SM buffer. Add 20µL chloroform to inhibit any further cell growth.

Isolation of pure clones: Add 5µL of resuspended phage suspension to 500µL of *E. coli* MRF' cells (OD_{600}=1.0). Incubate at 37°C for 15 minutes. While phage/cell suspension is incubating, add 600µL of desired polysaccharide dye-labeled substrate (usually 1-2% w/v) to 3.0mL NZY top agar at 50°C and mix thoroughly. (Solution kept at 50°C until needed.) Transfer cell suspension to substrate/top agar solution and gently mix. Immediately pour solution onto small (90mm) NZY media plate and allow top agar to solidify completely

(approximately 30 minutes), then invert plate. Incubate plate at 39°C for 8-12 hours. Plate observed for a clearing zone (halo) around a single plaque (pure clone). (If a single plaque cannot be isolated, adjust titer and replate phage suspension.) Phage are resuspended in 500µL SM buffer and 20µL Chloroform is added to inhibit any further cell growth.

Excision of pure clone: Allow pure phage suspension to incubate at room temperature for 2 to 3 hours or overnight at 4°C. Add 100µL of pure phage suspension to 200µL *E. coli* MRF' cells (OD_{600}=1.0). Add 1.0µL of ExAssist helper phage (>1 x 10^6 pfu/mL; Stratagene). Incubate suspension at 37°C for 15 minutes. Add 3.0 mL of 2 x YT media to cell suspension. Incubate at 37°C for 2-2.5 hours while shaking. Transfer tube to 70°C for 20 minutes. Transfer 50-100 µL of phagemid suspension to a micro tube containing 200µL of *E. coli* Exp 505 cells (OD_{600}=1.0). Incubate suspension at 37°C for 45 minutes. Plate 100 µL of cell suspension on $LB_{kan\ 50}$ media (LB media with Kanamycin 50µg/mL). Incubate plate at 37°C for 8-12 hours. Observe plate for colonies. Any colonies that grow contain the pure phagemid. Pick a colony and grow a small (3-10mL) liquid culture for 8-12 hours. Culture media is liquid $LB_{kan\ 50}$.

Activity verification: Transfer 1.0mL of liquid culture to a sterile micro tube. Centrifuge at 13200 rpm (16000 g's) for 1 minute. Discard supernatant and add 200µL of phosphate buffer pH 6.2. Sonicate for 5 to 10 seconds on ice using a micro tip. Add 200 µL of appropriate substrate, mix gently and incubate at 37 °C for 1.5-2 hours. A negative control should also be run that contains only buffer and substrate. Add 1.0mL absolute ethanol (200 proof) to suspension and mixed. Centrifuge at 13200 rpm for 10 minutes. Observe supernatant for color. Amount of coloration may vary, but any tubes with more coloration than control is considered positive for activity. A spectrophotometer can be used for this step if so desired or needed. (For Azo-xylan, Megazyme, read at 590nm).

RFLP of pure clones from same Libraries: Transfer 1.0mL of liquid culture to a sterile micro tube. Centrifuge at 13200 rpm (16000 g's) for 1 minute. Follow QIAprep spin mini kit (Qiagen) protocol for plasmid isolation and use 40 µL holy water as the elution buffer. Transfer 10 µL plasmid DNA to a sterile micro tube. Add 1.5µL Buffer 3 (New England Biolabs), 1.5µL 100X BSA solution (New England Biolabs) and 2.0µL holy water. To this add 1.0µL Not 1 and 1.0µL Pst 1 restriction endonucleases (New England Biolabs). Incubate for 1.5 hours at 37°C. Add 3.0µL 6X Loading buffer (Invitrogen). Run 15µL of

digested sample on a 1.0% agarose gel for 1-1.5 hours at 120 volts. View the gel with a gel imager. Perform sequence analysis on all clones with a different digest pattern.

Table 6 describes various properties of exemplary enzymes of the invention.

Table 6

SEQ ID NO.	Topt*	Tstab**	pHopt*	Significant activities	pI	M_w	Notes
151, 152	50°C	<1 min at 65°C	5.5-9.0	AZO-xylan	5.7	40.2	
155, 156	50°C	<1 min at 65°C	5.5-8.0	AZO-xylan	8.8	62.7	
169, 170	50°C	> 1 min at 65°C; < 1 min at 85°C	7.0	AZO-xylan	8.7	36.7	
195, 196	50°C	>1 min at 65°C < 10 min, < 1 min 85°C	5.5	AZO-xylan	8.5	36.7	
215, 216	85°C	<3 min at 85°C	5.5-8.0	AZO-xylan	8.6	34.8	
47, 48	50°C	< 0.5 min at 65°C; < 1 min at 85°C	7.0-8.0	AZO-xylan	6.2	40.3	
191, 192	^{3}85°C	> 30 sec at 85°C	5.5	AZO-xylan	7.8	34.6	
247, 248	50°C	< 1 min at 65°C	8.0	AZO-xylan	9.4	43.5	
7, 8	50°C	> 1 min 85°C < 5 min	5.5	AZO-xylan	4.5	55.3	
221, 222	50-65°C	<1 min at 75°C	5.5	AZO-xylan	8.3	34.6	
163, 164	65°C	<1 min at 65°C	7.0	AZO-xylan	6.3	36.0	
19, 20	37°C	<5 min at 50°C	7.0 - 8.0	AZO-xylan	9.2	41.5	
87, 88	37 - 50°C	< 1 min at 85°C	8.0	AZO-xylan	5.2	36.7	
81, 82	50°C	< 1 min at 65°C	7.0 - 9.0	AZO-xylan	5.3	38.8	
91, 92	50°C	< 1 min at 65°C	7 - 8	AZO-xylan, AZO-CMC	5.4	39.0	
61, 62	37°C	<5 min at 50°C	7.0 - 9.0	AZO-xylan, AZO-CMC	5.4	40	
159, 160	85°C	< 30 sec at 85°C	5.5	AZO-xylan	8.3	34.5	
233, 234	50°C	> 30 sec < 1 min at 65°c; < 1 min at 85°C	7.0	AZO-xylan	8.5	35.1	
203, 204	50 - 65°C	> 1 min at 65°C < 5 min, < 1 min 85°C	5.5	AZO-xylan	9.5	21.7	
181, 182	^{3}85°C	> 1 min at 85°C	5.5-8.0	AZO-xylan	8.8	35.5	
227, 228	65°C	>1 min at 85°C < 5 min	5.5 - 7.0	AZO-xylan	7.8	25.8	
45, 46	^{3}45°C	^{3}5 min 45°C, <0.5 min 55°C	> 5.5	AZO-xylan	6.7	40.4	***
231, 232	65°C	>10 min at 50°C	5.5 - 7.0	AZO-xylan	8.4	31.4	
129, 130	65°C	<1min at 75°C	5.5	AZO-xylan	5.1	116	
93, 94	50°C	< 1 min at 60°C	8.0 - 9.0	AZO-xylan	5.3	39.1	
189, 190	65°C	<1 min at 65°C	5.5	AZO-xylan	9.2	20.3	****
49, 50	70°C	<20 min 70°C	>5	AZO-xylan	5.7	38.9	
85, 86	50°C	>5 min at 85°C	5.5 - 7.0	AZO-xylan	6.1	48.4	
99, 100	50°C	<1 min at 75°C	5.5 - 8.0	AZO-xylan	10.8	36.6	
123, 124	^{3}85°C	<30 sec 100 °C	5.5-7.0	AZO-xylan	6.1	44.1	
249, 250	45°C	>1 min 75°C < 10 min	5.5	AZO-xylan	5.3	93	
167, 168	85°C	< 5 min 85°C	5.5	AZO-xylan	9.5	21.7	
207, 208	75°C	< 5 min 65 °C	5.5	AZO-xylan	9.1	20.4	
251, 252	65-75°C	< 1 min 85 °C	5.5	AZO-xylan	8.8	20.4	*****
11, 12	<90°C	<40 min 70°C	>6	AZO-xylan	6.8	43.9	
177, 178	65°C	< 1 min at 75°C	5.5	AZO-xylan	8.7	44.6	
9, 10	50°C	<1min at 65°C	5.5 - 7.0	AZO-xylan	4.9	46.1	
43, 44	37°C	unstable	5.5-7.0	AZO-xylan	4.9	39.1	
113, 114	65 - 75°C	< 1 min at 75°C	5.5 - 8.0	AZO-xylan	5	41.2	

SEQ ID NO.	Topt*	Tstab**	pHopt*	Significant activities	pI	M_w	Notes
75, 76	50°C	< 1 min 85°C	7.0 - 9.0	AZO-xylan	4.7	39.4	
111, 112	37°C	>10 min 50°C	7 - 8	AZO-xylan	5.6	41.0	
117, 118	37°C	unstable	7-8	AZO-xylan	9.1	53.3	
115, 116	-	-	-	AZO-xylan	8.9	50.8	
125, 126	37°C	-	8.0	AZO-xylan	5.3	41.1	
137, 138	50°C	< 30 sec at 65°C	5.5	AZO-xylan	5.7	38.5	
69, 70	³85°C	< 5 min at 85°C	5.5-9.0	AZO-xylan	6.4	58.0	
205, 206	50°C	<1min at 65°C	5.5 - 8	AZO-xylan	4.3	35.1	
211, 212	50°C	<1min at 65°C	5.5	AZO-xylan	4.4	35.4	
197, 198	65°C	<1 min at 65°C	5.5	AZO-xylan	8.8	20.1	
31, 32	37°C	unstable	7.0	AZO-xylan	5.1	54.4	
13, 14	50°C	<1 min at 65°C	7	AZO-xylan	5.5	40.0	
65, 66	50°C	< 1 min at 65°C	5.5	AZO-xylan, AZO-CMC	4.8	55.5	
257, 258	37°C	unstable	5.5	AZO-xylan, AZO-barley β-glucan, AZO-CMC	5.3	100.8	
57, 58	50°C	<1min at 65°C	7.0	AZO-xylan	4.8	56.7	
185, 186	50-75°C	< 1 min at 80°C	5.5	AZO-xylan	8.8	23.2	
243, 244	75°C	>0.5 min @ 85°C	5.5	AZO-xylan	8.8	44.4	
77, 78	50°C	< 5 min at 65°C, < 1 min 85°C	5.5	AZO-xylan	5.3	44.5	
229, 230	37°C	³30 min 55°C, < 5 min 75°C	5.5	AZO-xylan	8.7	20.6	******
109, 110	65°C	>0.5 min @ 75°C	5.5	AZO-xylan	4.9	45.2	
193, 194	65°C	< 1 min at 75°C	5.5	AZO-xylan	5.4	29.1	
173, 174	65°C	< 1 min at 80°C	7.0	AZO-xylan	7.6	51.6	
59, 60	37°C	<1min at 65°C	7.0	AZO-xylan	6.6	42.5	
101, 102	50°C	>0.5 min @ 65°C	7.0	AZO-xylan	8.7	41.1	
55, 56	37°C	> 5 min at 50°C; < 1 min at 85°C	7.0	AZO-xylan	6.5	41.8	
15, 16	50°C	< 1 min at 65°C	7.0	AZO-xylan	6.4	40.2	
131, 132	-	-	-	AZO-xylan	5.6	42.1	
145, 146	65-85°C	< 1 min at 85°C	5.5	AZO-xylan	5.2	43.7	
219, 220	-	-	5.5	AZO-xylan	6.6	34.5	
253, 254	65°C	> .5 min at 85°C	5.5 - 7	AZO-xylan	7.8	34.6	
255, 256	65°C	> 1 min 65°C <3 min	5.5-7.0	AZO-xylan	8.3	35.0	

* pH or temperature optima determined by initial rates using AZO-AZO-xylan as a substrate
** thermal stability, time that enzyme retained significant activity (approx. > 50 %)
*** Dough conditioning
**** GSSM™ parent for thermal tolerance evolution for animal feed applications
***** N35D mutation made to increase low pH activity- based on public knowledge- mutant enzyme's relative activity at pH 4 significantly increased
****** Dough conditioning

EXAMPLE 2: GSSM™ SCREEN FOR THERMAL TOLERANT MUTANTS

The following example describes an exemplary method for screening for thermally tolerant enzymes.

Master Plates: Prepare plates for a colony picker by labeling 96 well plates and aliquoting 200 μL LB Amp100 into each well. (~20ml needed per 96 well plate). After the plates are

returned from the picker, remove media from row 6 from plate A. Replace with an inoculation of SEQ ID NO: 189. Place in a humidified 37°C incubator overnight.

Assay Plates: Pin tool cultures into a fresh 96 well plate (200 μL /well LB Amp100). Remove plastic cover and replace with Gas Permeable Seal. Place in a humidified incubator overnight. Remove the seal and replace plastic lid. Spin cultures down in tabletop centrifuge at 3000 rpm for 10 min. Remove supernatant by inversion onto a paper towel. Aliquot 45 μL Cit-Phos-KCl buffer pH 6 into each well. Replace the plastic lid with an aluminum plate seal. Use a roller to get a good seal. Resuspend cells in a plate shaker at level 6-7 for ~30 seconds.

Place the 96 well plate in 80°C incubator for 20 minutes. Do not stack. Thereafter, immediately remove plates to ice water to cool for a few minutes. Remove the aluminum seal and replace with a plastic lid. Add 30 μL of 2 % Azo-xylan. Mix as before on the plate shaker. Incubate 37°C in a humidified incubator overnight.

Add 200 μL ethanol to each well and pipette up and down a couple of times to mix. As an alternative to changing tips each time, rinse in an ethanol wash and dry by expelling into a paper towel. Spin the plates at 3000 rpm for 10 minutes. Remove 100 μL of supernatant to a fresh 96 well plate. Read the OD_{590}.

EXAMPLE 3: GSSM™ ASSAY FOR HIT VERIFICATION OF THERMAL TOLERANT MUTANTS

The following example describes an exemplary method for assaying for thermally tolerant enzymes.

Pin tool or pick clones into duplicate 96 well plates (200ul /well LB Amp100). Remove the plastic cover and replace with a Gas Permeable Seal. Place in a humidified incubator overnight. Remove the Seal and replace with a plastic lid. Pintool the clones to solid agar. Spin cultures down in tabletop centrifuge at 3000 rpm for 10 min. Remove the supernatant by inversion onto a paper towel. Aliquot 25 μl BPER/Lysozyme/DNase solution (see below) into each well. Resuspend cells in a plate shaker on level 6-7 for ~30 seconds.

Incubate the plate on ice for 15 minutes. Add 20 μL of Cit-Phos-KCl buffer pH 6 into each well. Replace the plastic lid with an aluminum plate seal. Use a roller to get a good seal. Mix on a plate shaker at level 6-7 for ~30 seconds.

Place one 96 well plate in an 80°C incubator for 20 minutes and the other at 37°C. Do not stack. Immediately remove the plates to watery ice to cool for a few minutes (use a large plastic tray if needed). Remove the aluminum seal. Add 30 μl of 2% Azo-xylan.

Seal with a plastic gas permeable seal. Mix as before on the plate shaker. Incubate a set of 37°C and 80°C plates in humidified incubator at 37°C for 2 hours and another set for 4 hours.

After incubation, let the plate sit for ~5 minutes at room temperature. Add 200 μL ethanol to each well and pipette up and down a couple of times to mix. Instead of changing tips each time, rinse in an ethanol wash and dry by expelling into a paper towel. But, use a new set of tips for each clone. Spin plates at 3000 rpm 10 minutes. Remove 100 μL of supernatant to a fresh 96 well plate. Read OD_{590}.

BPER/Lysozyme/DNase solution (4.74 mL total):
4.5 mL BPR
200 μL 10 mg/mL Lysozyme (made fresh in pH 6 Cit-phos-buffer)
40 μL 5 mg/mL DNase I (made fresh in pH 6 Cit-phos buffer

EXAMPLE 4: Xylanase assay with wheat arabinoxylan as substrate

The following example describes an exemplary xylanase assay that can be used, for example, to determine is an enzyme is within the scope of the invention.

SEQ ID NOS: 11, 12, 69, 70, 77, 78, 113, 114, 149, 150, 159, 160, 163, 164, 167, 168, 181, 182, 197, and 198 were subjected to an assay at pH 8 (Na-phosphate buffer) and 70°C using wheat arabinoxylan as a substrate. The enzymes were characterized as set forth in Table 7.

Table 7

SEQ ID NOS:	Protein Concentration (mg/ml)	volume of lysate added to each vial	#of vials	Units/ml*	protein (mg/mL)	U/mg
11, 12	42	0.5	10	163	22.0	7.4
113, 114	37	0.6	10	66	22.0	3.0
163, 164	35	0.6	10	25	22.0	1.1
197, 198	23	1.0	10	31	22.0	1.4
167, 168	10	2.2	10	228	22.0	10.4
77, 78	47	0.5	10	29	22.0	1.3
69, 70	18	1.3	10	36	22.0	1.7
181, 182	28	0.8	10	24	22.0	1.1
159, 160	25	0.9	10	43	22.0	2.0
149, 150	42	0.5	10	24	22.0	1.1

*Based on addition of 1 mL of water to each sample.
Units are umoles xylose released per minute based on a reducing sugar assay.

EXAMPLE 5: Generation of an exemplary xylanase of the invention

The following example describes the generation of an exemplary xylanase of the invention using gene site-saturation mutagenesis (GSSM™) technology, designated the

"9x" variant or mutant (the nucleic acid as set forth in SEQ ID NO:377, the polypeptide sequence as set forth in SEQ ID NO:378).

GSSM™ was used to create a comprehensive library of point mutations in the exemplary SEQ ID NO:190, "wild-type" xylanase (encoded by SEQ ID NO:189). The xylanase thermotolerance screen described above identified nine single site amino acid mutants (Figure 6A) (D8F, Q11H, N12L, G17I, G60H, P64V, S65V, G68A & S79P) that had improved thermal tolerance relative to the wild type enzyme (as measured following a heat challenge at 80°C for 20 minutes). Wild-type enzyme and all nine single site amino acid mutants were produced in *E. coli* and purified utilizing an N-terminal hexahistidine tag. There was no noticeable difference in activity due to the tag.

Figure 6 illustrates the nine single site amino acid mutants of "variant 9x", or, as set forth in SEQ ID NO:378 (encoded by SEQ ID NO:377), as generated by Gene Site Saturation Mutagenesis (GSSM™) of the exemplary SEQ ID NO:190 "wild-type" enzyme (encoded by SEQ ID NO:189). Figure 6A is a schematic diagram illustrating position, numbering and the amino acid change for the thermal tolerant point mutants of the "wild-type" gene (SEQ ID NO:190, encoded by SEQ ID NO:189). A library of all 64 codons was generated for every amino acid position in the gene (~13,000 mutants) and screened for mutations that increased thermal tolerance. The "9X" variant was generated by combining all 9 single-site mutants into one enzyme. The corresponding melting temperature transition midpoint (T_m) determined by DSC for each mutant enzyme and the "9X" (SEQ ID NO:378) variant is shown on the right. Figure 6B illustrates the unfolding of the "wild-type" (SEQ ID NO:190) and "9X" (SEQ ID NO:378) "variant/mutant" enzymes was monitored by DSC at a scan rate of 1°C/min. Baseline subtracted DSC data were normalized for protein concentration.

Xylanase activity assays

Enzymatic activities were determined using 400 ∝L of 2% Azo-xylan as substrate in 550 ∝L of CP (citrate-phosphate) buffer, pH 6.0 at the indicated temperatures. Activity measurements as a function of pH were determined using 50 mM Britton and Robinson buffer solutions (pH 3.0, 5.0, 6.0, 7.0, 8.0 and 9.0) prepared by mixing solutions of 0.1 M phosphoric acid solution, 0.1 M boric acid and 0.1 M acetic acid followed by pH adjustment with 1 M sodium hydroxide. Reactions were initiated by adding 50 ∝L of 0.1 mg/ml of purified enzyme. Time points were taken from 0 to 15 minutes where 50 ∝L of reaction mixture was added to 200 ∝L of precipitation solution (100% ethanol). When all

time points had been taken, samples were mixed, incubated for 10 minutes and centrifuged at 3000 g for 10 minutes at 4°C. Supernatant (150 ∝L) was aliquoted into a fresh 96 well plate and absorbance was measured at 590 nm. A_{590} values were plotted against time and the initial rate was determined from the slope of the line.

Differential Scanning Calorimetry (DSC).

Calorimetry was performed using a Model 6100 Nano II DSC apparatus (Calorimetry Sciences Corporation, American Fork, UT) using the DSCRun software package for data acquisition, CpCalc for analysis, CpConvert for conversion into molar heat capacity from microwatts and CpDeconvolute for deconvolution. Analysis was carried out with 1mg/ml recombinant protein in 20 mM potassium phosphate (pH 7.0) and 100 mM KCl at a scan rate of 1_{o}C/min. A constant pressure of 5 atm was maintained during all DSC experiments to prevent possible degassing of the solution on heating. The instrumental baseline was recorded routinely before the experiments with both cells filled with buffer. Reversibility of the thermally induced transitions was tested by reheating the solution in the calorimeter cell immediately after cooling the first run.

Thermal tolerance determination.

All enzymes were analyzed for thermal tolerance at 80°C in 20 mM potassium phosphate (pH 7.0) and 100 mM KCl. The enzymes were heated at 80°C for 0, 5, 10 or 30 minutes in thin-walled tubes and were cooled on ice. Residual activities were determined with Azo-xylan as substrate using the assay described above for activity measurement.

Polysaccharide Fingerprinting.

Polysaccharide fingerprints were determined by polysaccharide analysis using carbohydrate gel electrophoresis (PACE). Beechwood xylan (0.1 mg/mL, 100 ∝L, Sigma, Poole, Dorset, UK) or xylooligosaccharides (1 mM, 20 ∝L, Megazyme, Wicklow, Ireland) were treated with enzyme (1 – 3 ∝g) in a total volume of 250 ∝L for 16 hours. The reaction was buffered in 0.1 M ammonium acetate pH 5.5. Controls without substrates or enzymes were performed under the same conditions to identify any unspecific compounds in the enzymes, polysaccharides/oligosaccharides or labeling reagents. The reactions were stopped by boiling for 20 min. Assays were independently performed at least 2 times for each condition. Derivatization using ANTS (8-aminonaphthalene-1,3,6-trisulfonic acid, Molecular Probes, Leiden, The Netherlands), electrophoresis and imaging were carried out as described (Goubet, F., Jackson, P., Deery, M. and Dupree, P. (2002) *Anal. Biochem. 300*, 53–68).

Fitness Calculation.

The fitness (F_n), for a given enzyme variant, n, was calculated by equally weighting increase in denaturation temperature transition midpoint (T_m) and increase (or decrease) in enzymatic activity relative to the largest difference in each parameter across all variants: $F_n = F_{Tn} + F_{Vn}$, where $F_{Tn} = T_m$ fitness factor of the variant and F_{Vn} = activity fitness factor of the variant. The fitness factors for each (T_m and activity) are relative to the largest difference in T_m or rate across all of the variants. $F_{Tn} = (T_m - T_{mL}) / (T_{mH} - T_{mL})$ where T_{mn} is the T_m for the given variant, n, and T_{mL} is the lowest T_m across all variants and T_{mH} the highest T_m across all variants and $F_{Vn} = (V_n - V_L) / (V_H - V_L)$ where V_n is the relative rate for the given variant, n, and V_L is the lowest rate across all variants and V_H the highest rate across all variants.

Evolution by the GSSM™ method.

GSSM™ technology was used to create a comprehensive library of point mutations in the exemplary xylanase of the invention SEQ ID NO:190 (encoded by SEQ ID NO:189); including the exemplary xylanase of the invention SEQ ID NO:378 (encoded by SEQ ID NO:377). The xylanase thermotolerance screen described above identified nine single site amino acid mutants (Figure 6A), D8F, Q11H, N12L, G17I, G60H, P64V, S65V, G68A & S79P, that had improved thermal tolerance relative to the exemplary "wild type" enzyme SEQ ID NO:190 (encoded by SEQ ID NO:189), as measured following a heat challenge at 80°C for 20 minutes. Wild-type enzyme and all nine single site amino acid mutants were produced in *E. coli* and purified utilizing an N-terminal hexahistidine tag. There was no noticeable difference in activity due to the tag.

To determine the effect of the single amino acid mutations on enzymatic activity, all nine mutants were purified and their xylanase activity (initial rates at the wild-type temperature optimum, 70°C) was compared to that of the exemplary SEQ ID NO:190 "wild-type" enzyme. Enzyme activities were comparable to wild type (initial rate normalized to 1.0) for D8F, N12L, G17I, G60H, P64V, S65V G68A and S79P mutants (relative initial rates 0.65, 0.68, 0.76, 1.1, 1.0, 1.2, 0.98 and 0.84 respectively) confirming that these mutations do not significantly alter the enzymatic activity. Initial rates were measured 3 or more times and variance was typically less than 10 %. In contrast to these eight mutants, a notable reduction in enzymatic activity was observed for the best thermal tolerant, single site mutant, Q11H (relative initial rate 0.35).

Melting temperature (T_m) of "wild-type" and thermal tolerant single site amino acid mutant enzymes.

The purified SEQ ID NO:190 "wild-type" xylanase and the nine thermal tolerant single site amino acid mutants were analyzed using differential scanning calorimetry (DSC). Aggregation was apparent for the wild-type enzyme as evidenced by a shoulder in the DSC trace for its thermal denaturation, see Figure 6B. The evolved mutant enzymes showed no indication of aggregation. For all enzymes, thermally induced denaturation was irreversible and no discernible transition was observed in a second scan of the sample. Due to the irreversibility of denaturation, only the apparent T_m (melting temperature) could be calculated (as described, e.g., by Sanchez-Ruiz (1992) Biophys. J. 61:921–935; Beldarrain (2000) Biotechnol. Appl. Biochem. 31:77–84). The T_m of the wild-type enzyme was 61oC while the T_m's of all point mutants were increased and ranged from 64°C to 70°C (Figure 6A). The Q11H mutation introduced the largest increase (T_m = 70°C) over wild-type followed by P64V (69°C), G17I (67°C) and D8F (67°C).

The "9X" combined GSSM™ exemplary enzyme SEQ ID NO:378

The "9X" enzyme (SEQ ID NO:378) was constructed by combining the single-site changes of the nine thermal tolerant up-mutants by site-directed mutagenesis (Figure 6A). The "9X" (SEQ ID NO:378) enzyme was expressed in *E. coli* and purified to homogeneity. DSC was performed to determine the melting temperature. The T_m of "9X" enzyme was 34 degrees higher than SEQ ID NO:190, the "wild-type" enzyme, demonstrating a dramatic shift in its thermal stability (Figure 6B).

To evaluate the effect of the combined mutations and elevated melting temperature on the enzyme's biochemical properties, pH and temperature profiles were constructed and compared to SEQ ID NO:190, the "wild-type" enzyme. Figure 7 illustrates the biochemical characterization of "wild type" and "evolved" 9X mutant enzymes. Figure 7A illustrates the pH-dependence of activity for the wild-type and evolved 9X mutant enzymes. Xylanase activity was measured at 37°C at each pH and the initial velocity was plotted against absorbance at 590 nm to determine initial rates. Figure 7B illustrates the temperature-dependence of activity for the wild-type and evolved 9X mutant enzymes. The optimum temperatures of the wild-type and 9X mutant enzymes were measured over a temperature range of 25-100°C at pH 6.0 and are based on initial rates measured over 5 minutes. Figure 7C illustrates the thermal stability of wild-type and evolved 9X mutant enzymes. Thermal dependence of activity of the wild-type and evolved 9X mutant enzymes was measured by first heating the enzymes at each of the indicated temperatures for 5

minutes followed by cooling to room temperature and the measurement of residual activity (initial rate at 37°C, pH 6.0). For all experiments initial rates were measured 2 or more times and the variation was less than 10 %.

SEQ ID NO:190 and SEQ ID NO:378 (the "9X" mutant) enzyme had comparable pH/activity profiles with the highest activity between pH 5 and 6 (Figure 7A). Both enzymes had similar initial rate/temperature optima at 70°C, however, SEQ ID NO:190, the "wild-type" enzyme had higher activity at lower temperatures (25-50°C) whereas SEQ ID NO:378 (the "9X" mutant) retained more than 60% of its activity up to 100°C (determined by initial rate) in the presence of substrate (Figure 7B). The activity of SEQ ID NO:190, the "wild-type" enzyme was not detectable at temperatures above 70°C.

To determine the effect of the 9 combined mutations on enzyme thermal tolerance, residual activity was measured and compared to SEQ ID NO:190, the "wild-type" enzyme. Residual activity was determined by a heat challenge for 5 minutes at each temperature (37, 50, 60, 70, 80 and 90°C) followed by activity measurements at 37°C. SEQ ID NO:190 was completely inactivated above 70°C while the evolved 9X mutant displayed significant activity after heating at 70, 80 and even 90°C (Figure 7C). Furthermore, although the activity of the wild-type enzyme decreased with increasing temperature, the 9X variant was somewhat activated by heating at temperatures up to 60°C.

Generation of combinatorial GSSM™ variants using GeneReassembly™ technology.

To identify combinatorial variants of the 9 single site amino acid mutants with highest thermal tolerance and activity compared to the additively constructed SEQ ID NO:378 (the "9X" variant), a GeneReassembly™ library (U.S. Patent No. 6,537,776) of all possible mutant combinations (2^9) was constructed and screened. Using thermal tolerance as the screening criterion, 33 unique combinations of the nine mutations were identified as was the original 9X variant. A secondary screen was performed to select for variants with higher activity/expression than the evolved 9X. This screen yielded 10 variants with sequences possessing between 6 and 8 of the original single mutations in various combinations, as illustrated in Figure 8A. Figure 8 illustrates the combinatorial variants identified using GeneReassembly™ technology. Figure 8A illustrates the GeneReassembly™ library of all possible combinations of the 9 GSSM™ point mutations that was constructed and screened for variants with improved thermal tolerance and activity. Eleven variants including the 9X variant were obtained. As shown in the figure, the variants possessed 6, 7, 8, or 9 of the point mutations in various combinations. The corresponding melting temperature transition

midpoint (Tm) determined by DSC of each variant is shown on the right. Figure 8B illustrates the relative activity (initial rate measured over a 5 minute time period) of the 6X-2 and 9X variants compared to wild-type at the temperature optimum (70°C) and pH 6.0. Error bars show the range in the initial rate for 3 measurements.

The melting temperature (T_m) of each of the combinatorial variants was at least 28°C higher than wild type (Figure 8A) and all of the reassembly variants displayed higher relative activity than the 9X enzyme. The activity of one variant in particular, 6X-2, was greater than the wild-type enzyme and significantly better (1.7X) than the 9X enzyme (Figure 8B). Sequence comparison of the reassembly variants identified at least 6 mutations that were required for the enhanced thermostability (>20 degrees). All 33 unique variants found in the initial thermostability screen contained both Q11H and G17I mutations demonstrating their importance for thermal tolerance.

Analysis of wild-type and variant polysaccharide product fingerprints.

The products generated by the "wild-type," 6X-2 and 9X variants were compared by polysaccharide analysis using carbohydrate gel electrophoresis (PACE). Different substrates (oligosaccharides and polysaccharides) were tested for hydrolysis by the xylanases. The digestion products of the 3 xylanases tested were very similar, as illustrated in Figure 9. All three enzymes hydrolyzed $(Xyl)_6$ and $(Xyl)_5$, mainly into both $(Xyl)_3$ and $(Xyl)_2$, and $(Xyl)_4$ was hydrolyzed to $(Xyl)_2$ (Figure 9A). Only a small amount of hydrolysis of $(Xyl)_3$ into $(Xyl)_2$ and Xyl was observed indicating that $(Xyl)_3$ is a relatively poor substrate for the enzyme. No activity was detected on $(Xyl)_2$. Beechwood xylan, which contains glucuronosyl residues, was hydrolyzed by all three enzymes mainly into $(Xyl)_2$ and $(Xyl)_3$, but other bands were detected that migrated between oligoxylan bands (Figure 9B). In PACE analysis, each oligosaccharide has a specific migration depending on the sugar composition and degree of polymerization (Goubet, F., Jackson, P., Deery, M. and Dupree, P. (2002) *Anal. Biochem. 300*, 53–68), thus, these bands likely correspond to oligoglucuronoxylans. Therefore, the evolved enzymes retained the substrate specificity of the "wild-type" enzyme.

As noted above, Figure 9 illustrates the product fingerprints of "wild-type" SEQ ID NO:190 (encoded by SEQ ID NO:189), 6X-2 (SEQ ID NO:380, encoded by SEQ ID NO:379) and SEQ ID NO:378 (the "9X" mutant) enzyme variant, as determined by PACE. Figure 9A illustrates fingerprints obtained after hydrolysis of oligoxylans $(Xyl)_3$, $(Xyl)_4$, $(Xyl)_5$ and $(Xyl)_6$ by "wild-type" and variant enzymes. Control lanes contain oligosaccharide incubated under the assay conditions in the absence of enzyme. Figure 9B illustrates the

fingerprints obtained after hydrolysis of Beechwood xylan by wild-type and variant enzymes. Standards contained $(Xyl)_2$, $(Xyl)_3$, $(Xyl)_4$. All assays were performed at 37°C and pH 5.5.

A combination of laboratory gene evolution strategies was used to rapidly generate a highly active, thermostable xylanase optimized for process compatibility in a number of industrial market applications. GSSM™ methodology was employed to scan the entire sequence of the exemplary "wild type" xylanase SEQ ID NO:190 (encoded by SEQ ID NO:189) and to identify 9 point mutations that improve its thermal tolerance. Although it had no discernable effect on the hydrolysis product profile of the enzyme, as illustrated in Figure 9, the addition of the 9 mutations to the protein sequence resulted in a moderate reduction in enzymatic specific activity at SEQ ID NO:190 (the "wild-type")'s temperature optimum. 70°C, see Figure 9B. Using the GeneReassembly™ method to generate a combinatorial library of the 9 single site amino acid mutants, this reduction in activity was overcome. Ten thermostable variants (T_m's between 89°C and 94°C) with activity better than the "9X" variant were obtained from screening the GeneReassembly™ library. With a T_m of 90°C, enzymatic specific activity surpassing wild-type and a product fingerprint unaltered and comparable to SEQ ID NO:190 (the "wild-type"), the 6X-2 variant (SEQ ID NO:380, encoded by SEQ ID NO:379) is particularly notable. To our knowledge the shift in T_m obtained for these variants is the highest increase reported from the application of directed evolution technologies.

SEQ ID NO:380 (the 6X-2 variant) includes the following changes, as compared to SEQ ID NO:190 (the "wild-type"): D8F, Q11H, G17I, G60H, S65V and G68A. SEQ ID NO:379 includes the following nucleotide changes, as compared to the "wild type" SEQ ID NO:189: the nucleotides at positions 22 to 24 are TTC, the nucleotides at positions 31 to 33 are CAC, the nucleotides at positions 49 to 51 are ATA, the nucleotides at positions 178 to 180 are CAC, the nucleotides at positions 193 to 195 are GTG, the nucleotides at positions 202 to 204 are GCT.

In order to gauge the effectiveness of combinatorial mixing versus addition of the point mutants to the desired phenotype, a fitness parameter combining contributions both from changes in enzyme activity and thermostability was calculated for each mutant. The term fitness as described here is not an objective measure that can be compared to other enzymes, but rather a term that allows the measurement of the success of directed evolution of this particular xylanase. Since enzyme fitness, F, is calculated by equally weighting changes in T_m and enzyme activity for this set of variants, the maximum allowable fitness

value is 2 ($F_T \leq 1$ and $F_V \leq 1$, see above). In other words, if the variant with the best activity also had the highest T_m, its fitness value would be 2. With a fitness value near 2 (see Fig. 10B), the 6X-2 variant (SEQ ID NO:380, encoded by SEQ ID NO:379) is the closest to possessing the best possible combination of thermal stability and enzyme activity. The single site mutation that confers the highest value of fitness is S65V. Although the T_m of the S65V mutant is lower than that of the Q11H mutant (66°C verses 70°C respectively), it has a higher fitness value since its specific activity is not reduced relative to wild-type.

Figure 10A is a schematic diagram illustrating the level of thermal stability (represented by Tm) improvement over "wild-type" obtained by GSSM™ evolution. The single site amino acid mutant and the combinatorial variant with the highest thermal stability (Q11H and "9X" (SEQ ID NO:378), respectively) are shown in comparison to wild-type. Figure 10B illustrates a "fitness diagram" of enzyme improvement obtained by combining GSSM™ and GeneReassembly™ technologies. Fitness was determined using the formula F = FT + FV where fitness (F) is calculated by equally weighting thermal tolerance fitness (FT) and relative activity fitness (FV) as described above. The point mutation that confers the greatest fitness (S65V) is shown. Combining all 9 point mutations also improved fitness (SEQ ID NO:378, the "9X" variant). However, the largest improvement in fitness was obtained by combining GSSM™ and GeneReassembly™ methods to obtain the best variant, 6X-2 (SEQ ID NO:380).

The GeneReassembly™ method also allowed the identification of important residues that appear absolutely necessary for improved thermal stability. Two key residues, Q11H and G17I, were present in every GeneReassembly™ variant identified based on thermal tolerance (see Figure 6A). The structural determinants for thermal stability of proteins have been studied and several theories have been documented, e.g., by Kinjo (2001) Eur. Biophys. J. 30:378-384; Britton (1999) J. Mol. Biol. 293:1121-1132; Ladenstein (1998) Adv. Biochem. Eng. Biotechnol. 61:37-85; Britton (1995) Eur. J. Biochem. 229:688–695; Tanner (1996) Biochemistry 35:2597–2609; Vetriani (1998) Proc. Natl. Acad. Sci. USA 95:2300–2305. Hydrogen bonding patterns, ionic interactions, hydrophobic packing and decreased length of surface loops are among the key factors even though the contribution of each to protein stability is not fully understood. Given that most of the beneficial point substitutions identified from testing all possible single amino acid substitutions involved the replacement of relatively polar, charged or small (glycine) residues for much larger hydrophobic residues, it can surmised that hydrophobic interactions play the most significant

role in enhancing the thermostability of this protein. Even with a good understanding of the optimal interactions to enhance thermal tolerance, the prediction of where to make mutations that introduce such interactions is not straightforward. A nonrational approach using the GSSM™ method, however, allows rapid sampling of all sidechains at all positions within a protein structure. Such an approach leads to the discovery of amino acid substitutions that introduce functional interactions that could not have been foreseen.

EXAMPLE 6: Pre-treating paper pulp with xylanases of the invention

In one aspect, xylanases of the invention can be used to pretreat paper pulp. This example describes an exemplary routine screening protocol to determine whether a xylanase is useful in pretreating paper pulp; e.g., in reducing the use of bleaching chemicals (e.g., chlorine dioxide, ClO_2) when used to pretreat Kraft paper pulp.

The screening protocol has two alternative test parameters: Impact of xylanase treatment after an oxygen delignification step (post-O_2 pulp); and, Impact of xylanase in a process that does not include oxygen delignification (pre-O_2 brownstock).

For pulp treatment conditions that simulate process conditions in industrial situations, e.g., factories: pH 8.0; 70 °C; 60 min duration.

The process is schematically depicted in the Flow Diagram of Figure 11.

Twenty xylanases were identified by biochemical tests that were active under these conditions. Of the 20 xylanases, 6 were able to significantly reduce ClO_2 demand when they were used to pretreat Kraft pulp before it was chemically bleached. The six are: SEQ ID NO:182 (encoded by SEQ ID NO:181); SEQ ID NO:160 (encoded by SEQ ID NO:159); SEQ ID NO:198 (encoded by SEQ ID NO:197); SEQ ID NO:168 (encoded by SEQ ID NO:167); SEQ ID NO:216 (encoded by SEQ ID NO:215); SEQ ID NO:260 (encoded by SEQ ID NO:259). Others showed some activity but were not as good. Xylanases SEQ ID NO:182 (encoded by SEQ ID NO:181) and SEQ ID NO:160 (encoded by SEQ ID NO:159) are modular and contain a carbohydrate binding module in addition to the xylanase catalytic domain. It was demonstrated that truncated derivatives of these 2 xylanases containing just the catalytic domain are more effective in this application. The best xylanase, SEQ ID NO:160 (encoded by SEQ ID NO:159) was studied more comprehensively. Results can be summarized as follows:

- pretreatment of post-O_2 spruce/pine/fir (SPF) pulp with 2 units/g of SEQ ID NO:160 (encoded by SEQ ID NO:159) reduces subsequent ClO_2 use by 22% to reach 65%GE brightness;

- pretreatment of pre-O_2 brownstock SPF with 0.5 units/g SEQ ID NO:160 (encoded by SEQ ID NO:159) reduces subsequent ClO_2 use by 13% to reach 65%GE brightness;

- pretreatment of pre-O_2 Aspen pulp with 0.5 units/g SEQ ID NO:160 (encoded by SEQ ID NO:159) reduces ClO_2 use by at least 22%;

- pretreatment of pre-O_2 Douglas Fir/Hemlock pulp with 0.5 units/g SEQ ID NO:160 (encoded by SEQ ID NO:159) reduces ClO_2 use by at least 22%;

- under the treatment conditions employed, the reduction in yield from the xylanase treatment did not exceed 0.5% when compared with pulp that had been bleached at the same kappa factor but not treated with xylanase;

- optimal conditions for treating post-O_2 SPF pulp with SEQ ID NOS:159, 160 were: pH 6-7, enzyme dose 0.3 units/g, treatment time 20-25 min. Under these conditions, reduction in ClO_2 use of 28% was possible to reach 69%GE brightness.

In further experiments:

SEQ ID NO:160 (XYLA), encoded by SEQ ID NO: 159 = full length wild type xylanase:

- XYLA (E.c) = truncated variant of SEQ ID NOS:159, 160 containing only xylanase catalytic domain expressed in *E.coli*
- XYLA (P.f) = ditto but expressed in *P. fluorescens*

SEQ ID NO:182 (encoded by SEQ ID NO: 181) = second full-length wild type xylanase:

- XYLB (E.c) = truncated variant etc, etc expressed in *E.coli*
- XYLB (P.f) = ditto but expressed in *P. fluorescens*

<u>Dose Response Data for Lead Xylanases on Pre-O2 Brownstock</u>

<u>Conditions for xylanase stage (X-stage) as follows:</u>

pH 8

Temperature 70°C

Time 60 min

Kappa factor 0.24

For no-enzyme control, kappa factor was 0.30

Results showed a dose dependent increase in brightness for xylanase-treated samples at a lower charge of chlorine dioxide (ClO_2) (Kf 0.24 vs Kf 0.30).

In each case, the truncated derivative looked to be more effective that the full-length xylanase. Optimal xylanase dose looked to be around 0.6 to 0.7 U/g pulp.

Pretreatment of Intercontinental Pre-O_2 Brownstock with the best 4 Xylanases

Determination of ClO_2 Dose Response in D_o

Experimental outline

- Pre-O_2 Brownstock
  - Initial kappa 31.5
- X stage conditions
  - Xylanase charge 0.7 U/gm
  - Temperature 70°C
  - pH 8
  - Treatment time 1 hr
  - Pulp consistency 10%
- Bleach sequence XDE_p
  - Kappa factor 0.22, 0.26 and 0.30 (%D on pulp: 2.63, 3.12 and 3.60)

Final brightness after 3-stage bleach sequence versus Kappa factor (ClO_2 charge):

- XYLB - At 61.5 final brightness, X-stage enables reduction in ClO_2 use of 3.89 kg/ton pulp.
- XYLB (E.c) - At 61.5 final brightness, X-stage enables reduction in ClO_2 charge of 4.07 kg/ton pulp.
- XYLA - At 61.5 brightness, X-stage enables a reduction in ClO_2 use of 4.07 kg/ton pulp.
- XYLA (E.c) - At 61.5 final brightness, X-stage enables reduction in ClO_2 use of 4.90 kg/ton pulp.

Determination of ClO_2 Dose Response in D_o:

Enzyme	ClO_2 Savings in D_o (kg/ton OD)	Kf reduction in D_o
XYLB	3.89	11.7%
XYLB (E.c)	5.08	15.8%
XYLA	4.07	12.2%
XYLA (E.c)	4.90	14.7%

Xylanase 0.7 U/g, pH 8.0, 70 °C, 1 hr

Pulp: Pre-O_2 Brownstock, initial kappa 31.5

Percentage saving of ClO_2 is of little significance to the industry. Their primary concern is lbs of ClO_2 required per ton OD pulp. This makes sense when one considers that a lower percentage saving seen with a high initial kappa brownstock can be more valuable in terms of lbs of ClO_2 saved than a higher percentage reduction for a low initial kappa pulp which will require a lower total charge of ClO_2 to reach target brightness.

Relationship between Brightness, Yield and Kappa Factor for Bleached Control Pulp:

The results showed that bleaching with increasing doses of ClO_2 to achieve higher target brightness results in increased loss of pulp yield. This is an issue because pulp at this stage of the process has a value of almost $400 per ton and loss of cellulose costs money.

A benefit of xylanase (e.g., a xylanase of the invention) is that use of a lower ClO_2 dose can reduce yield losses as long as the action of the xylanase itself doesn't cancel out the gain.

Dose Response Data for Pretreatment of Pre-O_2 Brownstock with Xylanase XYLB (P.f):

Experimental outline

- Northwood Pre-O_2 Brownstock

–Initial kappa 28.0

–Initial consistency 32.46%

–Initial brightness 28.37

- X stage conditions

–Xylanase charge 0 to 2.70 U/gm

–Temperature 58°C to 61°C

–pH 8.2 to 8.5

–Treatment time 1hr

•Bleach sequence XDE_p

–Kappa factor 0.24

•ClO_2 saving calculated for Kappa factors between 0.24 and 0.30

The purpose of this experiment was to evaluate the best of the 4 xylanases on unwashed SPF brownstock. Results showed dose-dependent increases in final brightness for pulp treated with XYLB (E.c), with brightness achieved in presence of xylanase at lower Kf of 0.24, approaching brightness achieved at higher Kf of 0.30 asymptotically.

Relationship between Dose of Xylanase XYLB (E.c) and Chlorine Dioxide Saving (Pre-O_2 Brownstock):

ClO_2 Saving in % OD Pulp	ClO_2 Saving in kg/ton Pulp	Xylanase Dose in U/gm
0.299%	2.99	0.31
0.363%	3.63	0.51
0.406%	4.06	0.71
0.439%	4.39	0.91
0.483%	4.83	1.26
0.523%	5.32	1.80
0.587%	5.87	2.70

Optimum Xylanase Dose is between 0.5 and 0.9 U/gm

The optimum dose lies in the range 0.5 to 0.9 U/g. Above this dose there is a diminishing return per unit increment of xylanase. Reductions in chlorine dioxide dose per ton of pulp treated of this magnitude are commercially significant.

Three-stage biobleaching procedure

A three-stage biobleaching procedure was developed that would closely simulate the actual bleaching operations in a pulp mill bleach plant (Fig. 1). This bleach sequence is designated by (X)DoEp, in which X represents the xylanase treatment stage, D for chlorine dioxide bleaching stage, and Ep for alkaline peroxide extraction stage. The primary feedstock used in our application tests was Southern Softwood Kraft Brownstock (without oxygen delignification). The most effective xylanase candidates that showed high

bleach chemical reduction potential in the biobleaching assays were also tested on two species of hardwood Kraft pulp (maple and aspen). Upon completion of each biobleaching round, the ensuing pulp was used to produce TAPPI (Technical Association of Pulp and Paper Industries)-standard handsheets. The GE% brightness of each handsheet was measured, and the brightness values were used as the indication of how well each enzyme had performed on the pulp during the enzymatic pretreatment stage (X).

Results:

Out of approximately 110 xylanases that were screened using the (X)DoEp biobleaching sequence, 4 enzymes, i.e., XYLA (P.f); XYLB (P.f); SEQ ID NO216 (encoded by SEQ ID NO:215); SEQ ID NO:176 (encoded by SEQ ID NO: 175); showed the greatest potential for reducing the use of bleaching chemicals. While XYLA (P.f) and XYLB (P.f) exhibited equally high performance (best among the four good performers), XYLA (P.f) showed a better pH tolerance than XYLB (P.f). The results can be summarized as follows:

- It is possible to achieve a handsheet brightness of 60 (GE%) using a three-stage bleach sequence [(X)DoEp] that involves pretreatment of Southern Softwood Kraft Brownstock with the following four enzymes at the loading levels listed below (pH=8, 65 °C & 1 h):
    - XYLA (P.f) at 0.55 U/g pulp
    - XYLB (P.f) at 0.75 U/g pulp
    - SEQ ID NOS:215, 216 at 1.80 U/g pulp
    - SEQ ID NOS:175, 176 at 1.98 U/g pulp
- Pretreatment of Southern Softwood Kraft Brownstock with 2 U/g pulp of XYLA (P.f) reduces ClO_2 use by 18.7% to reach a final GE% brightness of 61.
- XYLA (P.f) exhibits good tolerance at higher pH and provides more than 14% chemical savings when the enzymatic pretreatment stage is run at pH=10.
- Pretreatment of Southern Softwood Kraft Brownstock with 2 U/g pulp of XYLB (P.f) reduces ClO_2 use by 16.3% to reach a final GE% brightness of 60.5.
- Pretreatment of aspen Kraft pulp with 2 U/g pulp of XYLA (P.f) and XYLB (P.f) reduces ClO_2 use by about 35% to reach a final GE% brightness of 77.
- Pretreatment of maple Kraft pulp with 2 U/g pulp of XYLA (P.f) and XYLB (P.f) reduces ClO_2 use by about 38% to reach a final GE% brightness of 79.

- The two best performing xylanases, namely XYLA (P.f) and XYLB (P.f), are truncated enzymes, containing just the catalytic domain, and were produced in *Pseudomonas fluorescens*.

While the invention has been described in detail with reference to certain preferred aspects thereof, it will be understood that modifications and variations are within the spirit and scope of that which is described and claimed.

WHAT IS CLAIMED IS:

1. An isolated or recombinant nucleic acid comprising a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID

NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, over a region of at least about 100 residues, wherein the nucleic acid encodes at least one polypeptide having a xylanase activity, and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection.

2. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is at least about 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63% or 64%.

3. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is at least about 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID

NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379.

4. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues, or the full length of a gene or a transcript.

5. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence comprises a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID

NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379.

6. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence encodes a polypeptide having a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322,

SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380.

7. The isolated or recombinant nucleic acid of claim 1, wherein the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

8. The isolated or recombinant nucleic acid of claim 1, wherein the xylanase activity comprises catalyzing hydrolysis of internal β-1,4-xylosidic linkages.

9. The isolated or recombinant nucleic acid of claim 8, wherein the xylanase activity comprises an endo-1,4-beta-xylanase activity.

10. The isolated or recombinant nucleic acid of claim 1, wherein the xylanase activity comprises hydrolyzing a xylan to produce a smaller molecular weight xylose and xylo-oligomer.

11. The isolated or recombinant nucleic acid of claim 10, wherein the xylan comprises an arabinoxylan.

12. The isolated or recombinant nucleic acid of claim 11, wherein the arabinoxylan comprises a water soluble arabinoxylan.

13. The isolated or recombinant nucleic acid of claim 12, wherein the water soluble arabinoxylan comprises a dough or a bread product.

14. The isolated or recombinant nucleic acid of claim 1, wherein the xylanase activity comprises hydrolyzing polysaccharides comprising 1,4-β-glycoside-linked D-xylopyranoses.

15. The isolated or recombinant nucleic acid of claim 1, wherein the xylanase activity comprises hydrolyzing hemicelluloses.

16. The isolated or recombinant nucleic acid of claim 15, wherein the xylanase activity comprises hydrolyzing hemicelluloses in a wood or paper pulp or a paper product.

17. The isolated or recombinant nucleic acid of claim 8, wherein the xylanase activity comprises catalyzing hydrolysis of xylans in a feed or a food product.

18. The isolated or recombinant nucleic acid of claim 17, wherein the feed or food product comprises a cereal-based animal feed, a wort or a beer, a milk or a milk product, a fruit or a vegetable.

19. The isolated or recombinant nucleic acid of claim 1, wherein the xylanase activity comprises catalyzing hydrolysis of xylans in a microbial cell or a plant cell.

20. The isolated or recombinant nucleic acid of claim 1, wherein the xylanase activity is thermostable.

21. The isolated or recombinant nucleic acid of claim 20, wherein the polypeptide retains a xylanase activity under conditions comprising a temperature range of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C.

22. The isolated or recombinant nucleic acid of claim 1, wherein the xylanase activity is thermotolerant.

23. The isolated or recombinant nucleic acid of claim 22, wherein the polypeptide retains a xylanase activity after exposure to a temperature in the range from greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C.

24. An isolated or recombinant nucleic acid, wherein the nucleic acid comprises a sequence that hybridizes under stringent conditions to a nucleic acid comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329,

SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, wherein the nucleic acid encodes a polypeptide having a xylanase activity.

25. The isolated or recombinant nucleic acid of claim 24, wherein the nucleic acid is at least about 50, 75, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more residues in length or the full length of the gene or transcript.

26. The isolated or recombinant nucleic acid of claim 24, wherein the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes.

27. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide with a xylanase activity, wherein the probe comprises at least 10 consecutive bases of a sequence comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID

NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, wherein the probe identifies the nucleic acid by binding or hybridization.

28. The nucleic acid probe of claim 27, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

29. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide having a xylanase activity, wherein the probe comprises a nucleic acid comprising at least about 10 consecutive residues of a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41,

SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139; SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID

NO:377 or SEQ ID NO:379, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection.

30. The nucleic acid probe of claim 29, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

31. An amplification primer pair for amplifying a nucleic acid encoding a polypeptide having a xylanase activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

32. The amplification primer pair of claim 31, wherein a member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence, or, about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence.

33. An amplification primer pair, wherein the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID

NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of the complementary strand of the first member.

34. A xylanase-encoding nucleic acid generated by amplification of a polynucleotide using an amplification primer pair as set forth in claim 33.

35. The xylanase-encoding nucleic acid of claim 34, wherein the amplification is by polymerase chain reaction (PCR).

36. The xylanase-encoding nucleic acid of claim 34, wherein the nucleic acid generated by amplification of a gene library.

37. The xylanase-encoding nucleic acid of claim 34, wherein the gene library is an environmental library.

38. An isolated or recombinant xylanase encoded by a xylanase-encoding nucleic acid as set forth in claim 34.

39. A method of amplifying a nucleic acid encoding a polypeptide having a xylanase activity comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic acid sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

40. An expression cassette comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

41. A vector comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

42. A cloning vehicle comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome.

43. The cloning vehicle of claim 42, wherein the viral vector comprises an adenovirus vector, a retroviral vector or an adeno-associated viral vector.

44. The cloning vehicle of claim 42, comprising a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

45. A transformed cell comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

46. A transformed cell comprising an expression cassette as set forth in claim 40.

47. The transformed cell of claim 40, wherein the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

48. A transgenic non-human animal comprising a sequence as set forth in claim 1 or claim 24.

49. The transgenic non-human animal of claim 48, wherein the animal is a mouse.

50. A transgenic plant comprising a sequence as set forth in claim 1 or claim 24.

51. The transgenic plant of claim 50, wherein the plant is a corn plant, a sorghum plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant, a grass, or a tobacco plant.

52. A transgenic seed comprising a sequence as set forth in claim 1 or claim 24.

53. The transgenic seed of claim 52, wherein the seed is a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a rice, a barley, a peanut or a tobacco plant seed.

54. An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

55. The antisense oligonucleotide of claim 49, wherein the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

56. A method of inhibiting the translation of a xylanase message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 24.

57. A double-stranded inhibitory RNA (RNAi) molecule comprising a subsequence of a sequence as set forth in claim 1 or claim 24.

58. The double-stranded inhibitory RNA (RNAi) molecule of claim 52, wherein the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length.

59. A method of inhibiting the expression of a xylanase in a cell comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (iRNA), wherein the RNA comprises a subsequence of a sequence as set forth in claim 1 or claim 24.

60. An isolated or recombinant polypeptide (i) having at least 50% sequence identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158,

SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380, over a region of at least about 100 residues, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection, or, (ii) encoded by a nucleic acid having at least 50% sequence identity to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID

NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, over a region of at least about 100 residues, and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection, or encoded by a nucleic acid capable of hybridizing under stringent conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID

NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID

NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379.

61. The isolated or recombinant polypeptide of claim 60, wherein the sequence identity is over a region of at least about at least about 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or is 100% sequence identity.

62. The isolated or recombinant polypeptide of claim 60, wherein the sequence identity is over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050 or more residues, or the full length of an enzyme.

63. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide has a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186,

SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380.

64. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide has a xylanase activity.

65. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity comprises catalyzing hydrolysis of internal β-1,4-xylosidic linkages.

66. The isolated or recombinant polypeptide of claim 65, wherein the xylanase activity comprises an endo-1,4-beta-xylanase activity.

67. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity comprises hydrolyzing a xylan to produce a smaller molecular weight xylose and xylo-oligomer.

68. The isolated or recombinant polypeptide of claim 67, wherein the xylan comprises an arabinoxylan.

69. The isolated or recombinant polypeptide of claim 68, wherein the arabinoxylan comprises a water soluble arabinoxylan.

70. The isolated or recombinant polypeptide of claim 69, wherein the water soluble arabinoxylan comprises a dough or a bread product.

71. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity comprises hydrolyzing polysaccharides comprising 1,4-β-glycoside-linked D-xylopyranoses.

72. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity comprises hydrolyzing hemicelluloses.

73. The isolated or recombinant polypeptide of claim 72, wherein the xylanase activity comprises hydrolyzing hemicelluloses in a wood or paper pulp or a paper product.

74. The isolated or recombinant polypeptide of claim 73, wherein the xylanase activity comprises catalyzing hydrolysis of xylans in a feed or a food product.

75. The isolated or recombinant polypeptide of claim 74, wherein the feed or food product comprises a cereal-based animal feed, a wort or a beer, a milk or a milk product, a fruit or a vegetable.

76. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity comprises catalyzing hydrolysis of xylans in a microbial cell or a plant cell.

77. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity is thermostable.

78. The isolated or recombinant polypeptide of claim 77, wherein the polypeptide retains a xylanase activity under conditions comprising a temperature range of between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 95°C, between about 70°C to about 75°C, or between about 90°C to about 95°C.

79. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity is thermotolerant.

80. The isolated or recombinant polypeptide of claim 79, wherein the polypeptide retains a xylanase activity after exposure to a temperature in the range from between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more.

81. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 60 and lacking a signal sequence or a prepro sequence.

82. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 60 and having a heterologous signal sequence or a heterologous prepro sequence.

83. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity comprises a specific activity at about 37°C in the range from about 100 to about 1000 units per milligram of protein, from about 500 to about 750 units per milligram of protein, from about 500 to about 1200 units per milligram of protein, or from about 750 to about 1000 units per milligram of protein.

84. The isolated or recombinant polypeptide of claim 79, wherein the thermotolerance comprises retention of at least half of the specific activity of the xylanase at 37°C after being heated to an elevated temperature.

85. The isolated or recombinant polypeptide of claim 79, wherein the thermotolerance comprises retention of specific activity at 37°C in the range from about 500 to about 1200 units per milligram of protein after being heated to an elevated temperature.

86. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises at least one glycosylation site.

87. The isolated or recombinant polypeptide of claim 86, wherein the glycosylation is an N-linked glycosylation.

88. The isolated or recombinant polypeptide of claim 87, wherein the polypeptide is glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

89. The isolated or recombinant polypeptide of claim 64, wherein the polypeptide retains a xylanase activity under conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0.

90. The isolated or recombinant polypeptide of claim 64, wherein the polypeptide retains a xylanase activity under conditions comprising about pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5.

91. A protein preparation comprising a polypeptide as set forth in claim 60, wherein the protein preparation comprises a liquid, a solid or a gel.

92. A heterodimer comprising a polypeptide as set forth in claim 60 and a second domain.

93. The heterodimer of claim 92, wherein the second domain is a polypeptide and the heterodimer is a fusion protein.

94. The heterodimer of claim 92, wherein the second domain is an epitope or a tag.

95. A homodimer comprising a polypeptide as set forth in claim 60.

96. An immobilized polypeptide, wherein the polypeptide comprises a sequence as set forth in claim 60, or a subsequence thereof.

97. The immobilized polypeptide of claim 96, wherein the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

98. An array comprising an immobilized polypeptide as set forth in claim 60.

99. An array comprising an immobilized nucleic acid as set forth in claim 1 or claim 24.

100. An isolated or recombinant antibody that specifically binds to a polypeptide as set forth in claim 60.

101. The isolated or recombinant antibody of claim 100, wherein the antibody is a monoclonal or a polyclonal antibody.

102. A hybridoma comprising an antibody that specifically binds to a polypeptide as set forth in claim 60.

103. A method of isolating or identifying a polypeptide with a xylanase activity comprising the steps of:

(a) providing an antibody as set forth in claim 100;

(b) providing a sample comprising polypeptides; and

(c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having a xylanase activity.

104. A method of making an anti-xylanase antibody comprising administering to a non-human animal a nucleic acid as set forth in claim 1 or claim 24 or a

subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-xylanase antibody.

105. A method of making an anti-xylanase antibody comprising administering to a non-human animal a polypeptide as set forth in claim 60 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-xylanase antibody.

106. A method of producing a recombinant polypeptide comprising the steps of: (a) providing a nucleic acid operably linked to a promoter, wherein the nucleic acid comprises a sequence as set forth in claim 1 or claim 24; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide.

107. The method of claim 106, further comprising transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell.

108. A method for identifying a polypeptide having a xylanase activity comprising the following steps:

(a) providing a polypeptide as set forth in claim 64;

(b) providing a xylanase substrate; and

(c) contacting the polypeptide with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having a xylanase activity.

109. A method for identifying a xylanase substrate comprising the following steps:

(a) providing a polypeptide as set forth in claim 64;

(b) providing a test substrate; and

(c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction

product, wherein a decrease in the amount of the substrate or an increase in the amount of a reaction product identifies the test substrate as a xylanase substrate.

110. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

(a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid has a sequence as set forth in claim 1 or claim 24;

(b) providing a test compound;

(c) contacting the polypeptide with the test compound; and

(d) determining whether the test compound of step (b) specifically binds to the polypeptide.

111. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

(a) providing a polypeptide as set forth in claim 60;

(b) providing a test compound;

(c) contacting the polypeptide with the test compound; and

(d) determining whether the test compound of step (b) specifically binds to the polypeptide.

112. A method for identifying a modulator of a xylanase activity comprising the following steps:

(a) providing a polypeptide as set forth in claim 64;

(b) providing a test compound;

(c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the xylanase, wherein a change in the xylanase activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the xylanase activity.

113. The method of claim 112, wherein the xylanase activity is measured by providing a xylanase substrate and detecting a decrease in the amount of the substrate or an

increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product.

114. The method of claim 113, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of a xylanase activity.

115. The method of claim 113, wherein an increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of a xylanase activity.

116. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises sequence as set forth in claim 60, a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

117. The computer system of claim 115, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

118. The computer system of claim 117, wherein the sequence comparison algorithm comprises a computer program that indicates polymorphisms.

119. The computer system of claim 117, further comprising an identifier that identifies one or more features in said sequence.

120. A computer readable medium having stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

121. A method for identifying a feature in a sequence comprising the steps of: (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and (b) identifying one or more features in the sequence with the computer program.

122. A method for comparing a first sequence to a second sequence comprising the steps of: (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60 or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and (b) determining differences between the first sequence and the second sequence with the computer program.

123. The method of claim 122, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

124. The method of claim 123, further comprising an identifier that identifies one or more features in a sequence.

125. The method of claim 124, comprising reading the first sequence using a computer program and identifying one or more features in the sequence.

126. A method for isolating or recovering a nucleic acid encoding a polypeptide with a xylanase activity from an environmental sample comprising the steps of:

(a) providing an amplification primer sequence pair as set forth in claim 31 or claim 33;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or

recovering a nucleic acid encoding a polypeptide with a xylanase activity from an environmental sample.

127. The method of claim 126, wherein each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID

NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, or a subsequence thereof.

128. A method for isolating or recovering a nucleic acid encoding a polypeptide with a xylanase activity from an environmental sample comprising the steps of:

(a) providing a polynucleotide probe comprising a sequence as set forth in claim 1 or claim 24, or a subsequence thereof;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with a xylanase activity from an environmental sample.

129. The method of claim 127 or claim 128, wherein the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample.

130. The method of claim 129, wherein the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

131. A method of generating a variant of a nucleic acid encoding a polypeptide with a xylanase activity comprising the steps of:

(a) providing a template nucleic acid comprising a sequence as set forth in claim 1 or claim 24; and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid.

132. The method of claim 131, further comprising expressing the variant nucleic acid to generate a variant xylanase polypeptide.

133. The method of claim 131, wherein the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof.

134. The method of claim 131, wherein the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

135. The method of claim 131, wherein the method is iteratively repeated until a xylanase having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced.

136. The method of claim 135, wherein the variant xylanase polypeptide is thermotolerant, and retains some activity after being exposed to an elevated temperature.

137. The method of claim 135, wherein the variant xylanase polypeptide has increased glycosylation as compared to the xylanase encoded by a template nucleic acid.

138. The method of claim 135, wherein the variant xylanase polypeptide has a xylanase activity under a high temperature, wherein the xylanase encoded by the template nucleic acid is not active under the high temperature.

139. The method of claim 131, wherein the method is iteratively repeated until a xylanase coding sequence having an altered codon usage from that of the template nucleic acid is produced.

140. The method of claim 131, wherein the method is iteratively repeated until a xylanase gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

141. A method for modifying codons in a nucleic acid encoding a polypeptide with a xylanase activity to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a xylanase activity comprising a sequence as set forth in claim 1 or claim 24; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

142. A method for modifying codons in a nucleic acid encoding a xylanase polypeptide, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a xylanase activity comprising a sequence as set forth in claim 1 or claim 24; and,

(b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a xylanase.

143. A method for modifying codons in a nucleic acid encoding a xylanase polypeptide to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a xylanase polypeptide comprising a sequence as set forth in claim 1 or claim 24; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

144. A method for modifying a codon in a nucleic acid encoding a polypeptide having a xylanase activity to decrease its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a xylanase polypeptide comprising a sequence as set forth in claim 1 or claim 24; and

(b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell.

145. The method of claim 144, wherein the host cell is a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

146. A method for producing a library of nucleic acids encoding a plurality of modified xylanase active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps:

(a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes

under stringent conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID

NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, or a subsequence thereof, and the nucleic acid encodes a xylanase active site or a xylanase substrate binding site;

(b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,

(c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified xylanase active sites or substrate binding sites.

147. The method of claim 145, comprising mutagenizing the first nucleic acid of step (a) by a method comprising an optimized directed evolution system, gene site-saturation mutagenesis (GSSM™), or a synthetic ligation reassembly (SLR).

148. The method of claim 145, comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof.

149. The method of claim 145, comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

150. A method for making a small molecule comprising the following steps:

(a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises a xylanase enzyme encoded by a nucleic acid comprising a sequence as set forth in claim 1 or claim 24;

(b) providing a substrate for at least one of the enzymes of step (a); and

(c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions.

151. A method for modifying a small molecule comprising the following steps:

(a) providing a xylanase enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence as set forth in claim 1 or claim 24;

(b) providing a small molecule; and

(c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the xylanase enzyme, thereby modifying a small molecule by a xylanase enzymatic reaction.

152. The method of claim 151, comprising a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the xylanase enzyme.

153. The method of claim 151, further comprising a plurality of additional enzymes under conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the plurality of enzymatic reactions.

154. The method of claim 153, further comprising the step of testing the library to determine if a particular modified small molecule which exhibits a desired activity is present within the library.

155. The method of claim 154, wherein the step of testing the library further comprises the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by

testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

156. A method for determining a functional fragment of a xylanase enzyme comprising the steps of:

(a) providing a xylanase enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and

(b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for a xylanase activity, thereby determining a functional fragment of a xylanase enzyme.

157. The method of claim 156, wherein the xylanase activity is measured by providing a xylanase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

158. A method for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis, the method comprising the following steps:

(a) making a modified cell by modifying the genetic composition of a cell, wherein the genetic composition is modified by addition to the cell of a nucleic acid comprising a sequence as set forth in claim 1 or claim 24;

(b) culturing the modified cell to generate a plurality of modified cells;

(c) measuring at least one metabolic parameter of the cell by monitoring the cell culture of step (b) in real time; and,

(d) analyzing the data of step (c) to determine if the measured parameter differs from a comparable measurement in an unmodified cell under similar conditions, thereby identifying an engineered phenotype in the cell using real-time metabolic flux analysis.

159. The method of claim 158, wherein the genetic composition of the cell is modified by a method comprising deletion of a sequence or modification of a sequence in the cell, or, knocking out the expression of a gene.

160. The method of claim 158, further comprising selecting a cell comprising a newly engineered phenotype.

161. The method of claim 160, further comprising culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.

162. An isolated or recombinant signal sequence consisting of a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43 or 1 to 44, of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID

NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380; or, consisting of a sequence as set forth in Table 4.

163. A chimeric polypeptide comprising at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 162, and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

164. The chimeric polypeptide of claim 163, wherein the heterologous polypeptide or peptide is not a xylanase.

165. The chimeric polypeptide of claim 163, wherein the heterologous polypeptide or peptide is amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP) or a xylanase catalytic domain (CD).

166. An isolated or recombinant nucleic acid encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 162 and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

167. A method of increasing thermotolerance or thermostability of a xylanase polypeptide, the method comprising glycosylating a xylanase, wherein the polypeptide comprises at least thirty contiguous amino acids of a polypeptide as set forth in claim 60, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24, thereby increasing the thermotolerance or thermostability of the xylanase.

168. A method for overexpressing a recombinant xylanase in a cell comprising expressing a vector comprising a nucleic acid sequence as set forth in claim 1 or claim 24, wherein overexpression is effected by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

169. A method of making a transgenic plant comprising the following steps:

(a) introducing a heterologous nucleic acid sequence into the cell, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 24, thereby producing a transformed plant cell;

(b) producing a transgenic plant from the transformed cell.

170. The method as set forth in claim 169, wherein the step (a) further comprises introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts.

171. The method as set forth in claim 169, wherein the step (a) comprises introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment or by using an *Agrobacterium tumefaciens* host.

172. A method of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps:

(a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 24;

(b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

173. A method for hydrolyzing, breaking up or disrupting a xylan-comprising composition comprising the following steps:

(a) providing a polypeptide having a xylanase activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing a composition comprising a xylan; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the xylanase hydrolyzes, breaks up or disrupts the xylan-comprising composition.

174. The method as set forth in claim 173, wherein the composition comprises a plant cell, a bacterial cell, a yeast cell, an insect cell, or an animal cell.

175. A dough or a bread product comprising a polypeptide as set forth in claim 64.

176. A method of dough conditioning comprising contacting a dough or a bread product with at least one polypeptide as set forth in claim 64 under conditions sufficient for conditioning the dough.

177. A beverage comprising a polypeptide as set forth in claim 64.

178. A method of beverage production comprising administration of at least one polypeptide as set forth in claim 64 to a beverage or a beverage precursor under conditions sufficient for decreasing the viscosity of the beverage.

179. The method of claim 178, wherein the beverage or beverage precursor is a wort or a beer.

180. A food, a feed or a nutritional supplement comprising a polypeptide as set forth in claim 64.

181. A method for utilizing a xylanase as a nutritional supplement in an animal diet, the method comprising:

preparing a nutritional supplement containing a xylanase enzyme comprising at least thirty contiguous amino acids of a polypeptide as set forth in claim 64; and

administering the nutritional supplement to an animal to increase utilization of a xylan contained in a feed or a food ingested by the animal.

182. The method of claim 181, wherein the animal is a human.

183. The method of claim 181, wherein the animal is a human.

184. The method of claim 181, wherein the animal is a ruminant or a monogastric animal.

185. The method of claim 181, wherein the xylanase enzyme is prepared by expression of a polynucleotide encoding the xylanase in an organism selected from the group consisting of a bacterium, a yeast, a plant, an insect, a fungus and an animal.

186. The method of claim 185, wherein the organism is selected from the group consisting of an *S. pombe*, *S. cerevisiae*, *Pichia pastoris*, *Pseudomonas* sp., *E. coli*, *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

187. An edible enzyme delivery matrix comprising a thermostable recombinant xylanase enzyme.

188. The edible enzyme delivery matrix of claim 187 comprising a polypeptide as set forth in claim 64.

189. A method for delivering a xylanase supplement to an animal, the method comprising:

preparing an edible enzyme delivery matrix in the form of pellets comprising a granulate edible carrier and a thermostable recombinant xylanase enzyme, wherein the pellets readily disperse the xylanase enzyme contained therein into aqueous media, and

administering the edible enzyme delivery matrix to the animal.

190. The method of claim 189, wherein the recombinant xylanase enzyme comprises a polypeptide as set forth in claim 64.

191. The method of claim 189, wherein the granulate edible carrier comprises a carrier selected from the group consisting of a grain germ, a grain germ that is spent of oil, a hay, an alfalfa, a timothy, a soy hull, a sunflower seed meal and a wheat midd.

192. The method of claim 189, wherein the edible carrier comprises grain germ that is spent of oil.

193. The method of claim 189, wherein the xylanase enzyme is glycosylated to provide thermostability at pelletizing conditions.

194. The method of claim 189, wherein the delivery matrix is formed by pelletizing a mixture comprising a grain germ and a xylanase.

195. The method of claim 189, wherein the pelletizing conditions include application of steam.

196. The method of claim 189, wherein the pelletizing conditions comprise application of a temperature in excess of about 80°C for about 5 minutes and the enzyme retains a specific activity of at least 350 to about 900 units per milligram of enzyme.

197. An isolated or recombinant nucleic acid comprising a sequence encoding a polypeptide having a xylanase activity and a signal sequence, wherein the nucleic acid comprises a sequence as set forth in claim 1.

198. The isolated or recombinant nucleic acid of claim 197, wherein the signal sequence is derived from another xylanase or a non-xylanase enzyme.

199. An isolated or recombinant nucleic acid comprising a sequence encoding a polypeptide having a xylanase activity, wherein the sequence does not contain a signal sequence and the nucleic acid comprises a sequence as set forth in claim 1.

200. An isolated or recombinant nucleic acid comprising a sequence as set forth in SEQ ID NO: 189, wherein SEQ ID NO: 189 contains one or more of the following mutations: the nucleotides at positions 22 to 24 are TTC, the nucleotides at positions 31 to 33 are CAC, the nucleotides at positions 34 to 36 are TTG, the nucleotides at positions 49 to 51 are ATA, the nucleotides at positions 31 to 33 are CAT, the nucleotides at positions 67 to 69 are ACG, the nucleotides at positions 178 to 180 are CAC, the nucleotides at positions 190 to 192 are TGT, the nucleotides at positions 190 to 192 are GTA, the nucleotides at positions 190 to 192 are GTT, the nucleotides at positions 193 to 195 are GTG, the nucleotides at positions 202 to 204 are GCT, the nucleotides at positions 235 to 237 are CCA, or the nucleotides at positions 235 to 237 are CCC.

201. A method for making a nucleic acid comprising a sequence as set forth in claim 200, wherein the mutations in SEQ ID NO: 189 are obtained by gene site saturated mutagenesis (GSSM™).

202. An isolated or recombinant polypeptide comprising an amino acid sequence comprising SEQ ID NO: 190, wherein SEQ ID NO: 190 contains one or more of the following mutations: the aspartic acid at amino acid position 8 is phenylalanine, the glutamine at amino acid position 11 is histidine, the asparagine at amino acid position 12 is leucine, the glycine at amino acid position 17 is isoleucine, the threonine at amino acid position 23 is threonine encoded by a codon other than the wild type codon, the glycine at amino acid position 60 is histidine, the proline at amino acid position 64 is cysteine, the proline at amino acid position 64 is valine, the serine at amino acid position 65 is valine, the glycine at amino acid position 68 is isoleucine, the glycine at amino acid position 68 is alanine, or the valine at amino acid position 79 is proline.

203. A method for reducing lignin in a wood or wood product comprising contacting the wood or wood product with a polypeptide as set forth in claim 64.

204. A detergent composition comprising a polypeptide as set forth in claim 64.

205. A pharmaceutical composition comprising a polypeptide as set forth in claim 64.

206. A method for eliminating or protecting animals from a microorganism comprising a xylan comprising administering a polypeptide as set forth in claim 64.

207. The method of claim 206, wherein the microorganism is a bacterium.

208. The method of claim 205, wherein the bacterium is a salmonellae.

209. An isolated or recombinant nucleic acid comprising SEQ ID NO:189, wherein SEQ ID NO:189 comprises one or more or all of the following sequence variations: the nucleotides at positions 22 to 24 are TTC, the nucleotides at positions 22 to 24 are TTT, the nucleotides at positions 31 to 33 are CAC, the nucleotides at positions 31 to 33 are CAT, the nucleotides at positions 34 to 36 are TTG, the nucleotides at positions 34 to 36 are TTA, the nucleotides at positions 34 to 36 are CTC, the nucleotides at positions 34 to 36 are CTT, the nucleotides at positions 34 to 36 are CTA, the nucleotides at positions 34 to 36 are CTG, the nucleotides at positions 49 to 51 are ATA, the nucleotides at positions 49 to 51 are ATT, the nucleotides at positions 49 to 51 are ATC, the nucleotides at positions 178 to 180 are CAC, the nucleotides at positions 178 to 180 are CAT, the nucleotides at positions 190 to 192 are TGT, the nucleotides at positions 190 to 192 are TGC, the nucleotides at positions 190 to 192 are GTA, the nucleotides at positions 190 to 192 are GTT, the nucleotides at positions 190 to 192 are GTC, the nucleotides at positions 190 to 192 are GTG, the nucleotides at positions 193 to 195 are GTG, the nucleotides at positions 193 to 195 are GTC, the nucleotides at positions 193 to 195 are GTA, the nucleotides at positions 193 to 195 are GTT, the nucleotides at positions 202 to 204 are ATA, the nucleotides at positions 202 to 204 are ATT, the nucleotides at positions 202 to 204 are ATC, the nucleotides at positions 202 to 204 are GCT, the nucleotides at positions 202 to 204 are GCG, the nucleotides at positions 202 to 204 are GCC, the nucleotides at positions 202 to 204 are GCA, the nucleotides at positions 235 to 237 are CCA, the nucleotides at positions 235 to 237 are CCC, or the nucleotides at positions 235 to 237 are CCG.

210. An isolated or recombinant polypeptide comprising an amino acid sequence comprising SEQ ID NO:190, wherein SEQ ID NO:190 comprises one or more or all of the following sequence variations: the aspartic acid at amino acid position 8 is phenylalanine, the glutamine at amino acid position 11 is histidine, the asparagine at amino

acid position 12 is leucine, the glycine at amino acid position 17 is isoleucine, the threonine at amino acid position 23 is threonine encoded by a codon other than the wild type codon, the glycine at amino acid position 60 is histidine, the proline at amino acid position 64 is cysteine, the proline at amino acid position 64 is valine, the serine at amino acid position 65 is valine, the glycine at amino acid position 68 is isoleucine, the glycine at amino acid position 68 is alanine, or the serine at amino acid position 79 is proline.

211. An isolated or recombinant nucleic acid comprising SEQ ID NO: 189, wherein SEQ ID NO:189 comprises one or more or all sequence variations set forth in Table 1 or Table 2.

212. An isolated or recombinant polypeptide encoded by the nucleic acid of claim 211.

213. An isolated or recombinant nucleic acid comprising SEQ ID NO:379, wherein SEQ ID NO:379 comprises one or more or all of the following sequence variations: the nucleotides at positions 22 to 24 are TTC, the nucleotides at positions 31 to 33 are CAC, the nucleotides at positions 49 to 51 are ATA, the nucleotides at positions 178 to 180 are CAC, the nucleotides at positions 193 to 195 are GTG, the nucleotides at positions 202 to 204 are GCT.

214. An isolated or recombinant polypeptide comprising SEQ ID NO:380, wherein SEQ ID NO:380 comprises one or more or all of the following sequence variations: D8F, Q11H, G17I, G60H, S65V and/or G68A.

215. The isolated or recombinant polypeptide of claim 210 or claim 214, wherein the polypeptide has a thermostable xylanase activity.

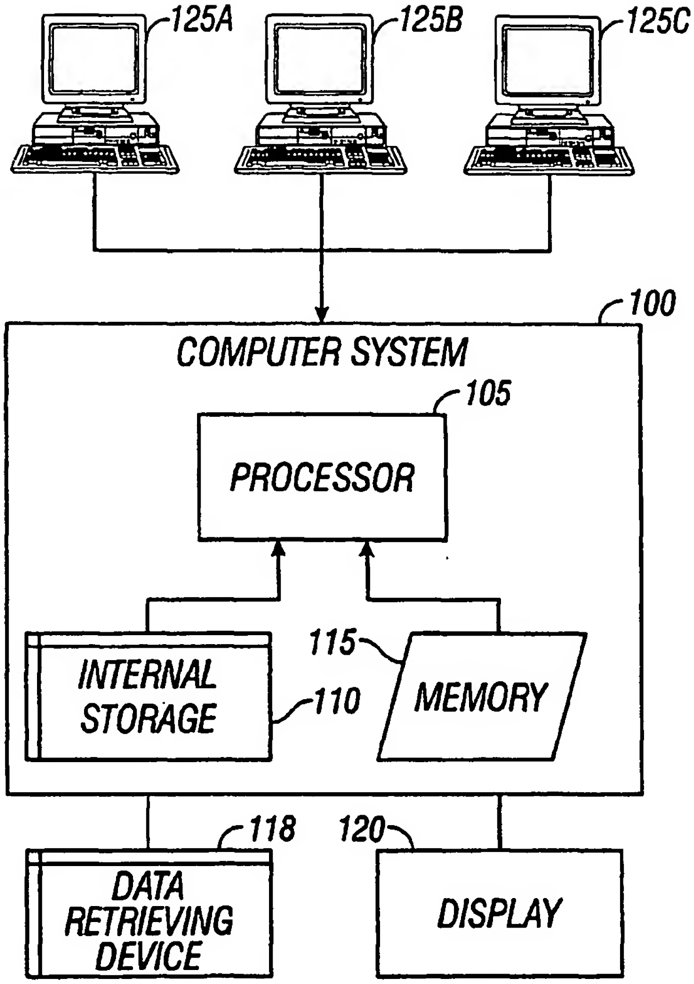

125A
125B
125C
100
COMPUTER SYSTEM
105
PROCESSOR
INTERNAL STORAGE
110
115
MEMORY
118
DATA RETRIEVING DEVICE
120
DISPLAY

FIG. 1

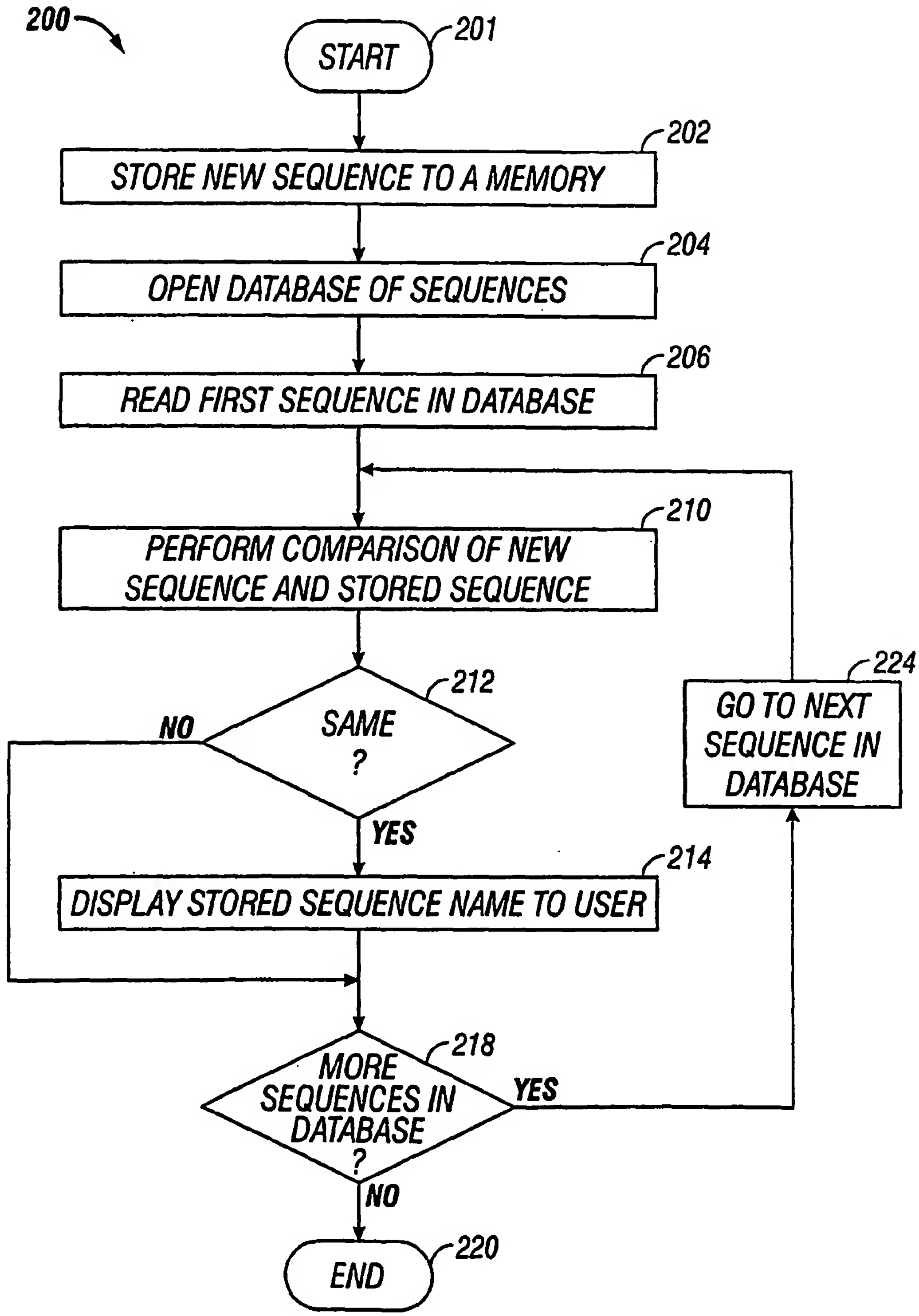

200
START
201
STORE NEW SEQUENCE TO A MEMORY
202
OPEN DATABASE OF SEQUENCES
204
READ FIRST SEQUENCE IN DATABASE
206
PERFORM COMPARISON OF NEW SEQUENCE AND STORED SEQUENCE
210
SAME ?
212
NO
YES
GO TO NEXT SEQUENCE IN DATABASE
224
DISPLAY STORED SEQUENCE NAME TO USER
214
MORE SEQUENCES IN DATABASE ?
218
YES
NO
END
220

FIG. 2

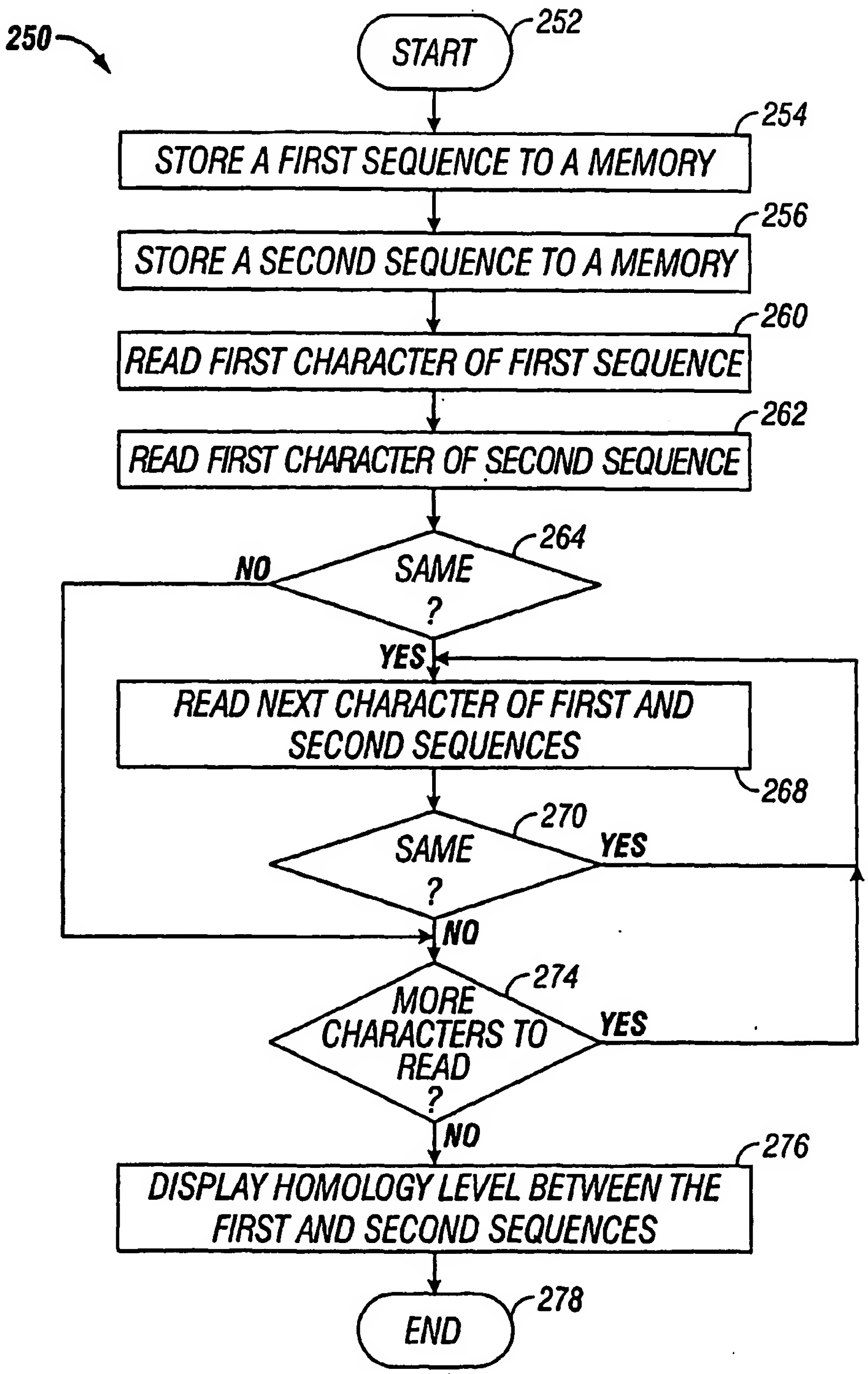

250
START
252
STORE A FIRST SEQUENCE TO A MEMORY
254
STORE A SECOND SEQUENCE TO A MEMORY
256
READ FIRST CHARACTER OF FIRST SEQUENCE
260
READ FIRST CHARACTER OF SECOND SEQUENCE
262
SAME ?
264
NO
YES
READ NEXT CHARACTER OF FIRST AND SECOND SEQUENCES
268
SAME ?
270
YES
NO
MORE CHARACTERS TO READ ?
274
YES
NO
DISPLAY HOMOLOGY LEVEL BETWEEN THE FIRST AND SECOND SEQUENCES
276
END
278

FIG. 3

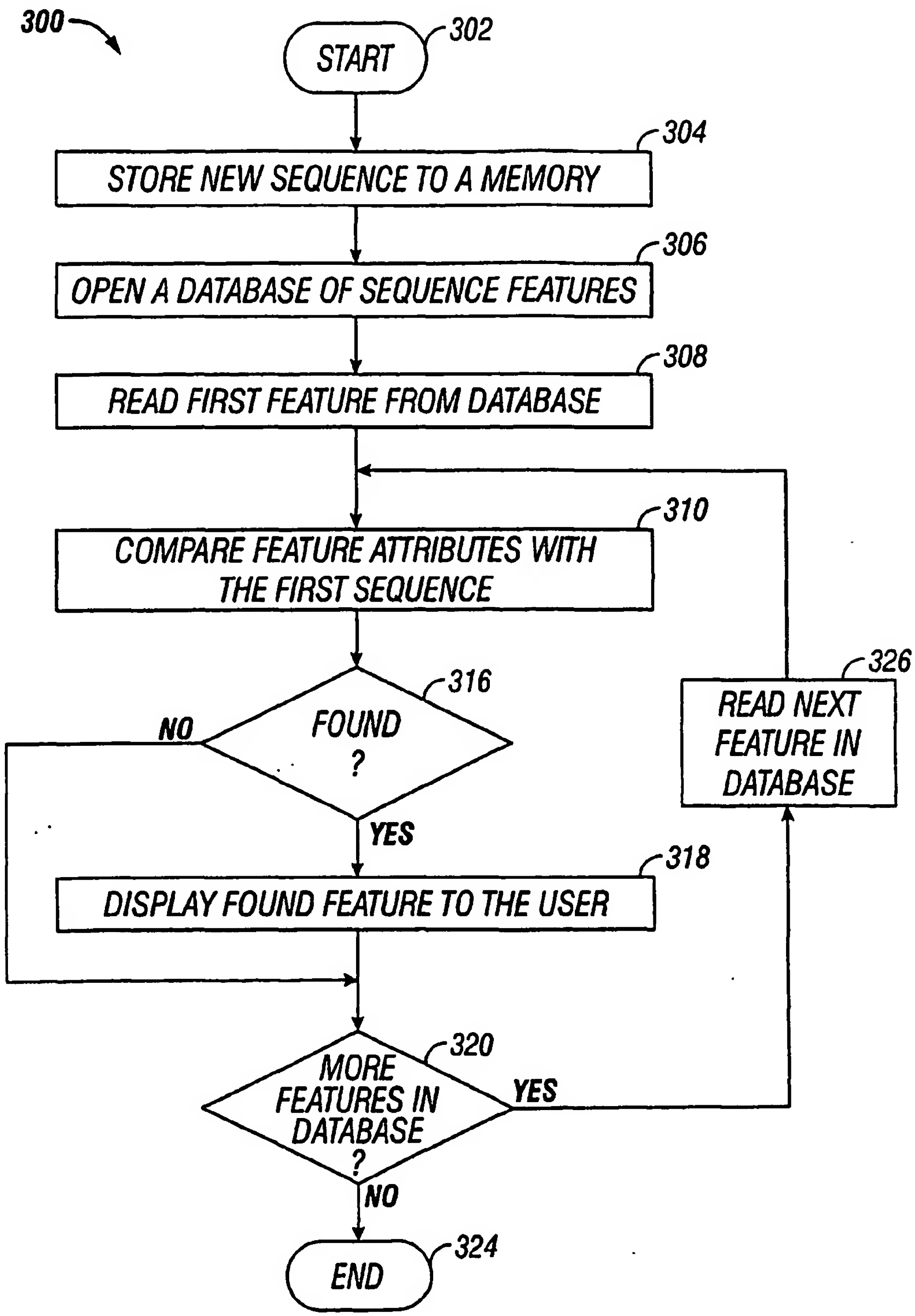

300
START
302
STORE NEW SEQUENCE TO A MEMORY
304
OPEN A DATABASE OF SEQUENCE FEATURES
306
READ FIRST FEATURE FROM DATABASE
308
COMPARE FEATURE ATTRIBUTES WITH THE FIRST SEQUENCE
310
FOUND ?
316
NO
YES
DISPLAY FOUND FEATURE TO THE USER
318
MORE FEATURES IN DATABASE ?
320
YES
NO
READ NEXT FEATURE IN DATABASE
326
END
324

FIG. 4

Figure 5: Thermal Tolerance of Wild-type Xylanase (SEQ ID NOS:189 and 190) vs. 8x Mutant

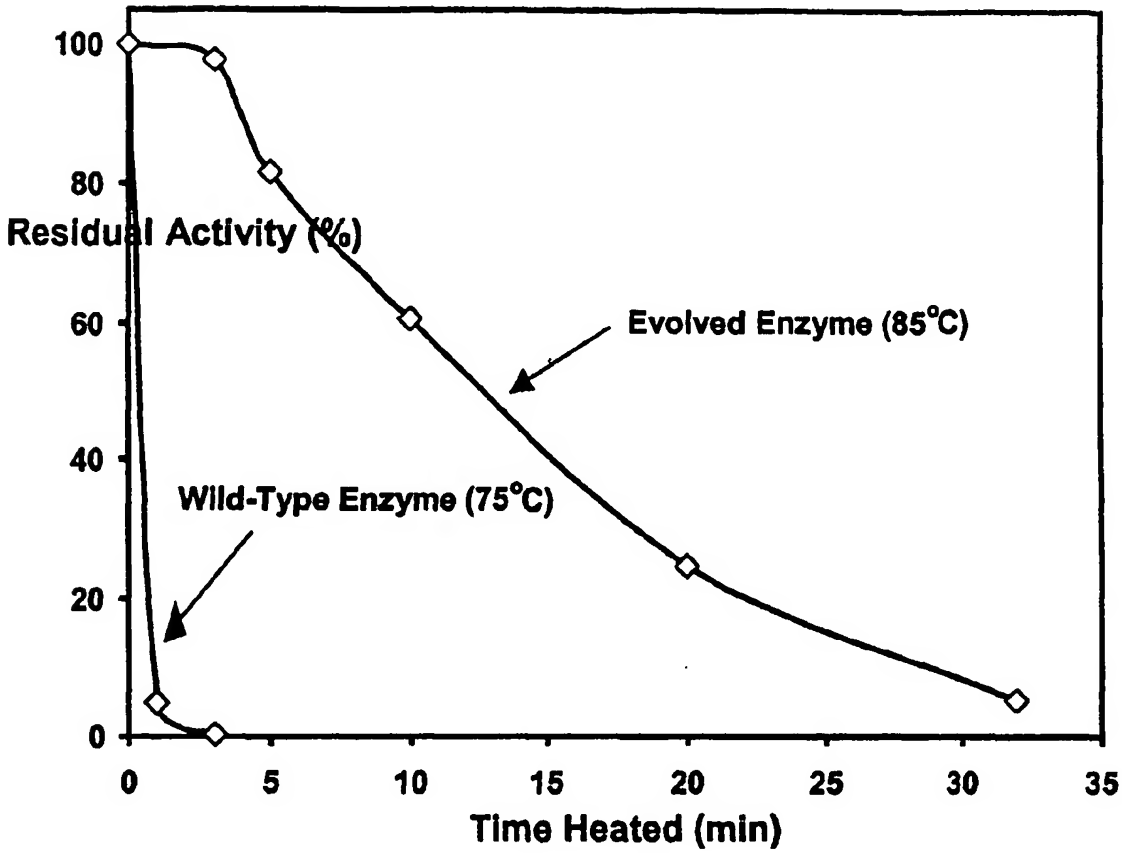
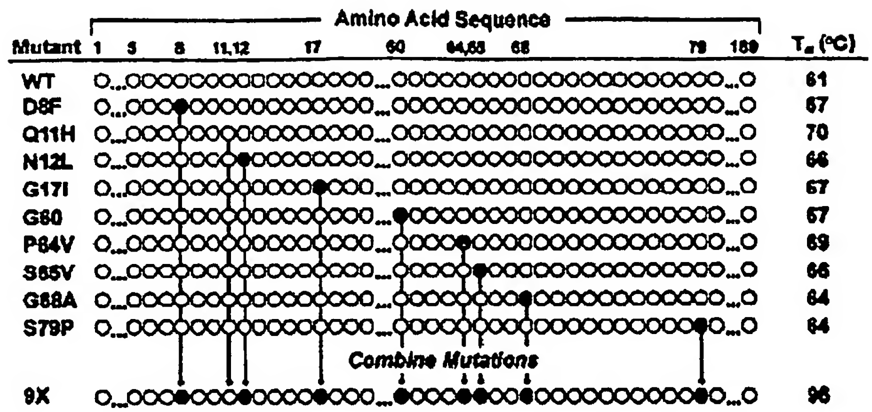


Figure 6

A


Amino Acid Sequence
Mutant 1 5 8 11,12 17 60 64,65 68 79 189 Tm (°C)
WT 61
D8F 67
Q11H 70
N12L 66
G17I 67
G60 67
P64V 69
S65V 66
G68A 64
S79P 64
Combine Mutations
9X 96

B

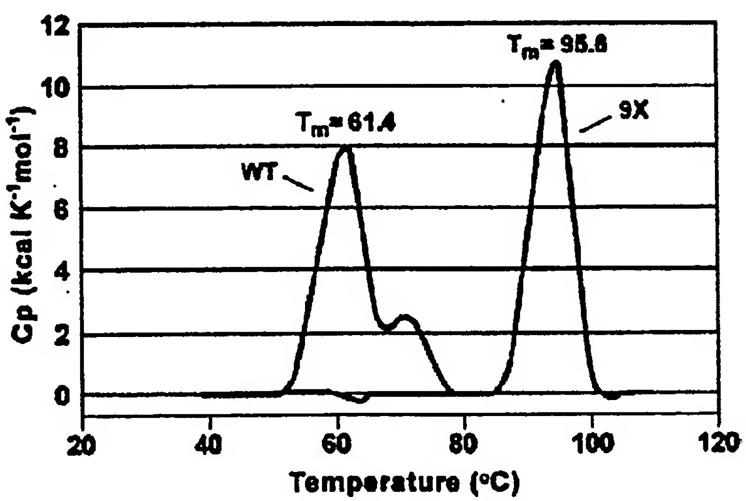
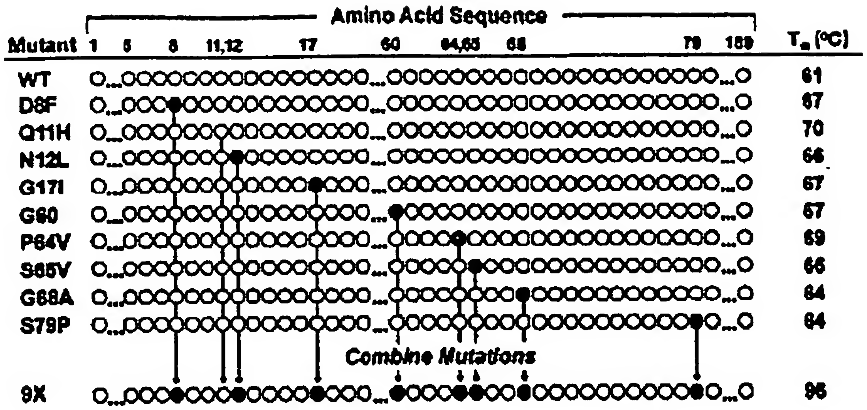

Tm= 95.6
Tm= 61.4
WT
9X
Cp (kcal K-1mol-1)
Temperature (°C)
0
2
4
6
8
10
12
20
40
60
80
100
120

Figure 6

A


Amino Acid Sequence
Mutant
1
5
8
11,12
17
60
64,65
68
79
189
Tm (°C)
WT
D8F
Q11H
N12L
G17I
G60
P64V
S65V
G68A
S79P
Combine Mutations
9X
61
67
70
66
67
67
69
66
64
64
95

B

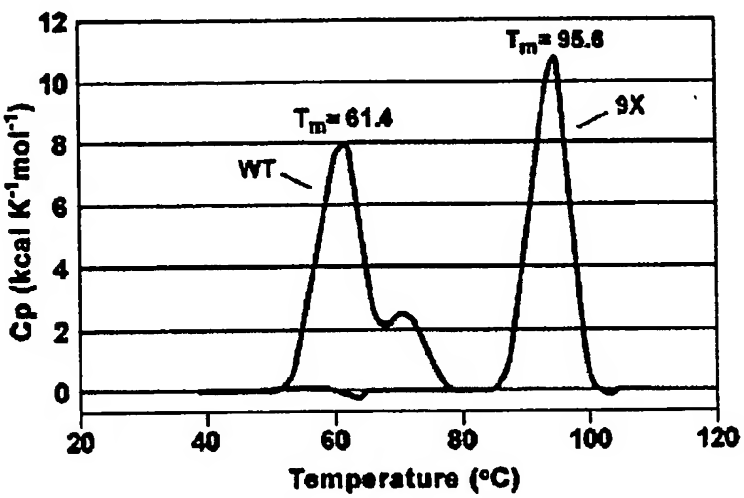

Tm= 95.6
Tm= 61.4
WT
9X
Cp (kcal K-1mol-1)
Temperature (°C)

Figure 7

A

B

C

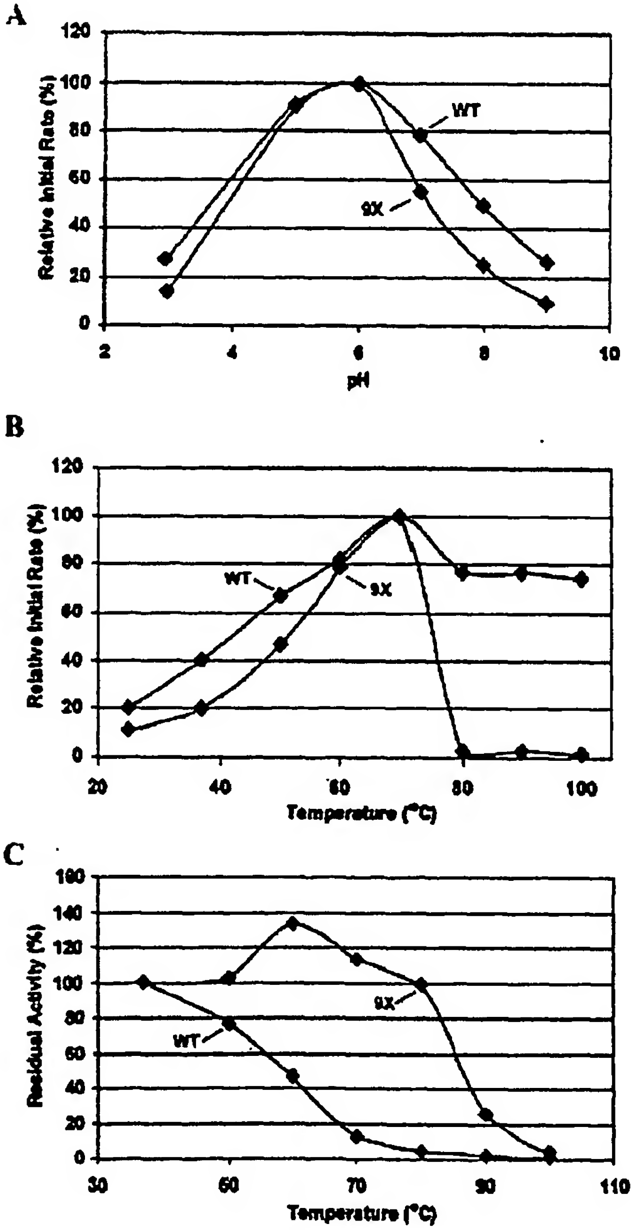

Relative Initial Rate (%)
pH
WT
9X
Temperature (°C)
Residual Activity (%)

Figure 7

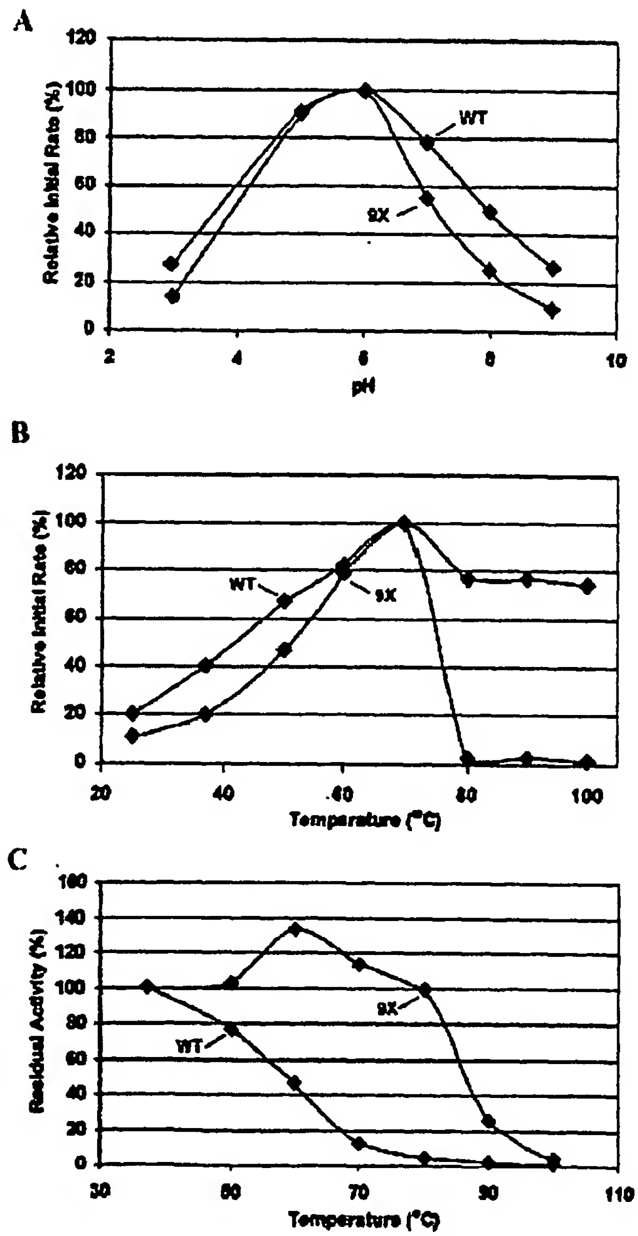
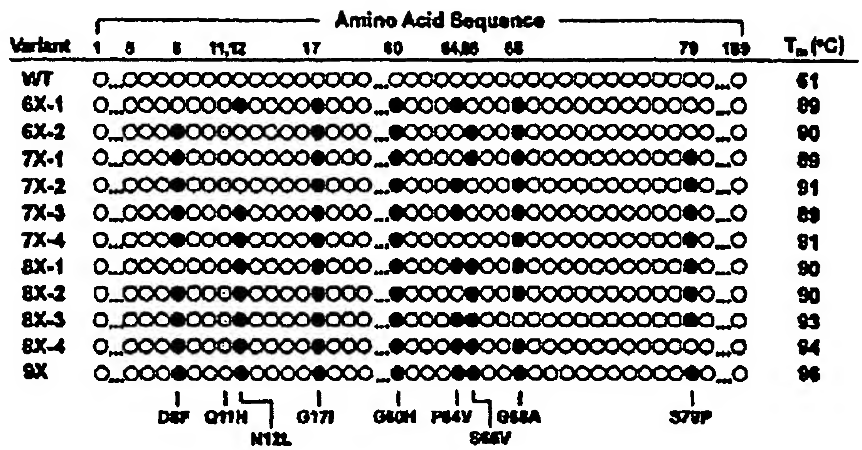

A
120
100
80
60
40
20
0
Relative Initial Rate (%)
2
4
6
8
10
pH
WT
9X
B
120
100
80
60
40
20
0
Relative Initial Rate (%)
20
40
60
80
100
Temperature (°C)
WT
9X
C
160
140
120
100
80
60
40
20
0
Residual Activity (%)
30
50
70
90
110
Temperature (°C)
WT
9X

Figure 8

A


Amino Acid Sequence
Variant
Tm (°C)
WT 61
6X-1 89
6X-2 90
7X-1 89
7X-2 91
7X-3 89
7X-4 91
8X-1 90
8X-2 90
8X-3 93
8X-4 94
9X 96

B

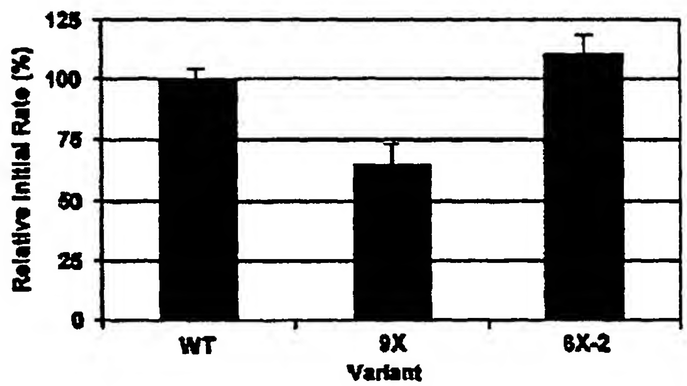
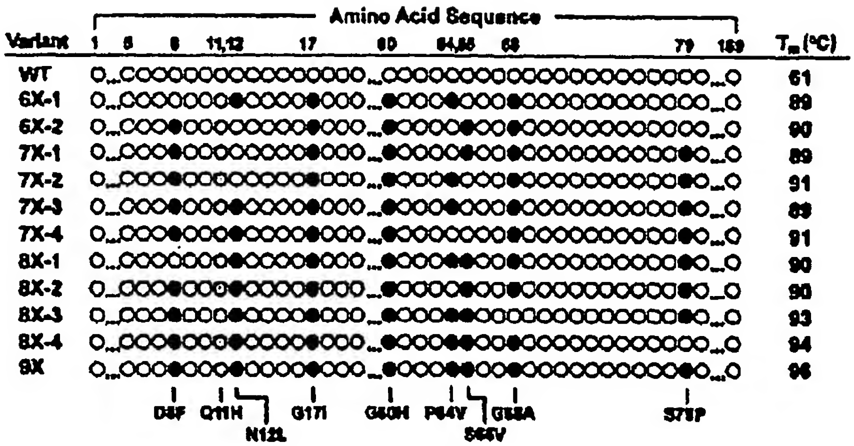

Relative Initial Rate (%)
125
100
75
50
25
0
WT
9X
6X-2
Variant

Figure 8

A


Amino Acid Sequence
Variant
WT
6X-1
6X-2
7X-1
7X-2
7X-3
7X-4
8X-1
8X-2
8X-3
8X-4
9X
Q11H
N12L
G17I
P64V
S66V

B

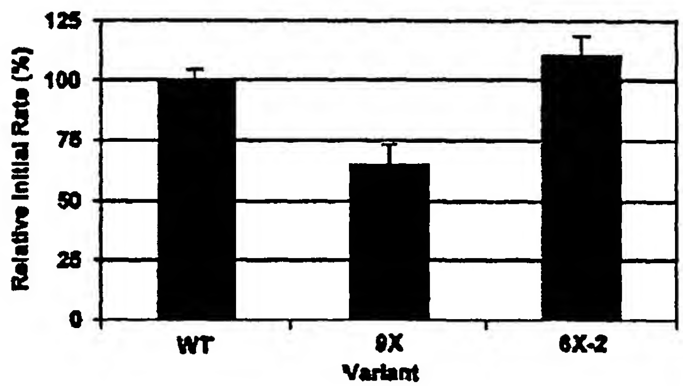

125
100
75
50
25
0
Relative Initial Rate (%)
WT
9X
6X-2
Variant

Figure 9

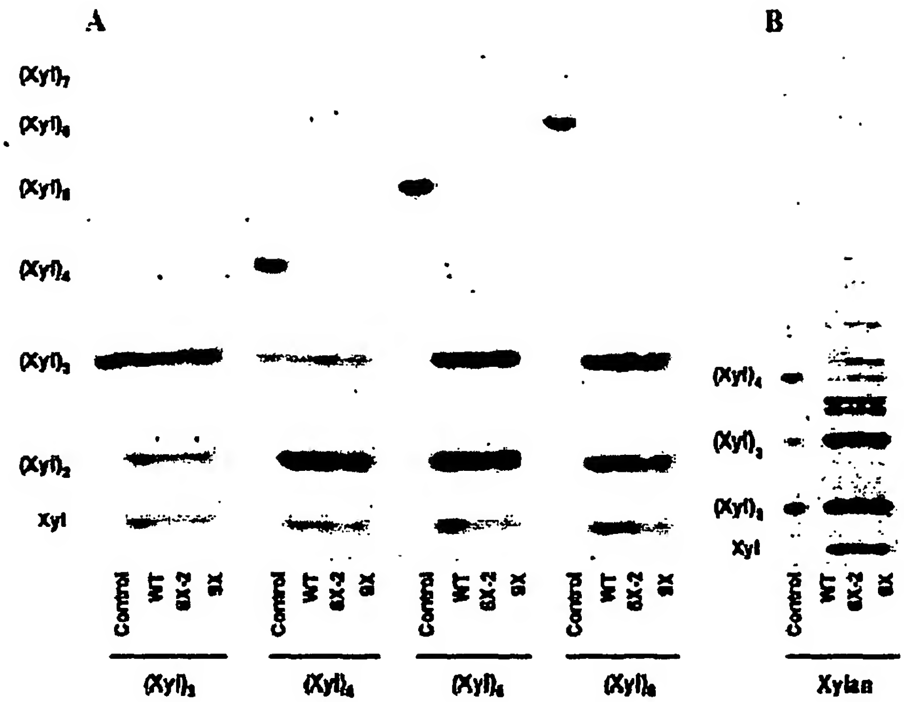

A
B
$(Xyl)_7$
$(Xyl)_6$
$(Xyl)_5$
$(Xyl)_4$
$(Xyl)_3$
$(Xyl)_2$
Xyl
Control
WT
8X-2
9X
$(Xyl)_3$
$(Xyl)_4$
$(Xyl)_5$
$(Xyl)_6$
$(Xyl)_4$
$(Xyl)_3$
$(Xyl)_2$
Xyl
Xylan

Figure 10

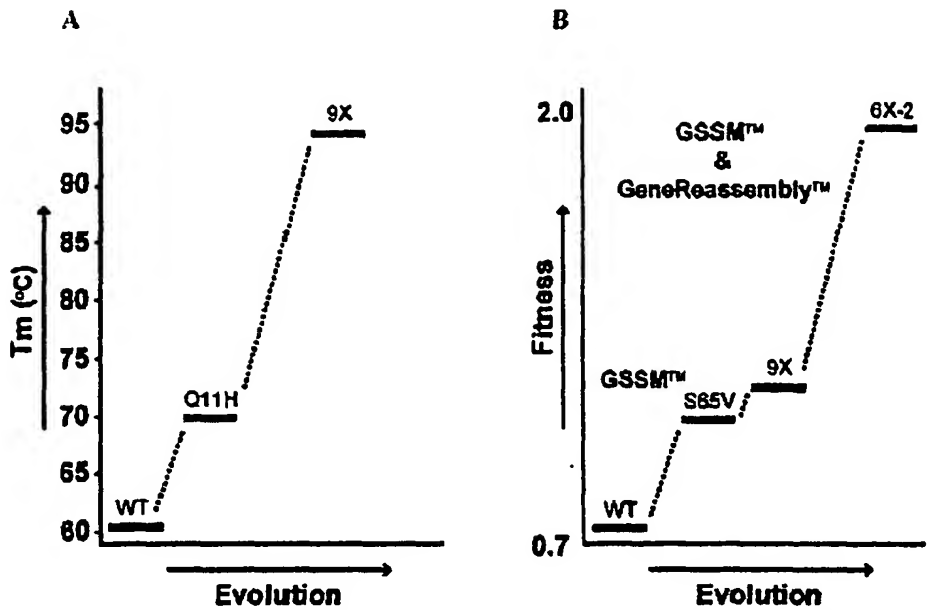

A
95
90
85
80
75
70
65
60
Tm (°C)
WT
Q11H
9X
Evolution
B
2.0
0.7
Fitness
GSSM™
& GeneReassembly™
GSSM™
WT
S65V
9X
6X-2
Evolution

Figure 10

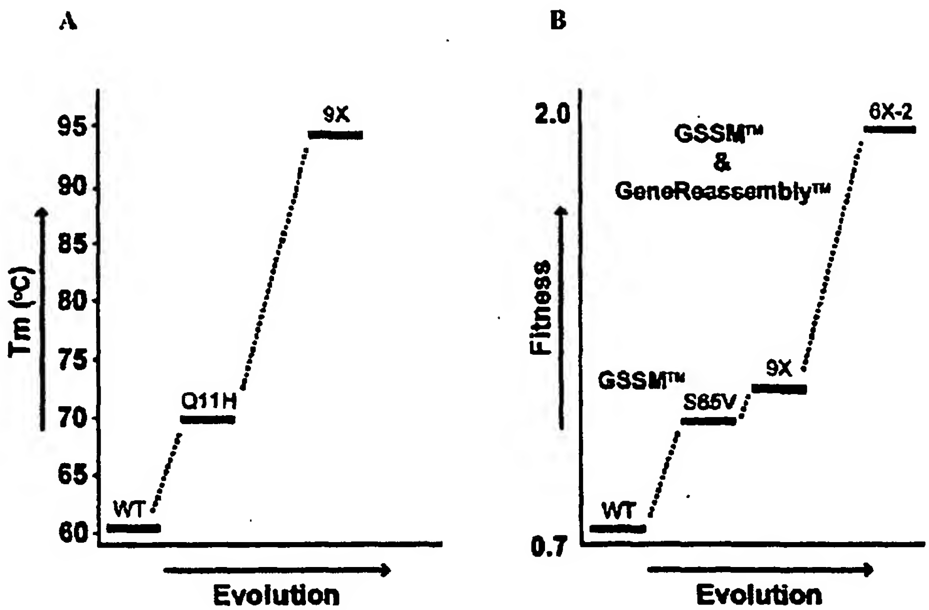
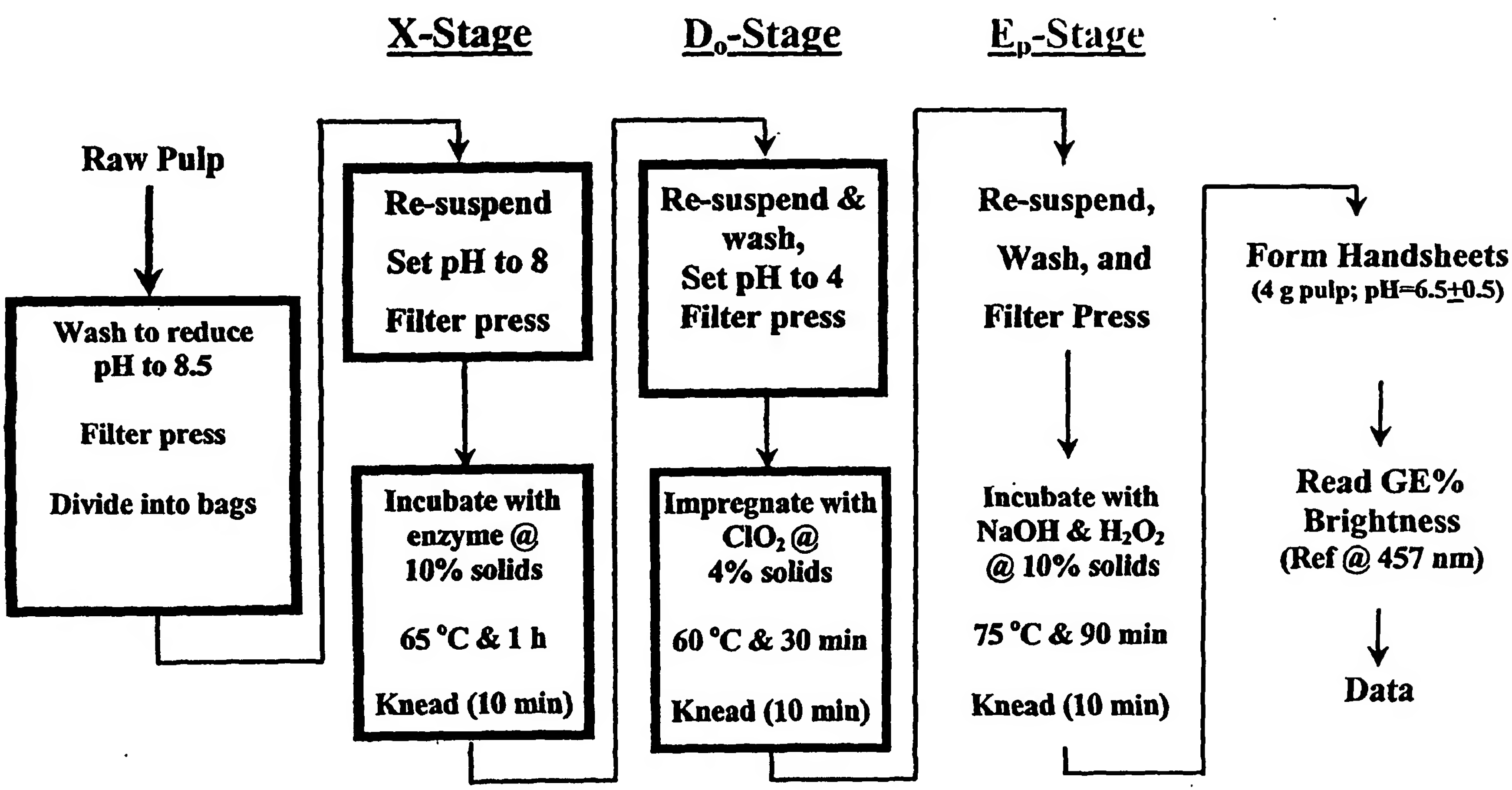

A
B
95
90
85
80
75
70
65
60
Tm (ºC)
WT
Q11H
9X
Evolution
2.0
0.7
Fitness
GSSM™
&
GeneReassembly™
GSSM™
WT
S65V
9X
6X-2
Evolution

Fig. 11. Diversa Applications Lab Biobleaching Scheme



SEQUENCE LISTING

<110> Steer, Brian
Callen, Walter
Healey, Shaun
Hazlewood, Geoff
Wu, Di
Blum, David
Esteghlalian, Alireza

<120> XYLANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AND USING THEM

<130>09010-290001 and 09010-290W01

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accgagggca tgagctacgc gatgatgatc gccgtgcagt acggccgcaa ggacgtgttc     240
gacaagctgt ggggttgggt catgaaatac atgttcatga ccgagggcct gcaccagggc     300
tacttcgcct ggtctgtgga ccccagcggc gtaccgaacg ccgacggtcc ggccccggac     360
ggcgaggaat acttcgcgat ggacctgttc ctggcctccg cgcgatgggg cgacggcgaa     420
ggcgtgtacg agtactcccg ccacgcccgc tcgatcctcc acacctgcgt gcaccagggc     480
gaggacggtg aaggctatcc gatgtggaac ccggagaacc atctgatcaa gttcatcccg     540
gaaaccgaat ggaccgaccc gtcctaccat ctgccgcact tctacgaggt gttcgccgag     600
cgcgccgacg aggccgaccg tccgttctgg gcgcaggccg ccaaggcgag ccgcgagtac     660
ctggtcaccg cctgccaccc gcagaccggc atgaaccccg aatactcaaa ctatgatggc     720
acgccgcacg tcgacgagcg cgaccactgg catttctact ccgacgccta ccgcaccgcc     780
ggcaacatcg ggctggactg cctgtggaac ggcgtcgtgc cggaactgtg cgatgcgaat     840
gcgcgtctgc agcgtttctt cctcgaacac gaccgcacct gcgtgtatgc gatcgacggc     900
acgccggtgg acgagaccgt gctgcacccg gtcggcttca tcgccgccac cgccgaaggc     960
tcgctcgccg cgatgcactc gcaggagccg gacgcgctcg acaacgcgat ccgctgggtg    1020
cgcctgctgt gggacacccc gatccgcacc ggcacgcgcc gctactacga caacttcctc    1080
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<211> 375
<212> PRT
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            20                  25                  30
Met Phe Glu Gly Pro Asp Lys Ile Tyr Trp Glu Asn Asp Glu Gly Leu
        35                  40                  45
Gly Tyr Val Met Asp Thr Gly Asn His Asp Val Arg Thr Glu Gly Met
    50                  55                  60
Ser Tyr Ala Met Met Ile Ala Val Gln Tyr Gly Arg Lys Asp Val Phe
65                  70                  75                  80
Asp Lys Leu Trp Gly Trp Val Met Lys Tyr Met Phe Met Thr Glu Gly
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```
                85                  90                  95
Leu His Gln Gly Tyr Phe Ala Trp Ser Val Asp Pro Ser Gly Val Pro
            100                 105                 110
Asn Ala Asp Gly Pro Ala Pro Asp Gly Glu Glu Tyr Phe Ala Met Asp
        115                 120                 125
Leu Phe Leu Ala Ser Ala Arg Trp Gly Asp Gly Glu Gly Val Tyr Glu
    130                 135                 140
Tyr Ser Arg His Ala Arg Ser Ile Leu His Thr Cys Val His Gln Gly
145                 150                 155                 160
Glu Asp Gly Glu Gly Tyr Pro Met Trp Asn Pro Glu Asn His Leu Ile
                165                 170                 175
Lys Phe Ile Pro Glu Thr Glu Trp Thr Asp Pro Ser Tyr His Leu Pro
            180                 185                 190
His Phe Tyr Glu Val Phe Ala Glu Arg Ala Asp Glu Ala Asp Arg Pro
        195                 200                 205
Phe Trp Ala Gln Ala Ala Lys Ala Ser Arg Glu Tyr Leu Val Thr Ala
    210                 215                 220
Cys His Pro Gln Thr Gly Met Asn Pro Glu Tyr Ser Asn Tyr Asp Gly
225                 230                 235                 240
Thr Pro His Val Asp Glu Arg Asp His Trp His Phe Tyr Ser Asp Ala
                245                 250                 255
Tyr Arg Thr Ala Gly Asn Ile Gly Leu Asp Cys Leu Trp Asn Gly Val
            260                 265                 270
Val Pro Glu Leu Cys Asp Ala Asn Ala Arg Leu Gln Arg Phe Phe Leu
        275                 280                 285
Glu His Asp Arg Thr Cys Val Tyr Ala Ile Asp Gly Thr Pro Val Asp
    290                 295                 300
Glu Thr Val Leu His Pro Val Gly Phe Ile Ala Ala Thr Ala Glu Gly
305                 310                 315                 320
Ser Leu Ala Ala Met His Ser Gln Glu Pro Asp Ala Leu Asp Asn Ala
                325                 330                 335
Ile Arg Trp Val Arg Leu Leu Trp Asp Thr Pro Ile Arg Thr Gly Thr
            340                 345                 350
Arg Arg Tyr Tyr Asp Asn Phe Leu Tyr Ala Phe Ala Phe Leu Ala Leu
        355                 360                 365
Ala Gly Glu Tyr Arg Thr Trp
    370                 375
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<210> 3
<211> 2196
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 3

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atgttcaaag aatggggaaa gaccgactcg gaaattacca caaaagtaaa caccgcgtgg      60
aacaaactgt ttgttaacgg ggtggaatcc ggagataatg ccgaaagaat ctatgtagag     120
actggaagcg acatggcgta catccatacc tttgacagca acgacgtgcg ctccgaagga     180
atgtcctacg gcatgatgat gtgcgtacag atgaacgatc agacaagatt taacaaactc     240
tggaaatggg caagaaccta tatgtacaat gaaacagacg ccggcagtaa ttccaggggc     300
tatttctcat ggcagtgcag tacaagcggc tcaaaaatgg ataagggccc cgctcctgac     360
ggcgaggaat actttattac ggcgctgttg ttcgcgcacg cccgctgggg gagcgcgtcc     420
ggtactacaa acataaacaa ttacgcgcag caagcaaggc agattatcta tgacttaacg     480
cgccgcaaac cggggaacgg agatccttac ggcgagcctt caatgtttaa tgtagacaac     540
tatatggtta gattcgccac acttggaaat tccgccacct ttacagaccc ctcataccat     600
ttaccggcat tctatgatgt ttgggcgctg gaattacagg cggactatga taatagtaaa     660
ctctacggta tctgggctga taaggctgac ttgaaaaaag acattgatta ctttaaacaa     720
gcggcgacca caagccgttc attctttgca aaaacgacaa acggtacaac cggacttgga     780
ccggattatg ccggctttga cggaacgcct aaaaatgaag gggatcacaa gtatttcgag     840
tatgacgcgt ggcgtatcgc gatgaacata ggtatggact acgcgtggtt cgcgaaagat     900
tcctggcaga agacatttgc cgacagaatt caggcgttct ttgtcagcaa gggagtcact     960
tcttacggaa accgctggac attggacggg actcaaaggg gagcggatca ctcgccgggt    1020
cttgtcggct gtaacgcggt cgcctctctc gcggcgacaa acgcgaacgc gtggaaattt    1080
atcgaagact tctggaacat cagcatgacg aaaggcaaat accgttacta tgacggatgt    1140
ctgtatatga tgagcatgct gcacttaagc ggcaacttta aggcgtatct ttctacaaat    1200
accacgcccg ccaacagttc cagcattacc ccgacaaccg cgtctttcga caagaagaca    1260
agcgcacaag ccgacattgc cgtaacagtg acgcttaacg ggaatacatt ctcaagtatc    1320
```

acaaacaacg gtacagccct tacaagcggc acagactact cagtgagtgg aacaaagtat 1380
acgataaaga aagaatacct tgcaaaacag cctgtaggaa caacgaagct cgcattcaac 1440
ttcagtgccg gaggaactcc ggaacttaca gttactataa cggacacggg cagctccagc 1500
atcagcccga caaccgcgac attcgacaaa aagaccggag cgcaagccga catcgccgta 1560
accatgacgc ttaatgggaa tactttgtcg aacatcaaaa acggttctgc acaacttaca 1620
agcggaactg actactcaac gagcggcagt acggtaacga ttaaaaaaga atacctggca 1680
aagcaggcta acggcacagt aacgcttacc ttcacattca gcgcaggcgc ggcccaaact 1740
attgacatca cggtaaaaga tacaaccggc ggagcggcgg gaataaaata caacttcgca 1800
actgacaacc tgcccaacgg gtacccgaag tacagttcaa gtgatatatc cgcgacaata 1860
accggaggag ctttggtaat aaccaaaacc ggaaataatt cgtccccgaa gattacattg 1920
cccttttagtg taacaggtaa cctttccggt tatacaggca taaagataaa tgtaaaggga 1980
gtatccggag atttcactta taaagtattg aatgccgcaa taggttctac aaatctcggc 2040
agcgtaaata acgcccccaat accaaacggc tcatttggag acgtaacaat accaataacc 2100
ggcggtacaa acaccggaga tttagatata tcgttctggc tcaataacac aaatgcttac 2160
gttattgaga ttaagagcat agagctggta aaatga 2196

<210> 4
<211> 711
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 4
Met Phe Lys Glu Trp Gly Lys Thr Asp Ser Glu Ile Thr Thr Lys Val
1 5 10 15
Asn Thr Ala Trp Asn Lys Leu Phe Val Asn Gly Val Glu Ser Gly Asp
20 25 30
Asn Ala Glu Arg Ile Tyr Val Glu Thr Gly Ser Asp Met Ala Tyr Ile
35 40 45
His Thr Phe Asp Ser Asn Asp Val Arg Ser Glu Gly Met Ser Tyr Gly
50 55 60
Met Met Met Cys Val Gln Met Asn Asp Gln Thr Arg Phe Asn Lys Leu
65 70 75 80
Trp Lys Trp Ala Arg Thr Tyr Met Tyr Asn Glu Thr Asp Ala Gly Ser
85 90 95
Asn Ser Arg Gly Tyr Phe Ser Trp Gln Cys Ser Thr Ser Gly Ser Lys
100 105 110
Met Asp Lys Gly Pro Ala Pro Asp Gly Glu Glu Tyr Phe Ile Thr Ala
115 120 125
Leu Leu Phe Ala His Ala Arg Trp Gly Ser Ala Ser Gly Thr Thr Asn
130 135 140
Ile Asn Asn Tyr Ala Gln Gln Ala Arg Gln Ile Ile Tyr Asp Leu Thr
145 150 155 160
Arg Arg Lys Pro Gly Asn Gly Asp Pro Tyr Gly Glu Pro Ser Met Phe
165 170 175
Asn Val Asp Asn Tyr Met Val Arg Phe Ala Thr Leu Gly Asn Ser Ala
180 185 190
Thr Phe Thr Asp Pro Ser Tyr His Leu Pro Ala Phe Tyr Asp Val Trp
195 200 205
Ala Leu Glu Leu Gln Ala Asp Tyr Asp Asn Ser Lys Leu Tyr Gly Ile
210 215 220
Trp Ala Asp Lys Ala Asp Leu Lys Lys Asp Ile Asp Tyr Phe Lys Gln
225 230 235 240
Ala Ala Thr Thr Ser Arg Ser Phe Phe Ala Lys Thr Thr Asn Gly Thr
245 250 255
Thr Gly Leu Gly Pro Asp Tyr Ala Gly Phe Asp Gly Thr Pro Lys Asn
260 265 270
Glu Gly Asp His Lys Tyr Phe Glu Tyr Asp Ala Trp Arg Ile Ala Met
275 280 285
Asn Ile Gly Met Asp Tyr Ala Trp Phe Ala Lys Asp Ser Trp Gln Lys
290 295 300
Thr Phe Ala Asp Arg Ile Gln Ala Phe Phe Val Ser Lys Gly Val Thr
305 310 315 320
Ser Tyr Gly Asn Arg Trp Thr Leu Asp Gly Thr Gln Arg Gly Ala Asp
325 330 335
His Ser Pro Gly Leu Val Gly Cys Asn Ala Val Ala Ser Leu Ala Ala
340 345 350

```
Thr Asn Ala Asn Ala Trp Lys Phe Ile Glu Asp Phe Trp Asn Ile Ser
        355                 360                 365
Met Thr Lys Gly Lys Tyr Arg Tyr Tyr Asp Gly Cys Leu Tyr Met Met
    370                 375                 380
Ser Met Leu His Leu Ser Gly Asn Phe Lys Ala Tyr Leu Ser Thr Asn
385                 390                 395                 400
Thr Thr Pro Ala Asn Ser Ser Ser Ile Thr Pro Thr Thr Ala Ser Phe
                405                 410                 415
Asp Lys Lys Thr Ser Ala Gln Ala Asp Ile Ala Val Thr Val Thr Leu
            420                 425                 430
Asn Gly Asn Thr Phe Ser Ser Ile Thr Asn Asn Gly Thr Ala Leu Thr
        435                 440                 445
Ser Gly Thr Asp Tyr Ser Val Ser Gly Thr Lys Tyr Thr Ile Lys Lys
    450                 455                 460
Glu Tyr Leu Ala Lys Gln Pro Val Gly Thr Thr Lys Leu Ala Phe Asn
465                 470                 475                 480
Phe Ser Ala Gly Gly Thr Pro Glu Leu Thr Val Thr Ile Thr Asp Thr
                485                 490                 495
Gly Ser Ser Ser Ile Ser Pro Thr Thr Ala Thr Phe Asp Lys Lys Thr
            500                 505                 510
Gly Ala Gln Ala Asp Ile Ala Val Thr Met Thr Leu Asn Gly Asn Thr
        515                 520                 525
Leu Ser Asn Ile Lys Asn Gly Ser Ala Gln Leu Thr Ser Gly Thr Asp
    530                 535                 540
Tyr Ser Thr Ser Gly Ser Thr Val Thr Ile Lys Lys Glu Tyr Leu Ala
545                 550                 555                 560
Lys Gln Ala Asn Gly Thr Val Thr Leu Thr Phe Thr Phe Ser Ala Gly
                565                 570                 575
Ala Ala Gln Thr Ile Asp Ile Thr Val Lys Asp Thr Thr Gly Gly Ala
            580                 585                 590
Ala Gly Ile Lys Tyr Asn Phe Ala Thr Asp Asn Leu Pro Asn Gly Tyr
        595                 600                 605
Pro Lys Tyr Ser Ser Ser Asp Ile Ser Ala Thr Ile Thr Gly Gly Ala
    610                 615                 620
Leu Val Ile Thr Lys Thr Gly Asn Asn Ser Ser Pro Lys Ile Thr Leu
625                 630                 635                 640
Pro Phe Ser Val Thr Gly Asn Leu Ser Gly Tyr Thr Gly Ile Lys Ile
                645                 650                 655
Asn Val Lys Gly Val Ser Gly Asp Phe Thr Tyr Lys Val Leu Asn Ala
            660                 665                 670
Ala Ile Gly Ser Thr Asn Leu Gly Ser Val Asn Asn Ala Pro Ile Pro
        675                 680                 685
Asn Gly Ser Phe Gly Asp Val Thr Ile Pro Ile Thr Gly Gly Thr Asn
    690                 695                 700
Thr Gly Asp Leu Asp Ile Ser
705                 710
```

<210> 5
<211> 2106
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 5

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atgcaaaacc tatttaagcg tgtgtttttc catcttctct tgcttgcctt gctggcaggc      60
tgtgctggcc cttctcccgt aacaccggag ccgaccgaaa tgccgaccca ggtccctaca     120
ccaacgccta gtcttggcgc ctacgagagc ggcgagtatc gcaacctgtt cgccgaggcg     180
cttggcaaat cggatgccga aattcaggcc aaaatcgatg ccgctttcca acaacttttc     240
tacggcgacg atgtttctga gcgcgtctat tacccggttg gcagcgacat gggctatatg     300
ctcgacaccg gcaacgacga tgtgcgctcc gagggcatgt cctacggcat gatgattgcc     360
gtccagatga acaagaagga agaattcgac cgcatctgga agtggaccaa aacctacatg     420
taccagaccg aaggtggtta caaaggttat tttgcctggc acgctaaaac ggacggcacc     480
caactggccg ccaacccggc ctctgacggt gaagtctggt ttgtgatggc gctcttcttt     540
gccgatgcgc gttggggcag cggcgaagga atttataact accgcgccca agcccaggaa     600
attctcgatg tggccttgaa cgccaaagaa ttgggcggca acctggcgac caacctgttc     660
gacccggaga ccaaacaggt cgtttttgtg ccgcagttgg gcaataactc gaaatttacc     720
gacgcttcgt accacatgcc ccatttctac gagttgtggg cgcgttgggc cgataaaaat     780
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aacgactttt gggccgaagc cgctaccgtt agccgcgagt tcctgcctac tgccgttcac 840
cccgaaaccg gcctggcccc taactattcc tacttcgatg gccgccctta caatgacgag 900
tatcacggcc agttccgcta cgacgctttc cgcgtgggcg cgaacatcgg catggattat 960
gtctggtttc acccctctga atggtatcgg gaacaagcca accgccaatt atctttcttc 1020
gcatcccagg gcatcgatga ttatgttgcc gaatattccc tggatggaaa accgctggcc 1080
gggcatcgcg ctacggggtt gattgccacc aatgctgtcc tggcctacgc cgcagacccc 1140
gaaattggtc aacccttcgt ccaggccctg tgggatgcag agcctccgac tggcaggtat 1200
cgctactatg acggcctgct ctacatgatg ggcctgctgc aagccagcgg caacttccgt 1260
atttacgagc cgggtattac gcctcgcgct gagttgccgc cccgccgcc tcgcgccatc 1320
gagggccgct tcgcgcccat taccgggcgg gccttgcttc tgattggccc gaatgcggat 1380
ggcgtcaacg cttacttcga caaactggtg acagcgccgg gcggcgtgaa tgtcgaacta 1440
tcgctcaaat cgcctgattt ggaagcgctc gacgccctgg cgaggaaata tcccaacagc 1500
acgctttcgg tcgggttgtc gctggatggc ccggtaacag aggcggatgc gcgggtggga 1560
gaattgctcg acgcgttggc tgtttatccg cgcccggtct tcctgcgcat cgggccggaa 1620
tttgatttgg cggcgagcgg ccaggggccg gaggaatatg tcgcggcctg gaaaacgctc 1680
cataacgaga ttcaggcgcg gggtagttcg aatatcgccc tggtgtggca tagcgccgca 1740
gcctgcgagt cgccctttgg cggtcatccg ctcgaagcgt ggtatcccgg tgatgagttt 1800
gtggattggg tggccgtttc gcgcactgcg cagtctgccg attgcgaggg gcagtccgtt 1860
gaggccgtct tgcagtttgc gcgtgagcga tacaaaccgg ttgtgttggt tgcatcgcca 1920
gcagaggaca tcttcgagtt cgtttacgcc aacaacgacg tgattcgcgc cctgctgtat 1980
ctgaacaccg agccgggcct gttcgacacc cccgaatttt tgagcggctg gaaggccgaa 2040
atcggtcagc agttctggct gcgcggcggc ccggcgcttt tttcgacact cggattggat 2100
gagtaa 2106

<210> 6
<211> 701
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(47)

<400> 6
Met Gln Asn Leu Phe Lys Arg Val Phe Phe His Leu Leu Leu Leu Ala
1 5 10 15
Leu Leu Ala Gly Cys Ala Gly Pro Ser Pro Val Thr Pro Glu Pro Thr
20 25 30
Glu Met Pro Thr Gln Val Pro Thr Pro Thr Pro Ser Leu Gly Ala Tyr
35 40 45
Glu Ser Gly Glu Tyr Arg Asn Leu Phe Ala Glu Ala Leu Gly Lys Ser
50 55 60
Asp Ala Glu Ile Gln Ala Lys Ile Asp Ala Ala Phe Gln Gln Leu Phe
65 70 75 80
Tyr Gly Asp Asp Val Ser Glu Arg Val Tyr Tyr Pro Val Gly Ser Asp
85 90 95
Met Gly Tyr Met Leu Asp Thr Gly Asn Asp Asp Val Arg Ser Glu Gly
100 105 110
Met Ser Tyr Gly Met Met Ile Ala Val Gln Met Asn Lys Lys Glu Glu
115 120 125
Phe Asp Arg Ile Trp Lys Trp Thr Lys Thr Tyr Met Tyr Gln Thr Glu
130 135 140
Gly Gly Tyr Lys Gly Tyr Phe Ala Trp His Ala Lys Thr Asp Gly Thr
145 150 155 160
Gln Leu Ala Ala Asn Pro Ala Ser Asp Gly Glu Val Trp Phe Val Met
165 170 175
Ala Leu Phe Phe Ala Asp Ala Arg Trp Gly Ser Gly Glu Gly Ile Tyr
180 185 190
Asn Tyr Arg Ala Gln Ala Gln Glu Ile Leu Asp Val Ala Leu Asn Ala
195 200 205
Lys Glu Leu Gly Gly Asn Leu Ala Thr Asn Leu Phe Asp Pro Glu Thr
210 215 220
Lys Gln Val Val Phe Val Pro Gln Leu Gly Asn Asn Ser Lys Phe Thr
225 230 235 240
Asp Ala Ser Tyr His Met Pro His Phe Tyr Glu Leu Trp Ala Arg Trp
245 250 255
Ala Asp Lys Asn Asn Asp Phe Trp Ala Glu Ala Ala Thr Val Ser Arg

                260   265   270
Glu Phe Leu Pro Thr Ala Val His Pro Glu Thr Gly Leu Ala Pro Asn
            275   280   285
Tyr Ser Tyr Phe Asp Gly Arg Pro Tyr Asn Asp Glu Tyr His Gly Gln
        290   295   300
Phe Arg Tyr Asp Ala Phe Arg Val Gly Ala Asn Ile Gly Met Asp Tyr
305   310   315   320
Val Trp Phe His Pro Ser Glu Trp Tyr Arg Glu Gln Ala Asn Arg Gln
                325   330   335
Leu Ser Phe Phe Ala Ser Gln Gly Ile Asp Asp Tyr Val Ala Glu Tyr
                340   345   350
Ser Leu Asp Gly Lys Pro Leu Ala Gly His Arg Ala Thr Gly Leu Ile
            355   360   365
Ala Thr Asn Ala Val Leu Ala Tyr Ala Ala Asp Pro Glu Ile Gly Gln
        370   375   380
Pro Phe Val Gln Ala Leu Trp Asp Ala Glu Pro Pro Thr Gly Arg Tyr
385   390   395   400
Arg Tyr Tyr Asp Gly Leu Leu Tyr Met Met Gly Leu Leu Gln Ala Ser
                405   410   415
Gly Asn Phe Arg Ile Tyr Glu Pro Gly Ile Thr Pro Arg Ala Glu Leu
                420   425   430
Pro Pro Pro Pro Pro Arg Ala Ile Glu Gly Arg Phe Ala Pro Ile Thr
            435   440   445
Gly Arg Ala Leu Leu Leu Ile Gly Pro Asn Ala Asp Gly Val Asn Ala
        450   455   460
Tyr Phe Asp Lys Leu Val Thr Ala Pro Gly Gly Val Asn Val Glu Leu
465   470   475   480
Ser Leu Lys Ser Pro Asp Leu Glu Ala Leu Asp Ala Leu Ala Arg Lys
                485   490   495
Tyr Pro Asn Ser Thr Leu Ser Val Gly Leu Ser Leu Asp Gly Pro Val
                500   505   510
Thr Glu Ala Asp Ala Arg Val Gly Glu Leu Leu Asp Ala Leu Ala Val
            515   520   525
Tyr Pro Arg Pro Val Phe Leu Arg Ile Gly Pro Glu Phe Asp Leu Ala
        530   535   540
Ala Ser Gly Gln Gly Pro Glu Glu Tyr Val Ala Ala Trp Lys Thr Leu
545   550   555   560
His Asn Glu Ile Gln Ala Arg Gly Ser Ser Asn Ile Ala Leu Val Trp
                565   570   575
His Ser Ala Ala Ala Cys Glu Ser Pro Phe Gly Gly His Pro Leu Glu
                580   585   590
Ala Trp Tyr Pro Gly Asp Glu Phe Val Asp Trp Val Ala Val Ser Arg
            595   600   605
Thr Ala Gln Ser Ala Asp Cys Glu Gly Gln Ser Val Glu Ala Val Leu
        610   615   620
Gln Phe Ala Arg Glu Arg Tyr Lys Pro Val Val Leu Val Ala Ser Pro
625   630   635   640
Ala Glu Asp Ile Phe Glu Phe Val Tyr Ala Asn Asn Asp Val Ile Arg
                645   650   655
Ala Leu Leu Tyr Leu Asn Thr Glu Pro Gly Leu Phe Asp Thr Pro Glu
                660   665   670
Phe Leu Ser Gly Trp Lys Ala Glu Ile Gly Gln Gln Phe Trp Leu Arg
            675   680   685
Gly Gly Pro Ala Leu Phe Ser Thr Leu Gly Leu Asp Glu
        690   695   700

<210> 7
<211> 1539
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 7
atggcacgtt taatcaccta ttgcttgatc ggcgtcttac tcgtgatgcc agtccttgcc 60
gcttgcagca cagcacctac gccaacgctg atgagccagc caacttccac gccgcaaccg 120
gccctgcaac cgacgccacc accgacgagc gtcccccggt cgatcggggc gtttgagtcc 180
ggtcagtatc gtaatctctt cacggaatta ctgggcaaga gcgaggccga gattcagcag 240

aagatcgatc aggcgtgggc gcagttgttc tacggcgaca acgacacgca gcgcgtttac 300
tatcccgtgg gtcgcgacag ggcctacatc aaagacatcg gcaacaatga tgtgcgcagt 360
gagggtatgt cgtacggtat gatgctggcg gtgcagctgg acaagcagga agagttcaac 420
aaattgtgga agtgggcgca cacctatatg ctgcaaaagg atggcccgta caaaggctat 480
tttgcgtggc atgccaatga gaacggtgaa cagctggatg cgggtcccgc ctccgatggc 540
gaagagtggt ttgtcatggc actgctcttc gcggcaaatc gctggggcaa cggtgaaggc 600
atctttaatt atcaggccga ggcgcagaag atcctggatg tgatgctgca taagagcgaa 660
gaggacaacg gtctcgccac cagcatgttc gatccggaca cgaagcaggt ggtgtttgtg 720
ccggccgggc gccaggccac attcaccgat ccgtcttatc acttgcccgc gttctatgaa 780
ctgtgggcgc gctgggctga caaggataac gatttttgga aagaagcggc gcaggccagc 840
cgcgaatttt ggaagaaggc ggcgcatccg gaaacgggcc tgatgtctga ctacgccgag 900
tttgacggca gaccccaggc cgattctgaa cacaaggatt ttcgctatga cgcgttccgt 960
gtggcgtcca atgtggcgct cgattgggcc tggttcgccg ccgatccgtg ggaggtggaa 1020
cagagcaatc ggttgttgga tttcttccgt tcacaaggca tggataagta tccgagtcta 1080
tacaacatcg atggcacgcc gttatccact aatcgctcgc cgggtttgat cgccatgaac 1140
gccacagctg gactcgcggc tgatccggaa aagagcaagg actttgtgca ggcgctatgg 1200
gatctggaaa ttcccagcgg acaatggcgc tattacgatg ggtgctgta tttcctggcg 1260
ctgttgcaag ccagcggcaa ctatcgcatc tacacgcccg atatgcccaa ggtggtgcgg 1320
cccacaccta cgcccgatcc gatcacgcaa gcgaaatttg cacccggcga tgacgcggtg 1380
ctgttcagtg tggaaacaga tgcactcgac gaatatgtga cggcgacggg ctttgagccg 1440
ggcggcgtga tgttgaacac tactttggac agcgcctctt ttgacgcacc actgcctgac 1500
agcgctctgc tgatcggatt ggacgtcagc gatcaataa 1539

<210> 8
<211> 512
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(57)

<400> 8
Met Ala Arg Leu Ile Thr Tyr Cys Leu Ile Gly Val Leu Leu Val Met
1 5 10 15
Pro Val Leu Ala Ala Cys Ser Thr Ala Pro Thr Pro Thr Leu Met Ser
20 25 30
Gln Pro Thr Ser Thr Pro Gln Pro Ala Leu Gln Pro Thr Pro Pro Pro
35 40 45
Thr Ser Val Pro Arg Ser Ile Gly Ala Phe Glu Ser Gly Gln Tyr Arg
50 55 60
Asn Leu Phe Thr Glu Leu Leu Gly Lys Ser Glu Ala Glu Ile Gln Gln
65 70 75 80
Lys Ile Asp Gln Ala Trp Ala Gln Leu Phe Tyr Gly Asp Asn Asp Thr
85 90 95
Gln Arg Val Tyr Tyr Pro Val Gly Arg Asp Arg Ala Tyr Ile Lys Asp
100 105 110
Ile Gly Asn Asn Asp Val Arg Ser Glu Gly Met Ser Tyr Gly Met Met
115 120 125
Leu Ala Val Gln Leu Asp Lys Gln Glu Glu Phe Asn Lys Leu Trp Lys
130 135 140
Trp Ala His Thr Tyr Met Leu Gln Lys Asp Gly Pro Tyr Lys Gly Tyr
145 150 155 160
Phe Ala Trp His Ala Asn Glu Asn Gly Glu Gln Leu Asp Ala Gly Pro
165 170 175
Ala Ser Asp Gly Glu Glu Trp Phe Val Met Ala Leu Leu Phe Ala Ala
180 185 190
Asn Arg Trp Gly Asn Gly Glu Gly Ile Phe Asn Tyr Gln Ala Glu Ala
195 200 205
Gln Lys Ile Leu Asp Val Met Leu His Lys Ser Glu Glu Asp Asn Gly
210 215 220
Leu Ala Thr Ser Met Phe Asp Pro Asp Thr Lys Gln Val Val Phe Val
225 230 235 240
Pro Ala Gly Arg Gln Ala Thr Phe Thr Asp Pro Ser Tyr His Leu Pro
245 250 255
Ala Phe Tyr Glu Leu Trp Ala Arg Trp Ala Asp Lys Asp Asn Asp Phe
260 265 270

```
Trp Lys Glu Ala Ala Gln Ala Ser Arg Glu Phe Trp Lys Lys Ala Ala
        275                 280                 285
His Pro Glu Thr Gly Leu Met Ser Asp Tyr Ala Glu Phe Asp Gly Arg
    290                 295                 300
Pro Gln Ala Asp Ser Glu His Lys Asp Phe Arg Tyr Asp Ala Phe Arg
305                 310                 315                 320
Val Ala Ser Asn Val Ala Leu Asp Trp Ala Trp Phe Ala Ala Asp Pro
                325                 330                 335
Trp Glu Val Glu Gln Ser Asn Arg Leu Leu Asp Phe Phe Arg Ser Gln
            340                 345                 350
Gly Met Asp Lys Tyr Pro Ser Leu Tyr Asn Ile Asp Gly Thr Pro Leu
        355                 360                 365
Ser Thr Asn Arg Ser Pro Gly Leu Ile Ala Met Asn Ala Thr Ala Gly
    370                 375                 380
Leu Ala Ala Asp Pro Glu Lys Ser Lys Asp Phe Val Gln Ala Leu Trp
385                 390                 395                 400
Asp Leu Glu Ile Pro Ser Gly Gln Trp Arg Tyr Tyr Asp Gly Val Leu
                405                 410                 415
Tyr Phe Leu Ala Leu Leu Gln Ala Ser Gly Asn Tyr Arg Ile Tyr Thr
            420                 425                 430
Pro Asp Met Pro Lys Val Val Arg Pro Thr Pro Thr Pro Asp Pro Ile
        435                 440                 445
Thr Gln Ala Lys Phe Ala Pro Gly Asp Asp Ala Val Leu Phe Ser Val
    450                 455                 460
Glu Thr Asp Ala Leu Asp Glu Tyr Val Thr Ala Thr Gly Phe Glu Pro
465                 470                 475                 480
Gly Gly Val Met Leu Asn Thr Thr Leu Asp Ser Ala Ser Phe Asp Ala
                485                 490                 495
Pro Leu Pro Asp Ser Ala Leu Leu Ile Gly Leu Asp Val Ser Asp Gln
            500                 505                 510
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<210> 9
<211> 1311
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 9

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atgtttccac gtctttcacc aagccgcttc aggcaagtta ccttaacctt gctcacgctc      60
ggccttgtgt cactgaccgg ttgtgcaggt aacagcaagc cggatgcaga caccagtact     120
gctggtgccg ttgctaccgg cgagtaccgc aatctgtttg ccgaaatcgg aaaaagcgaa     180
atagacatcc agcgcaaaat tgacgaggcg tttcagcact tgttttatgg cgacgcgaaa     240
gatgcagctg tctactatca agcgggtgga aacgagaatg gtccactcgc atatgtttac     300
gatgtgaaca gcaatgacgt gcgctcagaa ggcatgagct acggcatgat gattactgtt     360
caaatggaca aaaaagccga gttcgatgca atctggaact gggcgaaaac ctatatgtat     420
caagactccc ccacgcatcc agcgtttggt tactttgcct ggtccatgcg ccgcgatggt     480
gtcgccaatg acgatatgcc agcgccagat ggcgaggaat atttcgtgac cgctctctat     540
ttcgccgccg cccgctgggg taatggcgaa ggtattttca actaccaaca ggaagcggac     600
accattttga gccgcatgcg ccaccgccag gtgatcaccg gcccaaccaa tcgcggagta     660
atgactgcga ccaatctgtt ccacccggaa gaggcgcaag tgcgcttcac gcccgacatc     720
aataatgctg atcatacaga cgcgtcttac catctgccct cgttctatga aatttgggca     780
cgtgtcgcgc cgcaagaaga tcgcgcgttt tgggccaaag cggccgatgt gagccgcgac     840
tattttgcca aagccgccca ccctgtcact gcgttaacac cggactacgg taattttgat     900
ggcaccccgt gggcggcatc ctggcggccg gagtcggtag attttcgata cgatgcctgg     960
cgttccgtca tgaactggtc catggactat gcctggtggg gcaaagattc aggcgcacct    1020
gcgcgcagtg ataaattact cgcgttcttc gaaacccagg aaggcaaaat gaaccacctc    1080
tatagcctgg atggcaaacc gctgggtggt ggaccgaccc tcggcctaat ttccatgaat    1140
gcaacggcag ctatggcagc tactgatccc cgctggcaca atttgtgga aaagctctgg     1200
caacaacaac cccccacagg gcaataccgg tactacgacg gtgttctata cctgatggcg    1260
ctgctacatt gcgctgggga gtacaaagcg tggatccccg acggggaata a             1311
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<210> 10
<211> 436
<212> PRT
<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(36)

<400> 10
Met Phe Pro Arg Leu Ser Pro Ser Arg Phe Arg Gln Val Thr Leu Thr
1 5 10 15
Leu Leu Thr Leu Gly Leu Val Ser Leu Thr Gly Cys Ala Gly Asn Ser
20 25 30
Lys Pro Asp Ala Asp Thr Ser Thr Ala Gly Ala Val Ala Thr Gly Glu
35 40 45
Tyr Arg Asn Leu Phe Ala Glu Ile Gly Lys Ser Glu Ile Asp Ile Gln
50 55 60
Arg Lys Ile Asp Glu Ala Phe Gln His Leu Phe Tyr Gly Asp Ala Lys
65 70 75 80
Asp Ala Ala Val Tyr Tyr Gln Ala Gly Gly Asn Glu Asn Gly Pro Leu
85 90 95
Ala Tyr Val Tyr Asp Val Asn Ser Asn Asp Val Arg Ser Glu Gly Met
100 105 110
Ser Tyr Gly Met Met Ile Thr Val Gln Met Asp Lys Lys Ala Glu Phe
115 120 125
Asp Ala Ile Trp Asn Trp Ala Lys Thr Tyr Met Tyr Gln Asp Ser Pro
130 135 140
Thr His Pro Ala Phe Gly Tyr Phe Ala Trp Ser Met Arg Arg Asp Gly
145 150 155 160
Val Ala Asn Asp Asp Met Pro Ala Pro Asp Gly Glu Glu Tyr Phe Val
165 170 175
Thr Ala Leu Tyr Phe Ala Ala Ala Arg Trp Gly Asn Gly Glu Gly Ile
180 185 190
Phe Asn Tyr Gln Gln Glu Ala Asp Thr Ile Leu Ser Arg Met Arg His
195 200 205
Arg Gln Val Ile Thr Gly Pro Thr Asn Arg Gly Val Met Thr Ala Thr
210 215 220
Asn Leu Phe His Pro Glu Glu Ala Gln Val Arg Phe Thr Pro Asp Ile
225 230 235 240
Asn Asn Ala Asp His Thr Asp Ala Ser Tyr His Leu Pro Ser Phe Tyr
245 250 255
Glu Ile Trp Ala Arg Val Ala Pro Gln Glu Asp Arg Ala Phe Trp Ala
260 265 270
Lys Ala Ala Asp Val Ser Arg Asp Tyr Phe Ala Lys Ala Ala His Pro
275 280 285
Val Thr Ala Leu Thr Pro Asp Tyr Gly Asn Phe Asp Gly Thr Pro Trp
290 295 300
Ala Ala Ser Trp Arg Pro Glu Ser Val Asp Phe Arg Tyr Asp Ala Trp
305 310 315 320
Arg Ser Val Met Asn Trp Ser Met Asp Tyr Ala Trp Trp Gly Lys Asp
325 330 335
Ser Gly Ala Pro Ala Arg Ser Asp Lys Leu Leu Ala Phe Phe Glu Thr
340 345 350
Gln Glu Gly Lys Met Asn His Leu Tyr Ser Leu Asp Gly Lys Pro Leu
355 360 365
Gly Gly Gly Pro Thr Leu Gly Leu Ile Ser Met Asn Ala Thr Ala Ala
370 375 380
Met Ala Ala Thr Asp Pro Arg Trp His Asn Phe Val Glu Lys Leu Trp
385 390 395 400
Gln Gln Gln Pro Pro Thr Gly Gln Tyr Arg Tyr Tyr Asp Gly Val Leu
405 410 415
Tyr Leu Met Ala Leu Leu His Cys Ala Gly Glu Tyr Lys Ala Trp Ile
420 425 430
Pro Asp Gly Glu
435

<210> 11
<211> 1224
<212> DNA
<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 11
atgcggaacg tcgtgcgtaa accattgaca atcggactcg ctttaacact attattgccc 60
atgggaatga cggcaacatc agcgaagaat gcagattcct atgcgaaaaa acctcacatc 120
agcgcattga atgccccaca attggatcaa cgctacaaaa acgagttcac gattggtgcg 180
gcagtagaac cttatcaact acaaaatgaa aaagacgtac aaatgctaaa gcgccacttc 240
aacagcattg ttgccgagaa cgtaatgaaa ccgatcagca ttcaacctga ggaaggaaaa 300
ttcaattttg aacaagcgga tcgaattgtg aagttcgcta aggcaaatgg catggatatt 360
cgcttccata cactcgtttg gcacagccaa gtacctcaac ggttctttct tgacaaggaa 420
ggtaagccaa tggtcaatga aacagatcca gtgaaacgtg aacaaaataa acaactgctg 480
ttaaaacgac ttgaaactca tattaaaacg atcgtcgagc ggtacaaaga tgacattaag 540
tactgggacg ttgtaaatga ggttgtgggg gacgacggaa aactgcgcaa ctctccatgg 600
tatcaaatcg ccggcatcga ttatattaaa gtggcattcc aagcagctag aaaatatggc 660
ggagacaaca ttaagcttta catgaatgat tacaatacag aagtcgaacc gaagcgaacc 720
gctctttaca atttagtcaa acaactgaaa gaagagggtg ttccgatcga cggcatcggc 780
catcaatccc acatccaaat cggctggcct tctgaagcag aaatcgagaa aacgattaac 840
atgttcgccg ctttcggttt agacaaccaa atcactgagc ttgatgtgag catgtacggt 900
tggccgccgc gcgcttaccc gacgtatgac gccattccaa aacaaaagtt tttggatcag 960
gcagcgcgct atgatcgttt gttcaaactg tatgagaagt tgagcgataa aattagcaac 1020
gtcaccttct ggggcatcgc cgacaatcat acgtggctcg acagccgtgc ggatgtgtac 1080
tatgacgcca acgggaatgt tgtggttgac ccgaacgctc cgtacgcaaa agtggaaaaa 1140
gggaaaggaa aagatgcgcc gttcgttttt ggaccggatt acaaagtcaa acccgcatat 1200
tgggctatta ttgaccacaa atag 1224

<210> 12
<211> 407
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<400> 12
Met Arg Asn Val Val Arg Lys Pro Leu Thr Ile Gly Leu Ala Leu Thr
1 5 10 15
Leu Leu Leu Pro Met Gly Met Thr Ala Thr Ser Ala Lys Asn Ala Asp
20 25 30
Ser Tyr Ala Lys Lys Pro His Ile Ser Ala Leu Asn Ala Pro Gln Leu
35 40 45
Asp Gln Arg Tyr Lys Asn Glu Phe Thr Ile Gly Ala Ala Val Glu Pro
50 55 60
Tyr Gln Leu Gln Asn Glu Lys Asp Val Gln Met Leu Lys Arg His Phe
65 70 75 80
Asn Ser Ile Val Ala Glu Asn Val Met Lys Pro Ile Ser Ile Gln Pro
85 90 95
Glu Glu Gly Lys Phe Asn Phe Glu Gln Ala Asp Arg Ile Val Lys Phe
100 105 110
Ala Lys Ala Asn Gly Met Asp Ile Arg Phe His Thr Leu Val Trp His
115 120 125
Ser Gln Val Pro Gln Arg Phe Phe Leu Asp Lys Glu Gly Lys Pro Met
130 135 140
Val Asn Glu Thr Asp Pro Val Lys Arg Glu Gln Asn Lys Gln Leu Leu
145 150 155 160
Leu Lys Arg Leu Glu Thr His Ile Lys Thr Ile Val Glu Arg Tyr Lys
165 170 175
Asp Asp Ile Lys Tyr Trp Asp Val Val Asn Glu Val Val Gly Asp Asp
180 185 190
Gly Lys Leu Arg Asn Ser Pro Trp Tyr Gln Ile Ala Gly Ile Asp Tyr
195 200 205
Ile Lys Val Ala Phe Gln Ala Ala Arg Lys Tyr Gly Gly Asp Asn Ile
210 215 220
Lys Leu Tyr Met Asn Asp Tyr Asn Thr Glu Val Glu Pro Lys Arg Thr
225 230 235 240
Ala Leu Tyr Asn Leu Val Lys Gln Leu Lys Glu Glu Gly Val Pro Ile
245 250 255

```
Asp Gly Ile Gly His Gln Ser His Ile Gln Ile Gly Trp Pro Ser Glu
            260                 265                 270
Ala Glu Ile Glu Lys Thr Ile Asn Met Phe Ala Ala Phe Gly Leu Asp
        275                 280                 285
Asn Gln Ile Thr Glu Leu Asp Val Ser Met Tyr Gly Trp Pro Pro Arg
    290                 295                 300
Ala Tyr Pro Thr Tyr Asp Ala Ile Pro Lys Gln Lys Phe Leu Asp Gln
305                 310                 315                 320
Ala Ala Arg Tyr Asp Arg Leu Phe Lys Leu Tyr Glu Lys Leu Ser Asp
                325                 330                 335
Lys Ile Ser Asn Val Thr Phe Trp Gly Ile Ala Asp Asn His Thr Trp
            340                 345                 350
Leu Asp Ser Arg Ala Asp Val Tyr Tyr Asp Ala Asn Gly Asn Val Val
        355                 360                 365
Val Asp Pro Asn Ala Pro Tyr Ala Lys Val Glu Lys Gly Lys Gly Lys
    370                 375                 380
Asp Ala Pro Phe Val Phe Gly Pro Asp Tyr Lys Val Lys Pro Ala Tyr
385                 390                 395                 400
Trp Ala Ile Ile Asp His Lys
                405

<210> 13
<211> 1053
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 13
atgaaagacg cgctccagtg ctctcccctt ttcaaagcct atgaaaaata cttccgcatc      60
ggcgcggcgg ttagcagctt catgaccttt gatcccgctt accgcgccct gatccgccgc     120
cattacaatt ccctgacggc ggacaaccag atgaagccgg aaagcgtgtt ggatcgcacc     180
gcgaccctgg cgaagggcga cctgctccac gctgcggtgg atttcacccg tgtggacgcg     240
ctgatgtact ttgcacggga caacgggatc cccatgcggt atcacaccct ggcctggcac     300
aaccagacgc cccgctggtt cttcgcgaag gactggagcg acgcggaaag cgccgaaccc     360
gcctcaaagg aaaccatgct tgcccgtctg gaaaactata tcctggatgt catgaaccat     420
gtgaatacca agtttcccgg tctggtttac acctgggacg tggtaaacga agccattgag     480
ccagagctga aagccccggg attgtaccgg acctggagcc cctggttcaa aacctgcgga     540
gaagatttcc tctttaccgc tttccgggcc gcccgcaagg gacaggcgcc cggtcagacc     600
ctttgctata acgactataa cgccttcgag cccgtcaagc gggacgcgat tatcgatctg     660
ctgaagaagc tgcaggcgga aaacctggtg gataccatgg gtatgcaggg gcattatgtc     720
atggactgga tgaacatctc gctctgcgaa gaggccgccc gcgcctatgc cgccctgggc     780
ctgaaggtcc aggtcaccga gctggatatc cactgcaaca gcgacgatga agcccacagc     840
caaaagctgg cgcagcttta cggcgattat ttcgccatgc tgaagaagct gaaggaggaa     900
ggcgtcgaca tcgaagccgt caccttctgg ggcgtcaccg accaggacag ctggctcacc     960
ggtttccgta aagagacaag ctatcccctc ctcttcgacc gcgccaagca ggccaaggat    1020
gcctatgacg ccgtcatgaa agccgcggaa taa                                1053

<210> 14
<211> 350
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 14
Met Lys Asp Ala Leu Gln Cys Ser Pro Leu Phe Lys Ala Tyr Glu Lys
 1               5                  10                  15
Tyr Phe Arg Ile Gly Ala Ala Val Ser Ser Phe Met Thr Phe Asp Pro
            20                  25                  30
Ala Tyr Arg Ala Leu Ile Arg Arg His Tyr Asn Ser Leu Thr Ala Asp
        35                  40                  45
Asn Gln Met Lys Pro Glu Ser Val Leu Asp Arg Thr Ala Thr Leu Ala
    50                  55                  60
Lys Gly Asp Leu Leu His Ala Ala Val Asp Phe Thr Arg Val Asp Ala
65                  70                  75                  80
Leu Met Tyr Phe Ala Arg Asp Asn Gly Ile Pro Met Arg Tyr His Thr
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                85                  90                  95
Leu Ala Trp His Asn Gln Thr Pro Arg Trp Phe Phe Ala Lys Asp Trp
            100                 105                 110
Ser Asp Ala Glu Ser Ala Glu Pro Ala Ser Lys Glu Thr Met Leu Ala
        115                 120                 125
Arg Leu Glu Asn Tyr Ile Leu Asp Val Met Asn His Val Asn Thr Lys
    130                 135                 140
Phe Pro Gly Leu Val Tyr Thr Trp Asp Val Val Asn Glu Ala Ile Glu
145                 150                 155                 160
Pro Glu Leu Lys Ala Pro Gly Leu Tyr Arg Thr Trp Ser Pro Trp Phe
                165                 170                 175
Lys Thr Cys Gly Glu Asp Phe Leu Phe Thr Ala Phe Arg Ala Ala Arg
            180                 185                 190
Lys Gly Gln Ala Pro Gly Gln Thr Leu Cys Tyr Asn Asp Tyr Asn Ala
        195                 200                 205
Phe Glu Pro Val Lys Arg Asp Ala Ile Ile Asp Leu Leu Lys Lys Leu
    210                 215                 220
Gln Ala Glu Asn Leu Val Asp Thr Met Gly Met Gln Gly His Tyr Val
225                 230                 235                 240
Met Asp Trp Met Asn Ile Ser Leu Cys Glu Glu Ala Ala Arg Ala Tyr
                245                 250                 255
Ala Ala Leu Gly Leu Lys Val Gln Val Thr Glu Leu Asp Ile His Cys
            260                 265                 270
Asn Ser Asp Asp Glu Ala His Ser Gln Lys Leu Ala Gln Leu Tyr Gly
        275                 280                 285
Asp Tyr Phe Ala Met Leu Lys Lys Leu Lys Glu Glu Gly Val Asp Ile
    290                 295                 300
Glu Ala Val Thr Phe Trp Gly Val Thr Asp Gln Asp Ser Trp Leu Thr
305                 310                 315                 320
Gly Phe Arg Lys Glu Thr Ser Tyr Pro Leu Leu Phe Asp Arg Ala Lys
                325                 330                 335
Gln Ala Lys Asp Ala Tyr Asp Ala Val Met Lys Ala Ala Glu
            340                 345                 350
```

<210> 15
<211> 1110
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 15

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atgaaacgtc ctctagtcaa tctcctgaca accgcctgcc tcctcgttgc cgcaaatgct      60
gcagaaccca ccctccgcga agcctacgaa aagcactttg ccgtgggtgt cgcactcaat     120
accgctcaag tgactggtcg aaacaaagcc gcaggcgaac tcgccgcgaa gcagttcaat     180
tccatcaccg ctgagaatga catgaagtgg caatcgcttc atccagagct cgatacctac     240
cgctttgaat cggccgatgc ctatatcgac tttgccaaaa agaatgagat ggaagtcata     300
ggccacactc tcgtctggca cagccagacc cctcagtggg tgttccaagg cgacgatggc     360
aaacccgcga cacgggaaga acttctcaag cggatgcgcg atcacattca caaggtcgcc     420
ggccgataca agggtaaggt caagggctgg gacgtcgtca atgaggcgct ctccgacgga     480
ggtcaggaca ttctacgcga atctccgtgg cggcgaatca tcggagacga tttcatcgat     540
cacgctttcc gctacgcccg cgaagccgac ccaaaggcag aactttacta caacgactac     600
aacctcgaaa tccctcgcaa acgcgagaac tgcatcaagc tcgtcaaggg catgcttgag     660
cgcggcgtcc ccatcgacgg cattggaacg caatcccatt ttcagcttgg cttcccatcg     720
ctggaagatg tcgagaccac gattgaagag tttggaaaac tcggccttaa ggtcatgatt     780
accgaactcg atgtggatgt cctccctcgc aataacccag gcgtcgccga catcagtcag     840
cgcgagcaag gtagcaatcc ctacactgag ggcctgcccg aggatgttca aaagcagctt     900
acgaaacgct acgaagacat cttcaagatc tacctaaagc accagaaaac ggtcacccgc     960
gtgaccttct ggggcctcga tgatggtcaa tcatggttga atggctttcc tgttagaggc    1020
cgcaccaatc acccgctact tttcgatcgt gaactcaaac cgaagcccgt tcttccagtc    1080
ttgatagagc tcggcaagaa gaagcgataa                                     1110
```

<210> 16
<211> 369
<212> PRT
<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(20)

<400> 16
Met Lys Arg Pro Leu Val Asn Leu Leu Thr Thr Ala Cys Leu Leu Val
1 5 10 15
Ala Ala Asn Ala Ala Glu Pro Thr Leu Arg Glu Ala Tyr Glu Lys His
20 25 30
Phe Ala Val Gly Val Ala Leu Asn Thr Ala Gln Val Thr Gly Arg Asn
35 40 45
Lys Ala Ala Gly Glu Leu Ala Ala Lys Gln Phe Asn Ser Ile Thr Ala
50 55 60
Glu Asn Asp Met Lys Trp Gln Ser Leu His Pro Glu Leu Asp Thr Tyr
65 70 75 80
Arg Phe Glu Ser Ala Asp Ala Tyr Ile Asp Phe Ala Lys Lys Asn Glu
85 90 95
Met Glu Val Ile Gly His Thr Leu Val Trp His Ser Gln Thr Pro Gln
100 105 110
Trp Val Phe Gln Gly Asp Asp Gly Lys Pro Ala Thr Arg Glu Glu Leu
115 120 125
Leu Lys Arg Met Arg Asp His Ile His Lys Val Ala Gly Arg Tyr Lys
130 135 140
Gly Lys Val Lys Gly Trp Asp Val Val Asn Glu Ala Leu Ser Asp Gly
145 150 155 160
Gly Gln Asp Ile Leu Arg Glu Ser Pro Trp Arg Arg Ile Ile Gly Asp
165 170 175
Asp Phe Ile Asp His Ala Phe Arg Tyr Ala Arg Glu Ala Asp Pro Lys
180 185 190
Ala Glu Leu Tyr Tyr Asn Asp Tyr Asn Leu Glu Ile Pro Arg Lys Arg
195 200 205
Glu Asn Cys Ile Lys Leu Val Lys Gly Met Leu Glu Arg Gly Val Pro
210 215 220
Ile Asp Gly Ile Gly Thr Gln Ser His Phe Gln Leu Gly Phe Pro Ser
225 230 235 240
Leu Glu Asp Val Glu Thr Thr Ile Glu Glu Phe Gly Lys Leu Gly Leu
245 250 255
Lys Val Met Ile Thr Glu Leu Asp Val Asp Val Leu Pro Arg Asn Asn
260 265 270
Pro Gly Val Ala Asp Ile Ser Gln Arg Glu Gln Gly Ser Asn Pro Tyr
275 280 285
Thr Glu Gly Leu Pro Glu Asp Val Gln Lys Gln Leu Thr Lys Arg Tyr
290 295 300
Glu Asp Ile Phe Lys Ile Tyr Leu Lys His Gln Lys Thr Val Thr Arg
305 310 315 320
Val Thr Phe Trp Gly Leu Asp Asp Gly Gln Ser Trp Leu Asn Gly Phe
325 330 335
Pro Val Arg Gly Arg Thr Asn His Pro Leu Leu Phe Asp Arg Glu Leu
340 345 350
Lys Pro Lys Pro Val Leu Pro Val Leu Ile Glu Leu Gly Lys Lys Lys
355 360 365
Arg

<210> 17
<211> 1035
<212> DNA
<213> Bacteria

<400> 17
atgtcccggc acgtcatcgc cctgtccgcc gccgtctgcc tcgcggccgg cctcgccgcc 60
gcgcccgcga gcgccgagcc gcgtccccgg acgctcggcg aactggccaa gaagcaccac 120
aagtacttcg gctcggccac cgacaacccc gagttcaccg acgccgccta tctgaagctc 180
ctcggcagcg agttcgggca gaccaccccc ggcaacgcca tgaagtggta cgccaccgaa 240
cccgcgcccg gcgtcttcga cttcaccgcg ggcgacgagg tcgtggcctt cgccaaggcc 300
catcaccaga aggtccgcgg ccacaccctc gtctggcaca gccagctccc cgcctggctc 360
accgagcgca gctggaccgc cgcggaactg cgcccccgtcc tcaagaatca catccagaag 420
gtggcccggc actacaaggg caaggtcatc cactgggacg tcgtcaacga ggccttcaac 480

gaggacggca cctaccgcga gtcggtcttc tacaagacgc tcggccccgg ctacatcgcc 540
gacgccctgc gctgggccca cgaggccgac ccgcacgcca agctgtacct caacgactac 600
aacgtcgacg ggatcggccc caagagcgac gcctactacc gcctgatcaa gcagctgaag 660
gccgacggcg tcccggtgga gggcttcggc atccaggggc acctggcgct ccagtacggc 720
ttccccgccg acgtcaagca gaacatgcag cgcttcgccg acctcggcgt cgaggtcgcg 780
gtcaccgagc tcgacatccg gatgaacctc ccggcgaccc cttcgatgct cgccacccag 840
gccacctggt acgccgacta cgtcaaggcc tgcctggagg tcaggaagtg cgtcggcgtc 900
accatctggg actacaccga caagtactcg tggatcccct ccgtcttccc cggtgagggc 960
gccgcgctgc cctacgacga gaacctggcg cccaagcccg cctaccacgc gatcaggaag 1020
gtgctgggcg gatga 1035

<210> 18
<211> 344
<212> PRT
<213> Bacteria

<220>
<221> SIGNAL
<222> (1)...(31)

<400> 18
Met Ser Arg His Val Ile Ala Leu Ser Ala Ala Val Cys Leu Ala Ala
1 5 10 15
Gly Leu Ala Ala Ala Pro Ala Ser Ala Glu Pro Arg Pro Arg Thr Leu
20 25 30
Gly Glu Leu Ala Lys Lys His His Lys Tyr Phe Gly Ser Ala Thr Asp
35 40 45
Asn Pro Glu Phe Thr Asp Ala Ala Tyr Leu Lys Leu Leu Gly Ser Glu
50 55 60
Phe Gly Gln Thr Thr Pro Gly Asn Ala Met Lys Trp Tyr Ala Thr Glu
65 70 75 80
Pro Ala Pro Gly Val Phe Asp Phe Thr Ala Gly Asp Glu Val Val Ala
85 90 95
Phe Ala Lys Ala His His Gln Lys Val Arg Gly His Thr Leu Val Trp
100 105 110
His Ser Gln Leu Pro Ala Trp Leu Thr Glu Arg Ser Trp Thr Ala Ala
115 120 125
Glu Leu Arg Pro Val Leu Lys Asn His Ile Gln Lys Val Ala Arg His
130 135 140
Tyr Lys Gly Lys Val Ile His Trp Asp Val Val Asn Glu Ala Phe Asn
145 150 155 160
Glu Asp Gly Thr Tyr Arg Glu Ser Val Phe Tyr Lys Thr Leu Gly Pro
165 170 175
Gly Tyr Ile Ala Asp Ala Leu Arg Trp Ala His Glu Ala Asp Pro His
180 185 190
Ala Lys Leu Tyr Leu Asn Asp Tyr Asn Val Asp Gly Ile Gly Pro Lys
195 200 205
Ser Asp Ala Tyr Tyr Arg Leu Ile Lys Gln Leu Lys Ala Asp Gly Val
210 215 220
Pro Val Glu Gly Phe Gly Ile Gln Gly His Leu Ala Leu Gln Tyr Gly
225 230 235 240
Phe Pro Ala Asp Val Lys Gln Asn Met Gln Arg Phe Ala Asp Leu Gly
245 250 255
Val Glu Val Ala Val Thr Glu Leu Asp Ile Arg Met Asn Leu Pro Ala
260 265 270
Thr Pro Ser Met Leu Ala Thr Gln Ala Thr Trp Tyr Ala Asp Tyr Val
275 280 285
Lys Ala Cys Leu Glu Val Arg Lys Cys Val Gly Val Thr Ile Trp Asp
290 295 300
Tyr Thr Asp Lys Tyr Ser Trp Ile Pro Ser Val Phe Pro Gly Glu Gly
305 310 315 320
Ala Ala Leu Pro Tyr Asp Glu Asn Leu Ala Pro Lys Pro Ala Tyr His
325 330 335
Ala Ile Arg Lys Val Leu Gly Gly
340

<210> 19
<211> 1152
<212> DNA

<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 19
atgaagatgt taaaaactat tgttgtggct gtagcagcct tactatccag tcctactgct 60
tcagccactt tacagaacct gaagcgggct cctgattcat tgaccttgaa agatgcattt 120
gagggtaagt tttatatagg aacagcatta aaccttgatc agatatggga gcgcgatcag 180
gctgcggtcg cggtggtcaa aacgcagttc aactccatag ttgctgagaa ttgtatgaaa 240
agtatgtttt tgcaaccaag ggaaggtgag tttgatttta gggatgcgga ccgttttgtc 300
gcgtttggag aaaaaaataa aatgcaaatt atcggtcata cgctgatttg gcattcgcag 360
acaccagctt ggtttttgt cgataaaaat gggaaagagg tcacccgaga ggtacttatc 420
gagcgcatgc ggaagcatat acaaaccgtt gtttcccgct ataagggaag ggtgtttggt 480
tgggatgtgg tgaacgaagc catattggat aatggagaat ggcgtaaaag caaattctac 540
cagattatcg ggccacaatt tattgaattg gccttcaaat ttgcgcatga cgcagatcca 600
aatgcagaat tatattataa cgattattca actgctatcc ccgaaaaaag aaaggggatt 660
atgcgcatgg tgcagcaggt aaaggctgcc ggtgggcagg tcactggaat tggtatgcag 720
gaacacaacg cattggacaa tccaccggtc gatgaagtcg aaaaaaccat actcggattt 780
gcaagccttg gtgcgaaggt aatggttacg gaaatggata tttcggtcct gccgcatgta 840
cgtcccaata tgggcgcaga aatagggggag cgtcatgcct acagtaaagc gatgaatccg 900
tacgaaaaag gacttcctgt aacgaaaatg aacgagttgg gagcgagata tgtagcgttt 960
tttaatttat atctcaaaca tcgggataaa atatcgcgtg tgacattgtg gggtgttggc 1020
gatggagatt catggaagaa tggttggcct attcccggac gtacagacta tccattgtta 1080
ttcgatcgga attaccaacc caaacctttt gtaaaagata ttattgcgtt gactcaaaaa 1140
aaaaagaaat aa 1152

<210> 20
<211> 383
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(29)

<400> 20
Met Lys Met Leu Lys Thr Ile Val Val Ala Val Ala Ala Leu Leu Ser
1 5 10 15
Ser Pro Thr Ala Ser Ala Thr Leu Gln Asn Leu Lys Arg Ala Pro Asp
20 25 30
Ser Leu Thr Leu Lys Asp Ala Phe Glu Gly Lys Phe Tyr Ile Gly Thr
35 40 45
Ala Leu Asn Leu Asp Gln Ile Trp Glu Arg Asp Gln Ala Ala Val Ala
50 55 60
Val Val Lys Thr Gln Phe Asn Ser Ile Val Ala Glu Asn Cys Met Lys
65 70 75 80
Ser Met Phe Leu Gln Pro Arg Glu Gly Glu Phe Asp Phe Arg Asp Ala
85 90 95
Asp Arg Phe Val Ala Phe Gly Glu Lys Asn Lys Met Gln Ile Ile Gly
100 105 110
His Thr Leu Ile Trp His Ser Gln Thr Pro Ala Trp Phe Phe Val Asp
115 120 125
Lys Asn Gly Lys Glu Val Thr Arg Glu Val Leu Ile Glu Arg Met Arg
130 135 140
Lys His Ile Gln Thr Val Val Ser Arg Tyr Lys Gly Arg Val Phe Gly
145 150 155 160
Trp Asp Val Val Asn Glu Ala Ile Leu Asp Asn Gly Glu Trp Arg Lys
165 170 175
Ser Lys Phe Tyr Gln Ile Ile Gly Pro Gln Phe Ile Glu Leu Ala Phe
180 185 190
Lys Phe Ala His Asp Ala Asp Pro Asn Ala Glu Leu Tyr Tyr Asn Asp
195 200 205
Tyr Ser Thr Ala Ile Pro Glu Lys Arg Lys Gly Ile Met Arg Met Val
210 215 220
Gln Gln Val Lys Ala Ala Gly Gly Gln Val Thr Gly Ile Gly Met Gln
225 230 235 240

Glu His Asn Ala Leu Asp Asn Pro Pro Val Asp Glu Val Glu Lys Thr
245 250 255
Ile Leu Gly Phe Ala Ser Leu Gly Ala Lys Val Met Val Thr Glu Met
260 265 270
Asp Ile Ser Val Leu Pro His Val Arg Pro Asn Met Gly Ala Glu Ile
275 280 285
Gly Glu Arg His Ala Tyr Ser Lys Ala Met Asn Pro Tyr Glu Lys Gly
290 295 300
Leu Pro Val Thr Lys Met Asn Glu Leu Gly Ala Arg Tyr Val Ala Phe
305 310 315 320
Phe Asn Leu Tyr Leu Lys His Arg Asp Lys Ile Ser Arg Val Thr Leu
325 330 335
Trp Gly Val Gly Asp Gly Asp Ser Trp Lys Asn Gly Trp Pro Ile Pro
340 345 350
Gly Arg Thr Asp Tyr Pro Leu Leu Phe Asp Arg Asn Tyr Gln Pro Lys
355 360 365
Pro Phe Val Lys Asp Ile Ile Ala Leu Thr Gln Lys Lys Lys Lys
370 375 380

<210> 21
<211> 1119
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 21
atgcggattc actggctggg gctcagctca cgcgcaagcc tgatgacggc ggcgctcctg 60
gctgtcacag gcaccaccaa atccgaggac tcgcccgcaa ctttgaaaga cgccttcaag 120
gattgtttcc ggatcggggt cgcgctcaac cagcggcaat ttaccgagca agataccaac 180
ggcgcgacgt tggtgaaacg gcagttcaac gccatctcac ccgaaaacgt gatgaagtgg 240
gcgaacattc atccccgacc cgggcccgat gggtataact tcgaggcggc tgaccgttac 300
gtcgagtttg gcgagaagaa cggaatgttc atcgtcggcc atacgctcgt ttggcacttc 360
caaacgccgc gctgggtact ccagggcgat ggcactaacg cggcgacgcg cgagctgctg 420
ctgcagcgga tgcgcgatca catccacacg gtcgtaggcc ggtacaaagg gcggatcaag 480
gcttgggacg tggtcaacga agcgctgaac gaagatggca ctctgcggcg gtcgcagtgg 540
taccggatca tcggcgaaga ctacatcgtc aaggctttcg aatatgcgca tgaggccgat 600
ccgtccgcgg aattgcgata caacgattac gccatcgaga atgagcggaa gcgcgacggc 660
gtaatcgcgc tcgtgaagaa acttcaggcg cagaaggtcc cacttggggg gctgggctcg 720
cagacgcatg ccaacctgac ctggcctaac gccgaatcgc tggacaccgc cctcacggcc 780
ttcaccgaac tgggtatccc gatctcaatc acggaactgg atgtgaccgc ctcgcaacgc 840
ggtcagctca accagagcgc cgaggtgtcg cagaatggac aggcggggga gggaggcgtg 900
gtggacgggg cgaatcagaa gctcgccgag cagtacgcca acttcttccg cgtctttctg 960
aagcatcgca aaaacattga gctcgtgacg ttttggggcg tcacggatcg tgactcctgg 1020
cggcgcattg gcaaaccgct gctatttaac gcagaatggc aacccaagcc ggcctttcac 1080
gccgtcatcg ccgaggcgaa aaagatcagt gggcaatga 1119

<210> 22
<211> 372
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<400> 22
Met Arg Ile His Trp Leu Gly Leu Ser Ser Arg Ala Ser Leu Met Thr
1 5 10 15
Ala Ala Leu Leu Ala Val Thr Gly Thr Thr Lys Ser Glu Asp Ser Pro
20 25 30
Ala Thr Leu Lys Asp Ala Phe Lys Asp Cys Phe Arg Ile Gly Val Ala
35 40 45
Leu Asn Gln Arg Gln Phe Thr Glu Gln Asp Thr Asn Gly Ala Thr Leu
50 55 60
Val Lys Arg Gln Phe Asn Ala Ile Ser Pro Glu Asn Val Met Lys Trp

```
65                  70                  75                  80
Ala Asn Ile His Pro Arg Pro Gly Pro Asp Gly Tyr Asn Phe Glu Ala
                85                  90                  95
Ala Asp Arg Tyr Val Glu Phe Gly Glu Lys Asn Gly Met Phe Ile Val
            100                 105                 110
Gly His Thr Leu Val Trp His Phe Gln Thr Pro Arg Trp Val Leu Gln
        115                 120                 125
Gly Asp Gly Thr Asn Ala Ala Thr Arg Glu Leu Leu Leu Gln Arg Met
    130                 135                 140
Arg Asp His Ile His Thr Val Val Gly Arg Tyr Lys Gly Arg Ile Lys
145                 150                 155                 160
Ala Trp Asp Val Val Asn Glu Ala Leu Asn Glu Asp Gly Thr Leu Arg
                165                 170                 175
Arg Ser Gln Trp Tyr Arg Ile Ile Gly Glu Asp Tyr Ile Val Lys Ala
            180                 185                 190
Phe Glu Tyr Ala His Glu Ala Asp Pro Ser Ala Glu Leu Arg Tyr Asn
        195                 200                 205
Asp Tyr Ala Ile Glu Asn Glu Arg Lys Arg Asp Gly Val Ile Ala Leu
    210                 215                 220
Val Lys Lys Leu Gln Ala Gln Lys Val Pro Leu Gly Gly Leu Gly Ser
225                 230                 235                 240
Gln Thr His Ala Asn Leu Thr Trp Pro Asn Ala Glu Ser Leu Asp Thr
                245                 250                 255
Ala Leu Thr Ala Phe Thr Glu Leu Gly Ile Pro Ile Ser Ile Thr Glu
            260                 265                 270
Leu Asp Val Thr Ala Ser Gln Arg Gly Gln Leu Asn Gln Ser Ala Glu
        275                 280                 285
Val Ser Gln Asn Gly Gln Ala Gly Glu Gly Gly Val Val Asp Gly Ala
    290                 295                 300
Asn Gln Lys Leu Ala Glu Gln Tyr Ala Asn Phe Phe Arg Val Phe Leu
305                 310                 315                 320
Lys His Arg Lys Asn Ile Glu Leu Val Thr Phe Trp Gly Val Thr Asp
                325                 330                 335
Arg Asp Ser Trp Arg Arg Ile Gly Lys Pro Leu Leu Phe Asn Ala Glu
            340                 345                 350
Trp Gln Pro Lys Pro Ala Phe His Ala Val Ile Ala Glu Ala Lys Lys
        355                 360                 365
Ile Ser Gly Gln
    370
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<210> 23
<211> 1137
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 23

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atgaggacaa aacaagtttt taaattaacc acgctcgctt tattattaac agcagttgtt      60
agtagctgtt ctgccccaaa agcggcaaaa gaagatacgc ttaaagatgc ctccagggga     120
aaattcttta ttggtgctgc tgttaatgtt gaccaaatgg caggaaagga ttctcttgca     180
attgaagttg ttaaaaagaa ctttagctca attgtggccg agaattgcat gaaaatggaa     240
aacatccatc ctgtaaaagg tgaatttttc ttcgatgaag ccgatgcata tgttgaattt     300
ggcgaaaaaa acaacatgaa aatcattggt cacacattga tttggcattc acaagccgcc     360
aaatgggcat ttgttgatga tgaaggcaaa gatgtatcgc gcgaagaatt aattgaacgg     420
atgcgcaacc acatccatac cattgtaggc cgctataaag gtcgtgtaca tggctgggac     480
gttgttaatg aggctattct ggataacggc gaatggcgtc agagcaaatg gtataccatt     540
attggacccg aatttgttca gcttgctttt gagtttgccc acgaagccga ccccaacgct     600
gaattgtatt acaacgacta caacgagtgg attccggcta aaagagacgg catttacaac     660
atggttaagg atttaatcga caaaggcgtt aaagttgatg gaattggcct acagggtcac     720
attgctcttg actctcccag catcgaactt tacgaagaag ccattgtaaa atatgcaagt     780
ctgggtgtgc aaacaatggt taccgaactc gatatcactg ttttaccatg gccatcgcag     840
caagttacag ccgatatatc ttttagtgca gagctatcaa ccgaatacaa tccatttgtt     900
aatggtttac ccgattcggt tagcgttgaa cttaccaacc gttttgccag tttcttcgag     960
ttgtttttga aacatcagga taaaattgac cgcgttactc tatggggtgt acacgatggt    1020
caatcatgga aaaacaactg gcccatcagg ggacgtaaag attatccgtt gttattcgac    1080
aggcaatatc agtccaaacc tgccgttcag cgcataatcg aattggctaa acaataa       1137
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<210> 24
<211> 378
<212> PRT
<213> Unknown

<220>
<223> obtained from an environmental sample

<221> SIGNAL
<222> (1)...(29)

<400> 24
Met Arg Thr Lys Gln Val Phe Lys Leu Thr Thr Leu Ala Leu Leu Leu
1 5 10 15
Thr Ala Val Val Ser Ser Cys Ser Ala Pro Lys Ala Ala Lys Glu Asp
20 25 30
Thr Leu Lys Asp Ala Leu Gln Gly Lys Phe Phe Ile Gly Ala Ala Val
35 40 45
Asn Val Asp Gln Met Ala Gly Lys Asp Ser Leu Ala Ile Glu Val Val
50 55 60
Lys Lys Asn Phe Ser Ser Ile Val Ala Glu Asn Cys Met Lys Met Glu
65 70 75 80
Asn Ile His Pro Val Lys Gly Glu Phe Phe Phe Asp Glu Ala Asp Ala
85 90 95
Tyr Val Glu Phe Gly Glu Lys Asn Asn Met Lys Ile Ile Gly His Thr
100 105 110
Leu Ile Trp His Ser Gln Ala Ala Lys Trp Ala Phe Val Asp Asp Glu
115 120 125
Gly Lys Asp Val Ser Arg Glu Glu Leu Ile Glu Arg Met Arg Asn His
130 135 140
Ile His Thr Ile Val Gly Arg Tyr Lys Gly Arg Val His Gly Trp Asp
145 150 155 160
Val Val Asn Glu Ala Ile Leu Asp Asn Gly Glu Trp Arg Gln Ser Lys
165 170 175
Trp Tyr Thr Ile Ile Gly Pro Glu Phe Val Gln Leu Ala Phe Glu Phe
180 185 190
Ala His Glu Ala Asp Pro Asn Ala Glu Leu Tyr Tyr Asn Asp Tyr Asn
195 200 205
Glu Trp Ile Pro Ala Lys Arg Asp Gly Ile Tyr Asn Met Val Lys Asp
210 215 220
Leu Ile Asp Lys Gly Val Lys Val Asp Gly Ile Gly Leu Gln Gly His
225 230 235 240
Ile Ala Leu Asp Ser Pro Ser Ile Glu Leu Tyr Glu Glu Ala Ile Val
245 250 255
Lys Tyr Ala Ser Leu Gly Val Gln Thr Met Val Thr Glu Leu Asp Ile
260 265 270
Thr Val Leu Pro Trp Pro Ser Gln Gln Val Thr Ala Asp Ile Ser Phe
275 280 285
Ser Ala Glu Leu Ser Thr Glu Tyr Asn Pro Phe Val Asn Gly Leu Pro
290 295 300
Asp Ser Val Ser Val Glu Leu Thr Asn Arg Phe Ala Ser Phe Phe Glu
305 310 315 320
Leu Phe Leu Lys His Gln Asp Lys Ile Asp Arg Val Thr Leu Trp Gly
325 330 335
Val His Asp Gly Gln Ser Trp Lys Asn Asn Trp Pro Ile Arg Gly Arg
340 345 350
Lys Asp Tyr Pro Leu Leu Phe Asp Arg Gln Tyr Gln Ser Lys Pro Ala
355 360 365
Val Gln Arg Ile Ile Glu Leu Ala Lys Gln
370 375

<210> 25
<211> 978
<212> DNA
<213> Unknown

<220>
<223> obtained from an environmental sample

<400> 25
gtggatccaa agaattcctt acgcgcctta gctcaaaagc gaggaattgg gtttgggacg 60
gcagtttggg ttgagcctct gtctaacgat tcgagatatc ggacggtgtt ggcgcaggag 120
ttcaatatgg tgacgccaga gaatgagatg aagtttgagc cgacgcatcc agaacgggag 180
cgctacgatt ttacagcagc cgataccctt gttgactttg ccaagaacca taacatgcag 240
gtgcgcggac ataccctggt ttggcatgaa agtctccccg attggctaac gactcaaacg 300
tggacgcgtg aggagttgat gtccatctta gaagaacaca tcaatacagt tgtcgatcgc 360
tatcgggggc aattagttgc ctgggatgtg gtgaatgaag cgatcgccaa cgataaaaac 420
gcactcagag atacgatttg gctgcgaaca atcgggccag agtatataga gaaggcattt 480
cgctgggcgc atgcagccga ccctcaagca cgtttatttt acaacgatta tggcggcgag 540
gaagtggggg gaaagtctga ggccatctat ggcatgctta aagatttgct gcaacagggt 600
gtcccgattc acggggttgg cttgcaaatg cacgttagta taaaaaaccc tcccaatccc 660
gaaaaagtgg cggcaaatat caagcgcctg aacgatctgg gattggaagt gcatataact 720
gagatggatg tgaaaacctg ggatggcatc ggtacgaagc agcaacgact tgcggctcag 780
gcacaagtgt atcggaacat gatgcaggtg tgtttggaag ctgagaactg taaggcgttt 840
tcgttgtggg gggtaagcga tcgctattct tggattcccc ggatttttaa gaagccggat 900
gcaccactga tttttgatga tttagggcgt ccgaaacccg cttacaatgc cctgaaagaa 960
gtcctcaagc ggcgttaa 978

<210> 26
<211> 325
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 26
Val Asp Pro Lys Asn Ser Leu Arg Ala Leu Ala Gln Lys Arg Gly Ile
1 5 10 15
Gly Phe Gly Thr Ala Val Trp Val Glu Pro Leu Ser Asn Asp Ser Arg
20 25 30
Tyr Arg Thr Val Leu Ala Gln Glu Phe Asn Met Val Thr Pro Glu Asn
35 40 45
Glu Met Lys Phe Glu Pro Thr His Pro Glu Arg Glu Arg Tyr Asp Phe
50 55 60
Thr Ala Ala Asp Thr Leu Val Asp Phe Ala Lys Asn His Asn Met Gln
65 70 75 80
Val Arg Gly His Thr Leu Val Trp His Glu Ser Leu Pro Asp Trp Leu
85 90 95
Thr Thr Gln Thr Trp Thr Arg Glu Glu Leu Met Ser Ile Leu Glu Glu
100 105 110
His Ile Asn Thr Val Val Asp Arg Tyr Arg Gly Gln Leu Val Ala Trp
115 120 125
Asp Val Val Asn Glu Ala Ile Ala Asn Asp Lys Asn Ala Leu Arg Asp
130 135 140
Thr Ile Trp Leu Arg Thr Ile Gly Pro Glu Tyr Ile Glu Lys Ala Phe
145 150 155 160
Arg Trp Ala His Ala Ala Asp Pro Gln Ala Arg Leu Phe Tyr Asn Asp
165 170 175
Tyr Gly Gly Glu Glu Val Gly Gly Lys Ser Glu Ala Ile Tyr Gly Met
180 185 190
Leu Lys Asp Leu Leu Gln Gln Gly Val Pro Ile His Gly Val Gly Leu
195 200 205
Gln Met His Val Ser Ile Lys Asn Pro Pro Asn Pro Glu Lys Val Ala
210 215 220
Ala Asn Ile Lys Arg Leu Asn Asp Leu Gly Leu Glu Val His Ile Thr
225 230 235 240
Glu Met Asp Val Lys Thr Trp Asp Gly Ile Gly Thr Lys Gln Gln Arg
245 250 255
Leu Ala Ala Gln Ala Gln Val Tyr Arg Asn Met Met Gln Val Cys Leu
260 265 270
Glu Ala Glu Asn Cys Lys Ala Phe Ser Leu Trp Gly Val Ser Asp Arg
275 280 285
Tyr Ser Trp Ile Pro Arg Ile Phe Lys Lys Pro Asp Ala Pro Leu Ile
290 295 300
Phe Asp Asp Leu Gly Arg Pro Lys Pro Ala Tyr Asn Ala Leu Lys Glu
305 310 315 320
Val Leu Lys Arg Arg

325

<210> 27
<211> 1173
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 27
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atgaaatcct taacaaatca atccttcatg aaactcataa tctgtctggc attgccagtc      60
gcactactca gcatttcatg caaaaaaccc gccgaaccac tgaaaccggt tgaaggctta     120
aaagacagct tcaaagacaa gtttctcatg ggtgtggcgc tgaataaagc acagattctg     180
ggaagagata cattggtaca tgcttttaca gtacagcatt ttaattccat tactgcagaa     240
aacgaaatga agtgggaacg catccacccg cagcctgatg tatatgattt cacggttccg     300
gacagcctga ttgcttttgg cgaacgcaac ggcatgttta tagtcgggca tacactcgta     360
tggcactccc aggtgcccga ttgggttttc accgatgaga agggaaagcc tctgacccgc     420
gatgctctgc tccaacgcat gaaggatcat atttatgccg ttgtcggccg gtataagggc     480
aaggtggatg gctgggatgt ggtaaatgaa gcattggatg aagacggaca gctgcgcaaa     540
tccaggtggc atgaaatcat cggtgatgat tacattcaga aagcctttga gttcacccgg     600
gaggcagatc ccggtgcaga gctttattac aatgattaca acatagaact caaaaaaaag     660
cgggagggtg ctgtcaggct gctacaggaa ctgcagcaaa aaggcattaa aatcgacgga     720
gtgggcattc agggacattg gcacctgcac tcacctgatc tgcaagagat tgattcaagt     780
cttcaggcat acggacaact tggtctgaag gtcatgatca ccgaactgga tgttaacgtc     840
attcccgaac cttcaggtat tattggcgcc gatgttgcac agcgggcgga ttatcagagc     900
cagctgaatc catggcctga aagtttcccc gattccatgc agcaggttct ggccagccgg     960
tatgccgaac tgttcggatt gttcctgaag cacagcgata aggtaagccg ggtgaccttc    1020
tggggaattc acgatggcta ttcctggaag aacaactggc caataccggg ccgaacaact    1080
tatcccctcc tttttgaccg gaattaccag cctaaacctg cgtatgatgc tgtcattgaa    1140
ttgaccaaaa tacagccgga agccagtaac tga                                 1173
```

<210> 28
<211> 390
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(27)

<400> 28
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Met Lys Ser Leu Thr Asn Gln Ser Phe Met Lys Leu Ile Ile Cys Leu
 1               5                  10                  15
Ala Leu Pro Val Ala Leu Leu Ser Ile Ser Cys Lys Lys Pro Ala Glu
            20                  25                  30
Pro Leu Lys Pro Val Glu Gly Leu Lys Asp Ser Phe Lys Asp Lys Phe
        35                  40                  45
Leu Met Gly Val Ala Leu Asn Lys Ala Gln Ile Leu Gly Arg Asp Thr
    50                  55                  60
Leu Val His Ala Phe Thr Val Gln His Phe Asn Ser Ile Thr Ala Glu
65                  70                  75                  80
Asn Glu Met Lys Trp Glu Arg Ile His Pro Gln Pro Asp Val Tyr Asp
                85                  90                  95
Phe Thr Val Pro Asp Ser Leu Ile Ala Phe Gly Glu Arg Asn Gly Met
            100                 105                 110
Phe Ile Val Gly His Thr Leu Val Trp His Ser Gln Val Pro Asp Trp
        115                 120                 125
Val Phe Thr Asp Glu Lys Gly Lys Pro Leu Thr Arg Asp Ala Leu Leu
    130                 135                 140
Gln Arg Met Lys Asp His Ile Tyr Ala Val Val Gly Arg Tyr Lys Gly
145                 150                 155                 160
Lys Val Asp Gly Trp Asp Val Val Asn Glu Ala Leu Asp Glu Asp Gly
                165                 170                 175
Gln Leu Arg Lys Ser Arg Trp His Glu Ile Ile Gly Asp Asp Tyr Ile
            180                 185                 190
Gln Lys Ala Phe Glu Phe Thr Arg Glu Ala Asp Pro Gly Ala Glu Leu
```

195 200 205
Tyr Tyr Asn Asp Tyr Asn Ile Glu Leu Lys Lys Lys Arg Glu Gly Ala
210 215 220
Val Arg Leu Leu Gln Glu Leu Gln Gln Lys Gly Ile Lys Ile Asp Gly
225 230 235 240
Val Gly Ile Gln Gly His Trp His Leu His Ser Pro Asp Leu Gln Glu
245 250 255
Ile Asp Ser Ser Leu Gln Ala Tyr Gly Gln Leu Gly Leu Lys Val Met
260 265 270
Ile Thr Glu Leu Asp Val Asn Val Ile Pro Glu Pro Ser Gly Ile Ile
275 280 285
Gly Ala Asp Val Ala Gln Arg Ala Asp Tyr Gln Ser Gln Leu Asn Pro
290 295 300
Trp Pro Glu Ser Phe Pro Asp Ser Met Gln Gln Val Leu Ala Ser Arg
305 310 315 320
Tyr Ala Glu Leu Phe Gly Leu Phe Leu Lys His Ser Asp Lys Val Ser
325 330 335
Arg Val Thr Phe Trp Gly Ile His Asp Gly Tyr Ser Trp Lys Asn Asn
340 345 350
Trp Pro Ile Pro Gly Arg Thr Thr Tyr Pro Leu Leu Phe Asp Arg Asn
355 360 365
Tyr Gln Pro Lys Pro Ala Tyr Asp Ala Val Ile Glu Leu Thr Lys Ile
370 375 380
Gln Pro Glu Ala Ser Asn
385 390

<210> 29
<211> 2331
<212> DNA
<213> Archaea

<400> 29
atgacgatgc agagaaagta ctcatccgac gcgaacacac agtatgagtg gataaaatca 60
gctactgtac catctggtca gtgggtacag ctctctggaa cgtacacgat cccggccgga 120
gttaccgtgg aagatctcac gctttacttc gaatctcaaa atccaaccct tgagttctac 180
gtggatgacg tgaagatagt ggatacaact tccgcagaga taaagattga aatggaacct 240
gaaaaagaga tacctgctct gaaagaagta ctgaaagatt acttcaaagt cggagttgca 300
ctgccgtcca aggtcttcct caacccgaag gacatagaac tcatcacgaa acacttcaac 360
agcatcaccg cagaaaacga gatgaaaccg gatagtctgc tcgcgggcat cgaaaacggt 420
aagctgaagt tcaggtttga aacagcagac aaatacattc agttcgtcga ggaaaacggc 480
atggttataa gaggtcacac actggtgtgg cacaaccaga cacccgactg gttcttcaaa 540
gacgaaaacg gaaacctcct ctccaaagaa gcgatgacgg aaagactcaa agagtacatc 600
cacaccgttg tcggacactt caaaggaaaa gtctacgcat gggacgtggt gaacgaagcg 660
gtcgatccga accagccgga tggactgaga agatcaacct ggtaccagat catggggcct 720
gactacatag aactcgcctt caagttcgca agagaggcag atccagatgc aaaactcttc 780
tacaacgact acaacacatt cgatcccaga aagagagaca tcatctacaa cctcgtgaag 840
gatctcaaag agaagggact catcgatggc ataggaatgc agtgtcacat cagtcttgca 900
acagacatca aacagatcga agaggccatc aaaaagttca gcaccatacc cggtatagaa 960
attcacatca cagaactcga tatgagtgtc tacagagatt ccagttccaa ctacccagag 1020
gcaccgagga cggcactcat cgaacaggct cacaaaatga tgcagctctt tgagatcttc 1080
aagaagcaca gcaacgtgat cacgaacgtc acattctggg gtctcaagga cgattactcc 1140
tggagagcaa caagaagaaa cgactggccg ctcatcttcg acaaagatca ccaggcgaaa 1200
ctcgcttact gggcgatagt ggcacctgag gtccttccac cacttccaaa agaaagcagg 1260
atctccgaag gcgaagcagt ggtagtgggg atgatggacg actcgtacct gatgtcgaag 1320
ccgatagaga tccttgacga agaagggaac gtgaaggcaa cgatcagggc agtgtggaaa 1380
gacagcacga tctacatcta cggagaggta caggacaaga caaagaaacc agcagaagac 1440
ggagtggcca tattcatcaa cccgaacaac gaaagaacac cctatctgca gcctgatgac 1500
acctacgttg tgctgtggac gaactggaag acggaggtca acagagaaga cgtacaggtg 1560
aagaaattcg ttgggcctgg ctttagaaga tacagcttcg agatgtcgat cacgataccg 1620
ggtgtggagt tcaagaaaga cagctacata ggatttgacg ttgcggtgat agacgacggg 1680
aagtggtaca gctggagcga cacgacgaac agccagaaga cgaacacgat gaactacgga 1740
acgctgaagc tcgaaggaat aatggtagcg acagcaaaat acggaacacc ggtcatcgat 1800
ggagagatcg atgagatctg gaacacgaca gaggagatag agacgaaagc ggtggctatg 1860
ggatcgcttg acaagaatgc gacagcgaaa gtgagggtgc tgtgggacga gaactacctg 1920
tacgtacttg cgatcgtgaa agagcccgtt ctgaacaaag acaacagcaa cccgtgggag 1980
caggattccg tggagatctt cgtggatgag aacaaccaca agacaggata ctacgaagac 2040
gacgacgcgc agttcagggt gaactacatg aacgagcaga cctttggaac gggaggaagt 2100
ccagcgaggt tcaagacagc ggtgaagctg atcgaaggag gatacatagt tgaggcagcg 2160
atcaagtgga agacgatcaa gccaacaccg aacacagtga taggattcaa catccaggtg 2220

aacgatgcga acgagaaagg gcagagggtc ggtatcatct cctggagcga tcccacaaac 2280
aacagctggc aagatccttc aaagttcggt aacctcagac tcatcaagtg a 2331

<210> 30
<211> 776
<212> PRT
<213> Archaea

<400> 30
Met Thr Met Gln Arg Lys Tyr Ser Ser Asp Ala Asn Thr Gln Tyr Glu
1 5 10 15
Trp Ile Lys Ser Ala Thr Val Pro Ser Gly Gln Trp Val Gln Leu Ser
20 25 30
Gly Thr Tyr Thr Ile Pro Ala Gly Val Thr Val Glu Asp Leu Thr Leu
35 40 45
Tyr Phe Glu Ser Gln Asn Pro Thr Leu Glu Phe Tyr Val Asp Asp Val
50 55 60
Lys Ile Val Asp Thr Thr Ser Ala Glu Ile Lys Ile Glu Met Glu Pro
65 70 75 80
Glu Lys Glu Ile Pro Ala Leu Lys Glu Val Leu Lys Asp Tyr Phe Lys
85 90 95
Val Gly Val Ala Leu Pro Ser Lys Val Phe Leu Asn Pro Lys Asp Ile
100 105 110
Glu Leu Ile Thr Lys His Phe Asn Ser Ile Thr Ala Glu Asn Glu Met
115 120 125
Lys Pro Asp Ser Leu Leu Ala Gly Ile Glu Asn Gly Lys Leu Lys Phe
130 135 140
Arg Phe Glu Thr Ala Asp Lys Tyr Ile Gln Phe Val Glu Glu Asn Gly
145 150 155 160
Met Val Ile Arg Gly His Thr Leu Val Trp His Asn Gln Thr Pro Asp
165 170 175
Trp Phe Phe Lys Asp Glu Asn Gly Asn Leu Leu Ser Lys Glu Ala Met
180 185 190
Thr Glu Arg Leu Lys Glu Tyr Ile His Thr Val Val Gly His Phe Lys
195 200 205
Gly Lys Val Tyr Ala Trp Asp Val Val Asn Glu Ala Val Asp Pro Asn
210 215 220
Gln Pro Asp Gly Leu Arg Arg Ser Thr Trp Tyr Gln Ile Met Gly Pro
225 230 235 240
Asp Tyr Ile Glu Leu Ala Phe Lys Phe Ala Arg Glu Ala Asp Pro Asp
245 250 255
Ala Lys Leu Phe Tyr Asn Asp Tyr Asn Thr Phe Asp Pro Arg Lys Arg
260 265 270
Asp Ile Ile Tyr Asn Leu Val Lys Asp Leu Lys Glu Lys Gly Leu Ile
275 280 285
Asp Gly Ile Gly Met Gln Cys His Ile Ser Leu Ala Thr Asp Ile Lys
290 295 300
Gln Ile Glu Glu Ala Ile Lys Lys Phe Ser Thr Ile Pro Gly Ile Glu
305 310 315 320
Ile His Ile Thr Glu Leu Asp Met Ser Val Tyr Arg Asp Ser Ser Ser
325 330 335
Asn Tyr Pro Glu Ala Pro Arg Thr Ala Leu Ile Glu Gln Ala His Lys
340 345 350
Met Met Gln Leu Phe Glu Ile Phe Lys Lys His Ser Asn Val Ile Thr
355 360 365
Asn Val Thr Phe Trp Gly Leu Lys Asp Asp Tyr Ser Trp Arg Ala Thr
370 375 380
Arg Arg Asn Asp Trp Pro Leu Ile Phe Asp Lys Asp His Gln Ala Lys
385 390 395 400
Leu Ala Tyr Trp Ala Ile Val Ala Pro Glu Val Leu Pro Pro Leu Pro
405 410 415
Lys Glu Ser Arg Ile Ser Glu Gly Glu Ala Val Val Val Gly Met Met
420 425 430
Asp Asp Ser Tyr Leu Met Ser Lys Pro Ile Glu Ile Leu Asp Glu Glu
435 440 445
Gly Asn Val Lys Ala Thr Ile Arg Ala Val Trp Lys Asp Ser Thr Ile
450 455 460
Tyr Ile Tyr Gly Glu Val Gln Asp Lys Thr Lys Lys Pro Ala Glu Asp
465 470 475 480

Gly Val Ala Ile Phe Ile Asn Pro Asn Asn Glu Arg Thr Pro Tyr Leu
485 490 495
Gln Pro Asp Asp Thr Tyr Val Val Leu Trp Thr Asn Trp Lys Thr Glu
500 505 510
Val Asn Arg Glu Asp Val Gln Val Lys Lys Phe Val Gly Pro Gly Phe
515 520 525
Arg Arg Tyr Ser Phe Glu Met Ser Ile Thr Ile Pro Gly Val Glu Phe
530 535 540
Lys Lys Asp Ser Tyr Ile Gly Phe Asp Val Ala Val Ile Asp Asp Gly
545 550 555 560
Lys Trp Tyr Ser Trp Ser Asp Thr Thr Asn Ser Gln Lys Thr Asn Thr
565 570 575
Met Asn Tyr Gly Thr Leu Lys Leu Glu Gly Ile Met Val Ala Thr Ala
580 585 590
Lys Tyr Gly Thr Pro Val Ile Asp Gly Glu Ile Asp Glu Ile Trp Asn
595 600 605
Thr Thr Glu Glu Ile Glu Thr Lys Ala Val Ala Met Gly Ser Leu Asp
610 615 620
Lys Asn Ala Thr Ala Lys Val Arg Val Leu Trp Asp Glu Asn Tyr Leu
625 630 635 640
Tyr Val Leu Ala Ile Val Lys Glu Pro Val Leu Asn Lys Asp Asn Ser
645 650 655
Asn Pro Trp Glu Gln Asp Ser Val Glu Ile Phe Val Asp Glu Asn Asn
660 665 670
His Lys Thr Gly Tyr Tyr Glu Asp Asp Asp Ala Gln Phe Arg Val Asn
675 680 685
Tyr Met Asn Glu Gln Thr Phe Gly Thr Gly Gly Ser Pro Ala Arg Phe
690 695 700
Lys Thr Ala Val Lys Leu Ile Glu Gly Gly Tyr Ile Val Glu Ala Ala
705 710 715 720
Ile Lys Trp Lys Thr Ile Lys Pro Thr Pro Asn Thr Val Ile Gly Phe
725 730 735
Asn Ile Gln Val Asn Asp Ala Asn Glu Lys Gly Gln Arg Val Gly Ile
740 745 750
Ile Ser Trp Ser Asp Pro Thr Asn Asn Ser Trp Gln Asp Pro Ser Lys
755 760 765
Phe Gly Asn Leu Arg Leu Ile Lys
770 775

<210> 31
<211> 1134
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 31
gtggaaaccg tcggagcacc ggagctgagc tatgaaatcc ggaatttccg ggtggtggca 60
ccggacggag tgccggatat acagcccaca gccgcaccgg aagcgcaggc tgttccggaa 120
ggggagatgc cttccctgaa ggatgtatac gcgggcaaat tcgacttcgg tacggcgctg 180
ccccggaatg cattcaatga tatccagctg ctgagactgg tgaaggacca gttcaacatc 240
ctgacaccgg aaaatgagat gaaaccggat gcaatcctgg atgtgtacgg cagcaaaaaa 300
ctggcggaaa aggacgagac agcggtggct gtccggtttg aagcatgcaa gacgctgctt 360
cggttcgcac agtccaacgg cctgaaggtg cacggccata cgctgctgtg gcacaaccag 420
accccggaag ccctttcca cgaaggttat gacaccacca agccgatggc cggccgggaa 480
gtgatgttgg gccggatgga gaattacatc cgcgaagtgc tgacctggac cgaagaaaat 540
tatccgggcg tgatcgtttc ctgggacgtg gtgaatgaag caatcgacga cggaacgaac 600
cagctgcgca ccggtgccaa ctggtataag acggtcggac cggactacct ggcacgcgcg 660
tttgaatatg cccggaaata cgcggcggaa ggcgtgctgc tgtactacaa cgattacaat 720
accgcatacg gcggtaagct gtatgggatt gtggatctgc tggagagcct gattgccgag 780
ggcaatattg acggatacgg attccagatg caccacagcc tgggagaacc ttccatggat 840
atgattaccc gggcagtaga gaaaatagcc tcgctgggac tccggctgcg tgtgagcgaa 900
ctggacatca acgccggcaa ggcgacagag aaaaatttcg aagcccagaa gaacaagtac 960
aaacaggtga tgaagctgat gctccggttc aaggaccaga ctgaagcggt ccaggtgtgg 1020
ggcgtgacgg acatcatgag ctggcgcagg gacggatatc cgctgctgtt tgacaagaac 1080
atgaatccga aacccgcgtt cttcggtgtg atcgaagccg gaatggaaga ctga 1134

<210> 32

<211> 377
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 32
Val Glu Thr Val Gly Ala Pro Glu Leu Ser Tyr Glu Ile Arg Asn Phe
1 5 10 15
Arg Val Val Ala Pro Asp Gly Val Pro Asp Ile Gln Pro Thr Ala Ala
20 25 30
Pro Glu Ala Gln Ala Val Pro Glu Gly Glu Met Pro Ser Leu Lys Asp
35 40 45
Val Tyr Ala Gly Lys Phe Asp Phe Gly Thr Ala Leu Pro Arg Asn Ala
50 55 60
Phe Asn Asp Ile Gln Leu Leu Arg Leu Val Lys Asp Gln Phe Asn Ile
65 70 75 80
Leu Thr Pro Glu Asn Glu Met Lys Pro Asp Ala Ile Leu Asp Val Tyr
85 90 95
Gly Ser Lys Lys Leu Ala Glu Lys Asp Glu Thr Ala Val Ala Val Arg
100 105 110
Phe Glu Ala Cys Lys Thr Leu Leu Arg Phe Ala Gln Ser Asn Gly Leu
115 120 125
Lys Val His Gly His Thr Leu Leu Trp His Asn Gln Thr Pro Glu Ala
130 135 140
Leu Phe His Glu Gly Tyr Asp Thr Thr Lys Pro Met Ala Gly Arg Glu
145 150 155 160
Val Met Leu Gly Arg Met Glu Asn Tyr Ile Arg Glu Val Leu Thr Trp
165 170 175
Thr Glu Glu Asn Tyr Pro Gly Val Ile Val Ser Trp Asp Val Val Asn
180 185 190
Glu Ala Ile Asp Asp Gly Thr Asn Gln Leu Arg Thr Gly Ala Asn Trp
195 200 205
Tyr Lys Thr Val Gly Pro Asp Tyr Leu Ala Arg Ala Phe Glu Tyr Ala
210 215 220
Arg Lys Tyr Ala Ala Glu Gly Val Leu Leu Tyr Tyr Asn Asp Tyr Asn
225 230 235 240
Thr Ala Tyr Gly Gly Lys Leu Tyr Gly Ile Val Asp Leu Leu Glu Ser
245 250 255
Leu Ile Ala Glu Gly Asn Ile Asp Gly Tyr Gly Phe Gln Met His His
260 265 270
Ser Leu Gly Glu Pro Ser Met Asp Met Ile Thr Arg Ala Val Glu Lys
275 280 285
Ile Ala Ser Leu Gly Leu Arg Leu Arg Val Ser Glu Leu Asp Ile Asn
290 295 300
Ala Gly Lys Ala Thr Glu Lys Asn Phe Glu Ala Gln Lys Asn Lys Tyr
305 310 315 320
Lys Gln Val Met Lys Leu Met Leu Arg Phe Lys Asp Gln Thr Glu Ala
325 330 335
Val Gln Val Trp Gly Val Thr Asp Ile Met Ser Trp Arg Arg Asp Gly
340 345 350
Tyr Pro Leu Leu Phe Asp Lys Asn Met Asn Pro Lys Pro Ala Phe Phe
355 360 365
Gly Val Ile Glu Ala Gly Met Glu Asp
370 375

<210> 33
<211> 1815
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 33
atggttcgca aaaaactatt ttatatcgtc gcgttaatgc tgatgttcgg cgcaagtttt 60
acttccgctc aggacgcgga attttccctg cgcggtttag ccgagcgcaa taacttttat 120
gttggagcag ccgtttatac cactcatctg aatgatcctg tccatgttga aacactggca 180

cgagaattca atatgctcac gcctgaacag caggccaaac attgtgagtt ggaggcacag 240
caaggtcaat ttgactttcg gagtttcgat cgtttagtcg ccttcgccga agaacacaac 300
atggcgatac acggtcatgc gctggtctgg catagctgca caccgcaatg ggtggctaac 360
ggcgagtaca cccgtgacga agccattggt ctgctgcgcg actcgattat gaccattgtt 420
ggccgttaca aaggccgtat tccgatttgg gacgtcgtca atgaaggcat tgctgacagc 480
ggcggaacac tgcgcgatac gccatggcgg cagttaattg gcgatgatta catcgaactt 540
gccttccagt tcgctcatga agccgacccg gatgcgctgc tgttttacaa cgactataat 600
acggaaggca tgaaccctaa atcggacgcc atgtacgaga tggtgagcga ttttgtggcg 660
cgtggaattc cgattcacgg ggttgggctg caatcccatt tcatattagg cagttttgac 720
ccagaccaga ttgctcggaa cgtcgcgcgg cttggcgaac tcggtttaca agttcaattc 780
accgaggtcg atattcgata ttccggcgag gcgacagata atatcctcca gcggcaggcg 840
ggcgattacc atcgcctgat ggacgtttgc ctcggtaacg acgcctgtac tgcgtttatc 900
acctggggcg tgaccgataa atatacctgg ttgcggggcg cgaacctggg cttctacaac 960
aacctatcgg ttgaaccgct gctttttgac gatgactatg aacccaagcc cgcttatttt 1020
gcggtgctgg actcactagc gcgaagagcg ggcgaaaccc ccgttttgag cgatgacgag 1080
cttgcggcga tgatcggcgg cacagtccaa acggtcgaaa ttcccccgcc gacgaaaagc 1140
aatctcagtc aggaagcgcc ggacgccgtt cctggtgtga tctattacgc cgcctacccc 1200
ataagcatca cagttgacgg cgaagccaac gattgggaac gcattccgcg cggtatgatt 1260
gacagcggcc ccaccgtacc tcaggataac gacacgacaa tgacatttgc cgccgctgcc 1320
gacaaaacca atctatactt ccttgcagag gttacggaca gccaggtgtc ctacggaacg 1380
cacgacccgg ctactgcctg gtatcaggag gactcggttg agttttacct gaacacgaca 1440
ggcgatctaa ctaacaccgc ctaccaaccc ggcgtcgccc aaatcggtat catggcagcc 1500
aacatcgaca acgataatcc cggtgcaccg atcatcgggg gcggcaacag cgacatttcg 1560
caggtaaaag cgattgtcgt caaaaccgat accgggtatc tggtcgaggc gtctgttcca 1620
ctcatgaccg atgtctggac gattgaaccg aaacaagggg ctgtactcgg cttccaagtg 1680
catctcaatg gctcacgcac accggatgcc gaccgagaca ccaagttgat ctggtcgcta 1740
ctggatacgc tagatcagtc ctatagcaat cccagcctgt ttggccgact catcttctgg 1800
aacataaatc tctaa 1815

<210> 34
<211> 604
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(23)

<400> 34
Met Val Arg Lys Lys Leu Phe Tyr Ile Val Ala Leu Met Leu Met Phe
1 5 10 15
Gly Ala Ser Phe Thr Ser Ala Gln Asp Ala Glu Phe Ser Leu Arg Gly
20 25 30
Leu Ala Glu Arg Asn Asn Phe Tyr Val Gly Ala Ala Val Tyr Thr Thr
35 40 45
His Leu Asn Asp Pro Val His Val Glu Thr Leu Ala Arg Glu Phe Asn
50 55 60
Met Leu Thr Pro Glu Gln Gln Ala Lys His Cys Glu Leu Glu Ala Gln
65 70 75 80
Gln Gly Gln Phe Asp Phe Arg Ser Phe Asp Arg Leu Val Ala Phe Ala
85 90 95
Glu Glu His Asn Met Ala Ile His Gly His Ala Leu Val Trp His Ser
100 105 110
Cys Thr Pro Gln Trp Val Ala Asn Gly Glu Tyr Thr Arg Asp Glu Ala
115 120 125
Ile Gly Leu Leu Arg Asp Ser Ile Met Thr Ile Val Gly Arg Tyr Lys
130 135 140
Gly Arg Ile Pro Ile Trp Asp Val Val Asn Glu Gly Ile Ala Asp Ser
145 150 155 160
Gly Gly Thr Leu Arg Asp Thr Pro Trp Arg Gln Leu Ile Gly Asp Asp
165 170 175
Tyr Ile Glu Leu Ala Phe Gln Phe Ala His Glu Ala Asp Pro Asp Ala
180 185 190
Leu Leu Phe Tyr Asn Asp Tyr Asn Thr Glu Gly Met Asn Pro Lys Ser
195 200 205
Asp Ala Met Tyr Glu Met Val Ser Asp Phe Val Ala Arg Gly Ile Pro
210 215 220

Ile His Gly Val Gly Leu Gln Ser His Phe Ile Leu Gly Ser Phe Asp
225 230 235 240
Pro Asp Gln Ile Ala Arg Asn Val Ala Arg Leu Gly Glu Leu Gly Leu
245 250 255
Gln Val Gln Phe Thr Glu Val Asp Ile Arg Tyr Ser Gly Glu Ala Thr
260 265 270
Asp Asn Ile Leu Gln Arg Gln Ala Gly Asp Tyr His Arg Leu Met Asp
275 280 285
Val Cys Leu Gly Asn Asp Ala Cys Thr Ala Phe Ile Thr Trp Gly Val
290 295 300
Thr Asp Lys Tyr Thr Trp Leu Arg Gly Ala Asn Leu Gly Phe Tyr Asn
305 310 315 320
Asn Leu Ser Val Glu Pro Leu Leu Phe Asp Asp Asp Tyr Glu Pro Lys
325 330 335
Pro Ala Tyr Phe Ala Val Leu Asp Ser Leu Ala Arg Arg Ala Gly Glu
340 345 350
Thr Pro Val Leu Ser Asp Asp Glu Leu Ala Ala Met Ile Gly Gly Thr
355 360 365
Val Gln Thr Val Glu Ile Pro Pro Pro Thr Lys Ser Asn Leu Ser Gln
370 375 380
Glu Ala Pro Asp Ala Val Pro Gly Val Ile Tyr Tyr Ala Ala Tyr Pro
385 390 395 400
Ile Ser Ile Thr Val Asp Gly Glu Ala Asn Asp Trp Glu Arg Ile Pro
405 410 415
Arg Gly Met Ile Asp Ser Gly Pro Thr Val Pro Gln Asp Asn Asp Thr
420 425 430
Thr Met Thr Phe Ala Ala Ala Ala Asp Lys Thr Asn Leu Tyr Phe Leu
435 440 445
Ala Glu Val Thr Asp Ser Gln Val Ser Tyr Gly Thr His Asp Pro Ala
450 455 460
Thr Ala Trp Tyr Gln Glu Asp Ser Val Glu Phe Tyr Leu Asn Thr Thr
465 470 475 480
Gly Asp Leu Thr Asn Thr Ala Tyr Gln Pro Gly Val Ala Gln Ile Gly
485 490 495
Ile Met Ala Ala Asn Ile Asp Asn Asp Asn Pro Gly Ala Pro Ile Ile
500 505 510
Gly Gly Gly Asn Ser Asp Ile Ser Gln Val Lys Ala Ile Val Val Lys
515 520 525
Thr Asp Thr Gly Tyr Leu Val Glu Ala Ser Val Pro Leu Met Thr Asp
530 535 540
Val Trp Thr Ile Glu Pro Lys Gln Gly Ala Val Leu Gly Phe Gln Val
545 550 555 560
His Leu Asn Gly Ser Arg Thr Pro Asp Ala Asp Arg Asp Thr Lys Leu
565 570 575
Ile Trp Ser Leu Leu Asp Thr Leu Asp Gln Ser Tyr Ser Asn Pro Ser
580 585 590
Leu Phe Gly Arg Leu Ile Phe Trp Asn Ile Asn Leu
595 600

<210> 35
<211> 2286
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 35
atgaccttga ttacgccaag ctcgaaatta accctcacta aagggaacaa aagctggagc 60
tcgcgcgcct gcaggtcgac actagtggat ctcacgcttt acttcgaatc tcaaaatcca 120
acccttgagt tctacgtgga tgacgtgaag atagtggata caacttccgc agagataaag 180
attgaaatgg aacctgaaaa agagatacct gctctgaaag aagtactgaa agattacttc 240
aaagtcggag ttgcactgcc gtccaaggtc ttcctcaacc cgaaggacat agaactcatc 300
acgaaacact tcaacagcat caccgcagaa aacgagatga aaccggatag tctgctcgcg 360
ggcatcgaaa acggtaagct gaagttcagg tttgaaacag cagacaaata cattcagttc 420
gtcgaggaaa acggcatggt tataagaggt cacacactgg tgtggcacaa ccagacaccc 480
gactggttct tcaaagacga aaacggaaac ctcctctcca aagaagcgat gacggaaaga 540
ctcaaagagt acatccacac cgttgtcgga cacttcaaag gaaaagtcta cgcatgggac 600
gtggtgaacg aagcggtcga tccgaaccag ccggatggac tgagaagatc aacctggtac 660

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cagatcatgg ggcctgacta catagaactc gccttcaagt tcgcaagaga ggcagatcca     720
gatgcaaaac tcttctacaa cgactacaac acattcgatc ccagaaagag agacatcatc     780
tacaacctcg tgaaggatct caaagagaag ggactcatcg atggcatagg aatgcagtgt     840
cacatcagtc ttgcaacaga catcaaacag atcgaagagg ccatcaaaaa gttcagcacc     900
atacccggta tagaaattca catcacagaa ctcgatatga gtgtctacag agattccagt     960
tccaactacc cagaggcacc gaggacggca ctcatcgaac aggctcacaa aatgatgcag    1020
ctctttgaga tcttcaagaa gcacagcaac gtgatcacga acgtcacatt ctggggtctc    1080
aaggacgatt actcctggag agcaacaaga agaaacgact ggccgctcat cttcgacaaa    1140
gatcaccagg cgaaactcgc ttactgggcg atagtggcac ctgaggtcct tccaccactt    1200
ccaaaagaaa gcaggatctc cgaaggcgaa gcagtggtag tggggatgat ggacgactcg    1260
tacctgatgt cgaagccgat agagatcctt gacgaagaag ggaacgtgaa ggcaacgatc    1320
agggcagtgt ggaaagacag cacgatctac atctacggag aggtacagga caagacaaag    1380
aaaccagcag aagacggagt ggccatattc atcaacccga acaacgaaag aacaccctat    1440
ctgcagcctg atgacaccta cgttgtgctg tggacgaact ggaagacgga ggtcaacaga    1500
gaagacgtac aggtgaagaa attcgttggg cctggcttta gaagatacag cttcgagatg    1560
tcgatcacga taccgggtgt ggagttcaag aaagacagct acataggatt tgacgttgcg    1620
gtgatagacg acgggaagtg gtacagctgg agcgacacga cgaacagcca gaagacgaac    1680
acgatgaact acggaacgct gaagctcgaa ggaataatgg tagcgacagc aaaatacgga    1740
acaccggtca tcgatggaga gatcgatgag atctggaaca cgacagagga gatagagacg    1800
aaagcggtgg ctatgggatc gcttgacaag aatgcgacag cgaaagtgag ggtgctgtgg    1860
gacgagaact acctgtacgt acttgcgatc gtgaaagatc ccgttctgaa caaagacaac    1920
agcaacccgt gggagcagga ttccgtggag atcttcgtgg atgagaacaa ccacaagaca    1980
ggatactacg aagacgacga cgcgcagttc agggtgaact acatgaacga gcagaccttt    2040
ggaacgggag gaagtccagc gaggttcaag acagcggtga agctgatcga aggaggatac    2100
atagttgagg cagcgatcaa gtggaagacg atcaagccaa caccgaacac agtgatagga    2160
ttcaacatcc aggtgaacga tgcgaacgag aaagggcaga gggtcggtat catctcctgg    2220
agcgatccca caaacaacag ctggcaagat ccttcaaagt tcggtaacct cagactcatc    2280
aagtga                                                               2286
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<210> 36
<211> 761
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 36
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Met Thr Leu Ile Thr Pro Ser Ser Lys Leu Thr Leu Thr Lys Gly Asn
1               5                   10                  15
Lys Ser Trp Ser Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Leu Thr
            20                  25                  30
Leu Tyr Phe Glu Ser Gln Asn Pro Thr Leu Glu Phe Tyr Val Asp Asp
        35                  40                  45
Val Lys Ile Val Asp Thr Thr Ser Ala Glu Ile Lys Ile Glu Met Glu
    50                  55                  60
Pro Glu Lys Glu Ile Pro Ala Leu Lys Glu Val Leu Lys Asp Tyr Phe
65                  70                  75                  80
Lys Val Gly Val Ala Leu Pro Ser Lys Val Phe Leu Asn Pro Lys Asp
                85                  90                  95
Ile Glu Leu Ile Thr Lys His Phe Asn Ser Ile Thr Ala Glu Asn Glu
            100                 105                 110
Met Lys Pro Asp Ser Leu Leu Ala Gly Ile Glu Asn Gly Lys Leu Lys
        115                 120                 125
Phe Arg Phe Glu Thr Ala Asp Lys Tyr Ile Gln Phe Val Glu Glu Asn
    130                 135                 140
Gly Met Val Ile Arg Gly His Thr Leu Val Trp His Asn Gln Thr Pro
145                 150                 155                 160
Asp Trp Phe Phe Lys Asp Glu Asn Gly Asn Leu Leu Ser Lys Glu Ala
                165                 170                 175
Met Thr Glu Arg Leu Lys Glu Tyr Ile His Thr Val Val Gly His Phe
            180                 185                 190
Lys Gly Lys Val Tyr Ala Trp Asp Val Val Asn Glu Ala Val Asp Pro
        195                 200                 205
Asn Gln Pro Asp Gly Leu Arg Arg Ser Thr Trp Tyr Gln Ile Met Gly
    210                 215                 220
Pro Asp Tyr Ile Glu Leu Ala Phe Lys Phe Ala Arg Glu Ala Asp Pro
225                 230                 235                 240
Asp Ala Lys Leu Phe Tyr Asn Asp Tyr Asn Thr Phe Asp Pro Arg Lys
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245 250 255
Arg Asp Ile Ile Tyr Asn Leu Val Lys Asp Leu Lys Glu Lys Gly Leu
260 265 270
Ile Asp Gly Ile Gly Met Gln Cys His Ile Ser Leu Ala Thr Asp Ile
275 280 285
Lys Gln Ile Glu Glu Ala Ile Lys Lys Phe Ser Thr Ile Pro Gly Ile
290 295 300
Glu Ile His Ile Thr Glu Leu Asp Met Ser Val Tyr Arg Asp Ser Ser
305 310 315 320
Ser Asn Tyr Pro Glu Ala Pro Arg Thr Ala Leu Ile Glu Gln Ala His
325 330 335
Lys Met Met Gln Leu Phe Glu Ile Phe Lys Lys His Ser Asn Val Ile
340 345 350
Thr Asn Val Thr Phe Trp Gly Leu Lys Asp Asp Tyr Ser Trp Arg Ala
355 360 365
Thr Arg Arg Asn Asp Trp Pro Leu Ile Phe Asp Lys Asp His Gln Ala
370 375 380
Lys Leu Ala Tyr Trp Ala Ile Val Ala Pro Glu Val Leu Pro Pro Leu
385 390 395 400
Pro Lys Glu Ser Arg Ile Ser Glu Gly Glu Ala Val Val Val Gly Met
405 410 415
Met Asp Asp Ser Tyr Leu Met Ser Lys Pro Ile Glu Ile Leu Asp Glu
420 425 430
Glu Gly Asn Val Lys Ala Thr Ile Arg Ala Val Trp Lys Asp Ser Thr
435 440 445
Ile Tyr Ile Tyr Gly Glu Val Gln Asp Lys Thr Lys Lys Pro Ala Glu
450 455 460
Asp Gly Val Ala Ile Phe Ile Asn Pro Asn Asn Glu Arg Thr Pro Tyr
465 470 475 480
Leu Gln Pro Asp Asp Thr Tyr Val Val Leu Trp Thr Asn Trp Lys Thr
485 490 495
Glu Val Asn Arg Glu Asp Val Gln Val Lys Lys Phe Val Gly Pro Gly
500 505 510
Phe Arg Arg Tyr Ser Phe Glu Met Ser Ile Thr Ile Pro Gly Val Glu
515 520 525
Phe Lys Lys Asp Ser Tyr Ile Gly Phe Asp Val Ala Val Ile Asp Asp
530 535 540
Gly Lys Trp Tyr Ser Trp Ser Asp Thr Thr Asn Ser Gln Lys Thr Asn
545 550 555 560
Thr Met Asn Tyr Gly Thr Leu Lys Leu Glu Gly Ile Met Val Ala Thr
565 570 575
Ala Lys Tyr Gly Thr Pro Val Ile Asp Gly Glu Ile Asp Glu Ile Trp
580 585 590
Asn Thr Thr Glu Glu Ile Glu Thr Lys Ala Val Ala Met Gly Ser Leu
595 600 605
Asp Lys Asn Ala Thr Ala Lys Val Arg Val Leu Trp Asp Glu Asn Tyr
610 615 620
Leu Tyr Val Leu Ala Ile Val Lys Asp Pro Val Leu Asn Lys Asp Asn
625 630 635 640
Ser Asn Pro Trp Glu Gln Asp Ser Val Glu Ile Phe Val Asp Glu Asn
645 650 655
Asn His Lys Thr Gly Tyr Tyr Glu Asp Asp Asp Ala Gln Phe Arg Val
660 665 670
Asn Tyr Met Asn Glu Gln Thr Phe Gly Thr Gly Gly Ser Pro Ala Arg
675 680 685
Phe Lys Thr Ala Val Lys Leu Ile Glu Gly Gly Tyr Ile Val Glu Ala
690 695 700
Ala Ile Lys Trp Lys Thr Ile Lys Pro Thr Pro Asn Thr Val Ile Gly
705 710 715 720
Phe Asn Ile Gln Val Asn Asp Ala Asn Glu Lys Gly Gln Arg Val Gly
725 730 735
Ile Ile Ser Trp Ser Asp Pro Thr Asn Asn Ser Trp Gln Asp Pro Ser
740 745 750
Lys Phe Gly Asn Leu Arg Leu Ile Lys
755 760

<210> 37
<211> 2769
<212> DNA

<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 37
atgcacaaga agaacggcac ctattacctg agctactcta caaatccggc caacggcatg 60
cggattgact acatgaccag cacgagcccg accagtggct ttgtccatcg aggcacggtc 120
atggcgcagc cctggcagaa cagcaacaac aacaaccacg caaccagcac cgagtacaac 180
gggcagggct acatcttcta tcacaaccgt gcgttgtcga acgagcgtgc gggtggcaac 240
gtgctgcagc gctcggtgaa cgtggatcgc ctctacttca atgccgatgg cagcatccgt 300
caggtcactt ccagtgcaac cggcgtgccg gccctgaaaa ccctggatgc cttcctggtc 360
aagcctgccg agctgtatca caaggaaagc gggatcaaga ccgagcctgc cagtgaagga 420
acccaggcac tggttatgac ggctggtagc tgggtgcgcc tggccaatgt cgatttcggc 480
aatggcggcg ccactggttt ttccgcgcgt attgcggcaa ccggcagcgg cagcatccag 540
gtgatcctgg gcaatctgaa caacgccccg gtcggcacgc tggcagtgag cagcaccggc 600
aacctccaga cctggcaaga ccgcagcacc gccatcagca aggtgaccgg cgtgcatgac 660
gtgtatttgc gtgccaccgg caatgtgcat gtgcagcgtc actggttcgt ggcgtcggcg 720
ccggccgctg ccgcctcatc cagcagtcag gcaagcgtct ctgccagcag tcaggcaagt 780
gtttcttcca gtagccaggc aagcgttgcc tccagcagca gttccagccg cgcttcttcc 840
gccagcagtt cggtggcggc tggccaggtg gaggtcggtt atcgccttag cagcgaatgg 900
gccgccggct tctgcggcgt ggtcaccatc cgtaatccgg gtagttctcc ggtcaccagc 960
tggagtggca gtttcaacct gcctggcggc aagatcaccc agctgtggaa tgccaactgg 1020
acccagaacg gcagcaccgt gacggtatct tcccaggcct ggagcggtgc cattgctgca 1080
ggcgccacca tcaccacgcc gggcttctgc gccgagcgca cgagcagcaa tgcgtcctcc 1140
agtgtcgcca gcagcagtgt ctcctcatcg agcagcagtg ctgcggctgc cagctccagc 1200
gcggcttcca gcgtcccgtc cactggcagt ggcggggtgg gcagcagcgc atcctcggct 1260
agcagtgccg ctgcacccaa gggcgtgctt gaagtcggcc tgagcggcct ttccagccag 1320
gccatgttcg ccccgttgcg ggtcaggacg gacgctgcgg ccgccaacaa ggcctatgtt 1380
gaatggccca acaacggcgc caatcagtcg ctggcaacgc ctgccaacga tgccgcaggg 1440
caggtggagg tagccttcgt gctggcccag gcatccgcag tgcagtttga tatcgaagcg 1500
aatttcgcca acgcggaaga cgactccttc tacttccagc tcaacggtgg tgcctggcag 1560
accttcaaca acgccaccac ggtcggctgg cagaccctgc cggtcgcctc tctgggcaat 1620
ctggctgccg ggcgccatgt gctgaccctg ctgcgccgcg aggatggcgc gaagctgggc 1680
aaggtcgtcc tgagtgcggc acagagcagc atcagtcgtg ccacgccggt ggcctacgcg 1740
tcgccgaatg atgttgccaa cctgttcaag ctggccagct tcccgatcgg ggtggcggtc 1800
agtgccggca acgaaggtga cagcctgctg cgtagcggta cccgcgcagc agccgagcgt 1860
gcgctgaccg agaagcactt caacagtctg gtggccggca acatcatgaa gatgagctac 1920
ctgcatccgg ccgagaacac ctacaccttc acccaggcgg atgcgctggc cgactacgcc 1980
aagtccaagg gcatggtgtt gcatggccat gcgctggtct ggcatgcgga ctatcaggta 2040
cccaactgga tgaagaatta caccggagac tggtcgaaga tgctcgaagc ccacgtcacc 2100
accgtcgcca agcactatgc cggcaaggtg gtgagctggg atgtggtgaa tgaagccctg 2160
gccgatggca atgccaccgc caccaagggt ttccgtgcca ccgattcgat cttctatcag 2220
aagatgggct ccagtttcat cgagaaggcc tttattgctg cacgtgctgc cgacccgaat 2280
gccgacctgt attacaacga ctacggcatg gagggcggaa acagcaagtt caattactgc 2340
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atgcacatca acatcgactg gccttcgtcg gcccagatcc gcgctgtatt cagtgaagtg 2460
gtcaagcgtg gtctgaaggt gcgtatctcc gagctggata ttccggtgaa taccactgcc 2520
ggtcgttttg ccagcctgaa tgccacggcc aacgagctgc agaagaagaa gtatcgtgag 2580
gttgtggctg cctacctgga tgtggtgccg cccgagctgc gcggtggcat caccgtgtgg 2640
ggcctgagcg acaacggcag ctggctggtg acccccacca agccggactg gccgctgctg 2700
ttcgatgccg acctcaaggc caaggacgcc ctgagcggct ttgccgacgc cctgcgcggc 2760
gtacgctga 2769

<210> 38
<211> 922
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 38
Met His Lys Lys Asn Gly Thr Tyr Tyr Leu Ser Tyr Ser Thr Asn Pro
1 5 10 15
Ala Asn Gly Met Arg Ile Asp Tyr Met Thr Ser Thr Ser Pro Thr Ser
20 25 30
Gly Phe Val His Arg Gly Thr Val Met Ala Gln Pro Trp Gln Asn Ser
35 40 45

Asn Asn Asn Asn His Ala Thr Ser Thr Glu Tyr Asn Gly Gln Gly Tyr
50 55 60
Ile Phe Tyr His Asn Arg Ala Leu Ser Asn Glu Arg Ala Gly Gly Asn
65 70 75 80
Val Leu Gln Arg Ser Val Asn Val Asp Arg Leu Tyr Phe Asn Ala Asp
85 90 95
Gly Ser Ile Arg Gln Val Thr Ser Ser Ala Thr Gly Val Pro Ala Leu
100 105 110
Lys Thr Leu Asp Ala Phe Leu Val Lys Pro Ala Glu Leu Tyr His Lys
115 120 125
Glu Ser Gly Ile Lys Thr Glu Pro Ala Ser Glu Gly Thr Gln Ala Leu
130 135 140
Val Met Thr Ala Gly Ser Trp Val Arg Leu Ala Asn Val Asp Phe Gly
145 150 155 160
Asn Gly Gly Ala Thr Gly Phe Ser Ala Arg Ile Ala Ala Thr Gly Ser
165 170 175
Gly Ser Ile Gln Val Ile Leu Gly Asn Leu Asn Asn Ala Pro Val Gly
180 185 190
Thr Leu Ala Val Ser Ser Thr Gly Asn Leu Gln Thr Trp Gln Asp Arg
195 200 205
Ser Thr Ala Ile Ser Lys Val Thr Gly Val His Asp Val Tyr Leu Arg
210 215 220
Ala Thr Gly Asn Val His Val Gln Arg His Trp Phe Val Ala Ser Ala
225 230 235 240
Pro Ala Ala Ala Ala Ser Ser Ser Ser Gln Ala Ser Val Ser Ala Ser
245 250 255
Ser Gln Ala Ser Val Ser Ser Ser Ser Gln Ala Ser Val Ala Ser Ser
260 265 270
Ser Ser Ser Ser Arg Ala Ser Ser Ala Ser Ser Ser Val Ala Ala Gly
275 280 285
Gln Val Glu Val Gly Tyr Arg Leu Ser Ser Glu Trp Ala Ala Gly Phe
290 295 300
Cys Gly Val Val Thr Ile Arg Asn Pro Gly Ser Ser Pro Val Thr Ser
305 310 315 320
Trp Ser Gly Ser Phe Asn Leu Pro Gly Gly Lys Ile Thr Gln Leu Trp
325 330 335
Asn Ala Asn Trp Thr Gln Asn Gly Ser Thr Val Thr Val Ser Ser Gln
340 345 350
Ala Trp Ser Gly Ala Ile Ala Ala Gly Ala Thr Ile Thr Thr Pro Gly
355 360 365
Phe Cys Ala Glu Arg Thr Ser Ser Asn Ala Ser Ser Ser Val Ala Ser
370 375 380
Ser Ser Val Ser Ser Ser Ser Ser Ser Ala Ala Ala Ala Ser Ser Ser
385 390 395 400
Ala Ala Ser Ser Val Pro Ser Thr Gly Ser Gly Gly Val Gly Ser Ser
405 410 415
Ala Ser Ser Ala Ser Ser Ala Ala Ala Pro Lys Gly Val Leu Glu Val
420 425 430
Gly Leu Ser Gly Leu Ser Ser Gln Ala Met Phe Ala Pro Leu Arg Val
435 440 445
Arg Thr Asp Ala Ala Ala Ala Asn Lys Ala Tyr Val Glu Trp Pro Asn
450 455 460
Asn Gly Ala Asn Gln Ser Leu Ala Thr Pro Ala Asn Asp Ala Ala Gly
465 470 475 480
Gln Val Glu Val Ala Phe Val Leu Ala Gln Ala Ser Ala Val Gln Phe
485 490 495
Asp Ile Glu Ala Asn Phe Ala Asn Ala Glu Asp Asp Ser Phe Tyr Phe
500 505 510
Gln Leu Asn Gly Gly Ala Trp Gln Thr Phe Asn Asn Ala Thr Thr Val
515 520 525
Gly Trp Gln Thr Leu Pro Val Ala Ser Leu Gly Asn Leu Ala Ala Gly
530 535 540
Arg His Val Leu Thr Leu Leu Arg Arg Glu Asp Gly Ala Lys Leu Gly
545 550 555 560
Lys Val Val Leu Ser Ala Ala Gln Ser Ser Ile Ser Arg Ala Thr Pro
565 570 575
Val Ala Tyr Ala Ser Pro Asn Asp Val Ala Asn Leu Phe Lys Leu Ala
580 585 590
Ser Phe Pro Ile Gly Val Ala Val Ser Ala Gly Asn Glu Gly Asp Ser

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        595                     600                     605
Leu Leu Arg Ser Gly Thr Arg Ala Ala Ala Glu Arg Ala Leu Thr Glu
    610                     615                     620
Lys His Phe Asn Ser Leu Val Ala Gly Asn Ile Met Lys Met Ser Tyr
625                     630                     635                     640
Leu His Pro Ala Glu Asn Thr Tyr Thr Phe Thr Gln Ala Asp Ala Leu
                645                     650                     655
Ala Asp Tyr Ala Lys Ser Lys Gly Met Val Leu His Gly His Ala Leu
            660                     665                     670
Val Trp His Ala Asp Tyr Gln Val Pro Asn Trp Met Lys Asn Tyr Thr
        675                     680                     685
Gly Asp Trp Ser Lys Met Leu Glu Ala His Val Thr Thr Val Ala Lys
    690                     695                     700
His Tyr Ala Gly Lys Val Val Ser Trp Asp Val Val Asn Glu Ala Leu
705                     710                     715                     720
Ala Asp Gly Asn Ala Thr Ala Thr Lys Gly Phe Arg Ala Thr Asp Ser
                725                     730                     735
Ile Phe Tyr Gln Lys Met Gly Ser Ser Phe Ile Glu Lys Ala Phe Ile
            740                     745                     750
Ala Ala Arg Ala Ala Asp Pro Asn Ala Asp Leu Tyr Tyr Asn Asp Tyr
        755                     760                     765
Gly Met Glu Gly Gly Asn Ser Lys Phe Asn Tyr Cys Met Ala Met Val
    770                     775                     780
Asp Asp Phe Gln Lys Arg Gly Ile Pro Ile Asp Gly Ile Gly Phe Gln
785                     790                     795                     800
Met His Ile Asn Ile Asp Trp Pro Ser Ser Ala Gln Ile Arg Ala Val
                805                     810                     815
Phe Ser Glu Val Val Lys Arg Gly Leu Lys Val Arg Ile Ser Glu Leu
            820                     825                     830
Asp Ile Pro Val Asn Thr Thr Ala Gly Arg Phe Ala Ser Leu Asn Ala
        835                     840                     845
Thr Ala Asn Glu Leu Gln Lys Lys Lys Tyr Arg Glu Val Val Ala Ala
    850                     855                     860
Tyr Leu Asp Val Val Pro Pro Glu Leu Arg Gly Gly Ile Thr Val Trp
865                     870                     875                     880
Gly Leu Ser Asp Asn Gly Ser Trp Leu Val Thr Pro Thr Lys Pro Asp
                885                     890                     895
Trp Pro Leu Leu Phe Asp Ala Asp Leu Lys Ala Lys Asp Ala Leu Ser
            900                     905                     910
Gly Phe Ala Asp Ala Leu Arg Gly Val Arg
        915                     920
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<210> 39
<211> 1143
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 39

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atgaaaaaaa cgattgcaca tttcacctta tggatagtgt tttttctctt cacttcctgt      60
gctgttacgg cgcagaagaa tgcaaagaat acaagagtaa aacccactac cctaaaagag     120
gcttaccaag gtaaattcta tatcggtact gcgatgaact tgagacagat tcacggagat     180
gatccccaat ctgaaaatat tatcaaaaaa cagttcaatt ccatagttgc cgaaaactgc     240
atgaagagta tgtatcttca gccggaggaa ggaaaatttt tcttcgatga tgcggacaag     300
tttgtggatt ttggtcttca gaacaatatg ttcatcattg ggcattgtct gatttggcat     360
tcgcaggcgc caaaatggtt tttcaccgat gagaatggaa acacggtttc tccagaagtt     420
cttaaacaaa ggatgaaagc ccatattacc gccgtcgttt cccgttacaa agggaaaatc     480
aaaggttggg atgtggtgaa cgaagccatt atggaagatg gttcttaccg taaaagcaaa     540
ttttacgaga ttttgggaga agaatttatt ccgttggcat ttcagtatgc gcatgaagca     600
gatcctgatg cagaacttta ttacaacgat tataacgaat ggtatcccgg aaaaagagct     660
acggtgacca agataatccg cgatttcaaa actagaggaa tccgcatcga tgccatcgga     720
atgcaggctc atttcgggat ggattcgccc actgtagaag agtatgaaca aactattcag     780
ggctatataa aagaaggcgt gaaagtcaat attacggaac tcgatttgag tccacttcct     840
tctccttggg gaacttccgc caatgttgcc gatacgcagc aatatcagga aaaaatgaat     900
ccatacacca aaggacttcc tgcagatgtt gaaaaagcat gggaaaaccg ttatgtggat     960
tttttcaaac tgttcctaaa atatcatcag catattgagc gtgttacgtt ttggggcgtt    1020
agcgatatcg attcctggaa gaacgatttt ccggtaagag gacgtaccga ttatccacta    1080
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ccgtttaacc gtcaatatca agcaaaacct ttggttcaga aattaataga tttaacaaaa 1140
tag 1143

<210> 40
<211> 380
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(24)

<400> 40
Met Lys Lys Thr Ile Ala His Phe Thr Leu Trp Ile Val Phe Phe Leu
1 5 10 15
Phe Thr Ser Cys Ala Val Thr Ala Gln Lys Asn Ala Lys Asn Thr Arg
20 25 30
Val Lys Pro Thr Thr Leu Lys Glu Ala Tyr Gln Gly Lys Phe Tyr Ile
35 40 45
Gly Thr Ala Met Asn Leu Arg Gln Ile His Gly Asp Asp Pro Gln Ser
50 55 60
Glu Asn Ile Ile Lys Lys Gln Phe Asn Ser Ile Val Ala Glu Asn Cys
65 70 75 80
Met Lys Ser Met Tyr Leu Gln Pro Glu Glu Gly Lys Phe Phe Phe Asp
85 90 95
Asp Ala Asp Lys Phe Val Asp Phe Gly Leu Gln Asn Asn Met Phe Ile
100 105 110
Ile Gly His Cys Leu Ile Trp His Ser Gln Ala Pro Lys Trp Phe Phe
115 120 125
Thr Asp Glu Asn Gly Asn Thr Val Ser Pro Glu Val Leu Lys Gln Arg
130 135 140
Met Lys Ala His Ile Thr Ala Val Val Ser Arg Tyr Lys Gly Lys Ile
145 150 155 160
Lys Gly Trp Asp Val Val Asn Glu Ala Ile Met Glu Asp Gly Ser Tyr
165 170 175
Arg Lys Ser Lys Phe Tyr Glu Ile Leu Gly Glu Glu Phe Ile Pro Leu
180 185 190
Ala Phe Gln Tyr Ala His Glu Ala Asp Pro Asp Ala Glu Leu Tyr Tyr
195 200 205
Asn Asp Tyr Asn Glu Trp Tyr Pro Gly Lys Arg Ala Thr Val Thr Lys
210 215 220
Ile Ile Arg Asp Phe Lys Thr Arg Gly Ile Arg Ile Asp Ala Ile Gly
225 230 235 240
Met Gln Ala His Phe Gly Met Asp Ser Pro Thr Val Glu Glu Tyr Glu
245 250 255
Gln Thr Ile Gln Gly Tyr Ile Lys Glu Gly Val Lys Val Asn Ile Thr
260 265 270
Glu Leu Asp Leu Ser Pro Leu Pro Ser Pro Trp Gly Thr Ser Ala Asn
275 280 285
Val Ala Asp Thr Gln Gln Tyr Gln Glu Lys Met Asn Pro Tyr Thr Lys
290 295 300
Gly Leu Pro Ala Asp Val Glu Lys Ala Trp Glu Asn Arg Tyr Val Asp
305 310 315 320
Phe Phe Lys Leu Phe Leu Lys Tyr His Gln His Ile Glu Arg Val Thr
325 330 335
Phe Trp Gly Val Ser Asp Ile Asp Ser Trp Lys Asn Asp Phe Pro Val
340 345 350
Arg Gly Arg Thr Asp Tyr Pro Leu Pro Phe Asn Arg Gln Tyr Gln Ala
355 360 365
Lys Pro Leu Val Gln Lys Leu Ile Asp Leu Thr Lys
370 375 380

<210> 41
<211> 1893
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 41
atgatccatc aacaaaagcc caaccaagac atcggtaggc tattcaagcg cagctgcagc 60
tttgtcggta ttagcgcggc actggctgtt ttctcacaca ccgcaagtgc agcctgtact 120
tacaacattg ataaccaatg gggcagcggt tttgtcgcta gtattactgt aaagaatgac 180
actggtgcaa ccgtcaataa ctggagtgtg aattggcaat atgccaacaa tcgcatcacc 240
aatggttgga gtgcaaattt ctctggcagc aatccttaca ccgccaccaa tatgagctgg 300
aacggtagca ttgccgctgg ccagtcggtg acttttggtt tccagggcaa cactaacagc 360
aataccgttg agcgcccggt ggttaacggt tcactgtgcg gtactgcaac aacctcttca 420
gttcgctcca gcgtggctgc gacgtcttcc agtcgctcca gtgttgcgcc cagctcgatt 480
cctgcttcca gcactccgcg ttcaagcaca cctgccacct cttcttctgc ttccagcttc 540
tcagtaccgg ccaataattt tgcgcagaat ggcggcgtgg aatctggttt gaccaactgg 600
ggtacgactg cgggcaccgt gactcgctct actgccgata aacacagcgg tacagccagt 660
gccttaatta ccggccgcac tgctgcctgg aatggtttga cgtttaatgt gggcgcattg 720
accaacggca accagtacca agtcaacgtg tgggtgaaat tggctccagg tacgcccgac 780
agcgtactga ccttaaccgg taagcgtgta gacgatagcg atactactac ctacaacgaa 840
tacacacgcg tagcgactgt gactgcctct gccaatgagt ggcgtttgct ggaaggttac 900
tacacccaat ctggcagcac tgcattccag catttcatta tcgaagcaac ggatactact 960
gccagttatt acgcggatga tttcgccatc ggcggtcaag tcgtacaagt tccaagcagc 1020
agctcacgca gctcaagcag tgctccggcg gctagaaaat tcatcggcaa catcaccacc 1080
tcgggtgcag tgagatccga ctttactcgt tactggaacc aaattacacc agagaacgaa 1140
ggtaagtggg gttccgttga aggtactcgc aaccagtaca actgggcacc gctggatcgt 1200
atttatgctt acgctcgcca aaataatatt ccggtaaaag ctcacacgtt tgtgtggggt 1260
gcgcaatcac ccgcgtggct caataactta agcggaccgg aagtcgctgt tgaaattgaa 1320
caatggattc gcgattactg tactcgttac cctgacacgg cgatgattga cgtagtgaac 1380
gaagcggttc ctggccatca accggcaggt tatgcacaac gagcatttgg caataactgg 1440
atccaacgcg tgttccaatt ggctcgccaa tattgcccta actcgatcct gatcctgaat 1500
gattacaaca atatccgttg gcagcacaat gagtttattg cccttgcaaa agctcaaggc 1560
aattatattg atgcagtcgg cctgcaggcg catgaactga agggtatgac agcggcgcaa 1620
gtcaaaaccg caatcgacaa tatttggaac caagtgggca agcccatcta catttctgaa 1680
tacgacattg gcgataacaa tgaccaggtt caattgcaga atttccaggc gcatttccct 1740
gtattctggg accatccgca tgttaaaggc atcaccattt ggggttatgt caatggcaga 1800
acttggattg aaggctcggg cctgatttct gacaacggaa caccgcgccc cgcaatgact 1860
tggttgctga ataactatat caataagcag taa 1893

<210> 42
<211> 630
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(37)

<400> 42
Met Ile His Gln Gln Lys Pro Asn Gln Asp Ile Gly Arg Leu Phe Lys
1 5 10 15
Arg Ser Cys Ser Phe Val Gly Ile Ser Ala Ala Leu Ala Val Phe Ser
20 25 30
His Thr Ala Ser Ala Ala Cys Thr Tyr Asn Ile Asp Asn Gln Trp Gly
35 40 45
Ser Gly Phe Val Ala Ser Ile Thr Val Lys Asn Asp Thr Gly Ala Thr
50 55 60
Val Asn Asn Trp Ser Val Asn Trp Gln Tyr Ala Asn Asn Arg Ile Thr
65 70 75 80
Asn Gly Trp Ser Ala Asn Phe Ser Gly Ser Asn Pro Tyr Thr Ala Thr
85 90 95
Asn Met Ser Trp Asn Gly Ser Ile Ala Ala Gly Gln Ser Val Thr Phe
100 105 110
Gly Phe Gln Gly Asn Thr Asn Ser Asn Thr Val Glu Arg Pro Val Val
115 120 125
Asn Gly Ser Leu Cys Gly Thr Ala Thr Thr Ser Ser Val Arg Ser Ser
130 135 140
Val Ala Ala Thr Ser Ser Ser Arg Ser Ser Val Ala Pro Ser Ser Ile
145 150 155 160

Pro Ala Ser Ser Thr Pro Arg Ser Ser Thr Pro Ala Thr Ser Ser Ser
165 170 175
Ala Ser Ser Phe Ser Val Pro Ala Asn Asn Phe Ala Gln Asn Gly Gly
180 185 190
Val Glu Ser Gly Leu Thr Asn Trp Gly Thr Thr Ala Gly Thr Val Thr
195 200 205
Arg Ser Thr Ala Asp Lys His Ser Gly Thr Ala Ser Ala Leu Ile Thr
210 215 220
Gly Arg Thr Ala Ala Trp Asn Gly Leu Thr Phe Asn Val Gly Ala Leu
225 230 235 240
Thr Asn Gly Asn Gln Tyr Gln Val Asn Val Trp Val Lys Leu Ala Pro
245 250 255
Gly Thr Pro Asp Ser Val Leu Thr Leu Thr Gly Lys Arg Val Asp Asp
260 265 270
Ser Asp Thr Thr Thr Tyr Asn Glu Tyr Thr Arg Val Ala Thr Val Thr
275 280 285
Ala Ser Ala Asn Glu Trp Arg Leu Leu Glu Gly Tyr Tyr Thr Gln Ser
290 295 300
Gly Ser Thr Ala Phe Gln His Phe Ile Ile Glu Ala Thr Asp Thr Thr
305 310 315 320
Ala Ser Tyr Tyr Ala Asp Asp Phe Ala Ile Gly Gly Gln Val Val Gln
325 330 335
Val Pro Ser Ser Ser Ser Arg Ser Ser Ser Ser Ala Pro Ala Ala Arg
340 345 350
Lys Phe Ile Gly Asn Ile Thr Thr Ser Gly Ala Val Arg Ser Asp Phe
355 360 365
Thr Arg Tyr Trp Asn Gln Ile Thr Pro Glu Asn Glu Gly Lys Trp Gly
370 375 380
Ser Val Glu Gly Thr Arg Asn Gln Tyr Asn Trp Ala Pro Leu Asp Arg
385 390 395 400
Ile Tyr Ala Tyr Ala Arg Gln Asn Asn Ile Pro Val Lys Ala His Thr
405 410 415
Phe Val Trp Gly Ala Gln Ser Pro Ala Trp Leu Asn Asn Leu Ser Gly
420 425 430
Pro Glu Val Ala Val Glu Ile Glu Gln Trp Ile Arg Asp Tyr Cys Thr
435 440 445
Arg Tyr Pro Asp Thr Ala Met Ile Asp Val Val Asn Glu Ala Val Pro
450 455 460
Gly His Gln Pro Ala Gly Tyr Ala Gln Arg Ala Phe Gly Asn Asn Trp
465 470 475 480
Ile Gln Arg Val Phe Gln Leu Ala Arg Gln Tyr Cys Pro Asn Ser Ile
485 490 495
Leu Ile Leu Asn Asp Tyr Asn Asn Ile Arg Trp Gln His Asn Glu Phe
500 505 510
Ile Ala Leu Ala Lys Ala Gln Gly Asn Tyr Ile Asp Ala Val Gly Leu
515 520 525
Gln Ala His Glu Leu Lys Gly Met Thr Ala Ala Gln Val Lys Thr Ala
530 535 540
Ile Asp Asn Ile Trp Asn Gln Val Gly Lys Pro Ile Tyr Ile Ser Glu
545 550 555 560
Tyr Asp Ile Gly Asp Asn Asn Asp Gln Val Gln Leu Gln Asn Phe Gln
565 570 575
Ala His Phe Pro Val Phe Trp Asp His Pro His Val Lys Gly Ile Thr
580 585 590
Ile Trp Gly Tyr Val Asn Gly Arg Thr Trp Ile Glu Gly Ser Gly Leu
595 600 605
Ile Ser Asp Asn Gly Thr Pro Arg Pro Ala Met Thr Trp Leu Leu Asn
610 615 620
Asn Tyr Ile Asn Lys Gln
625 630

<210> 43
<211> 1011
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 43
atgcaaacaa atattaaagg aaataacatt ccatcattac acgaagttta tcaagatcac 60
tttttgatag gtgcagcagt taatccaaaa acattagact cacagcagga tttattgaga 120
aaacacttta acagtattac agctgaaaat gaaatgaaat ttgaagaatt gcaaccagaa 180
cctggccatt tcacgtttgg tgtagcagat gaaatcgttt catttgcaaa agaaaatgga 240
atgaaagtta gaggacatac attagtttgg cataatcaaa cgcctgattg gatgtttttg 300
aatgaagatg gatctgtcac agatcgagaa acgcttctag aaagaatgaa attacacatt 360
acaacagtta tgcagcatta caaaggtcaa gcttattgct gggatgttgt aaatgaggtg 420
attgctgacg agggtacaga gttattccgt aaatctaaat ggactgaaat tattggtgat 480
gattttgtag aaaaggcatt tgaatatgca catgaggctg atccagaagc tttactattc 540
tacaatgact ataatgaatc ccatcccaat aagcgtgaga aaattttcac acttgtaaaa 600
ggattagttg ataaggggat acctattcat ggaatcggtt tacaagcaca ttggaattta 660
acaggacctt cttatgaaga tattagagca gcactcgaga aatatgctac attgggattg 720
gaaatacacc ttaccgaatt ggatgtttct gtttttaatt atgaagatcg aagaacagat 780
ttaacagaac caactaaaga tatgcaagcg cttcaagcgg agcgttatac agaattattc 840
aagatattga gagaatatag tcatgtaatc agttcgatta ctttttgggg agctgcagat 900
gattatactt ggttagatga ttttcctgtc aaaggaagaa aaaactggcc atttgttttt 960
gatgaaaacc aagagccaaa agagtcattt tggaatatta ttgactttta a 1011

<210> 44
<211> 336
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 44
Met Gln Thr Asn Ile Lys Gly Asn Asn Ile Pro Ser Leu His Glu Val
1 5 10 15
Tyr Gln Asp His Phe Leu Ile Gly Ala Ala Val Asn Pro Lys Thr Leu
20 25 30
Asp Ser Gln Gln Asp Leu Leu Arg Lys His Phe Asn Ser Ile Thr Ala
35 40 45
Glu Asn Glu Met Lys Phe Glu Glu Leu Gln Pro Glu Pro Gly His Phe
50 55 60
Thr Phe Gly Val Ala Asp Glu Ile Val Ser Phe Ala Lys Glu Asn Gly
65 70 75 80
Met Lys Val Arg Gly His Thr Leu Val Trp His Asn Gln Thr Pro Asp
85 90 95
Trp Met Phe Leu Asn Glu Asp Gly Ser Val Thr Asp Arg Glu Thr Leu
100 105 110
Leu Glu Arg Met Lys Leu His Ile Thr Thr Val Met Gln His Tyr Lys
115 120 125
Gly Gln Ala Tyr Cys Trp Asp Val Val Asn Glu Val Ile Ala Asp Glu
130 135 140
Gly Thr Glu Leu Phe Arg Lys Ser Lys Trp Thr Glu Ile Ile Gly Asp
145 150 155 160
Asp Phe Val Glu Lys Ala Phe Glu Tyr Ala His Glu Ala Asp Pro Glu
165 170 175
Ala Leu Leu Phe Tyr Asn Asp Tyr Asn Glu Ser His Pro Asn Lys Arg
180 185 190
Glu Lys Ile Phe Thr Leu Val Lys Gly Leu Val Asp Lys Gly Ile Pro
195 200 205
Ile His Gly Ile Gly Leu Gln Ala His Trp Asn Leu Thr Gly Pro Ser
210 215 220
Tyr Glu Asp Ile Arg Ala Ala Leu Glu Lys Tyr Ala Thr Leu Gly Leu
225 230 235 240
Glu Ile His Leu Thr Glu Leu Asp Val Ser Val Phe Asn Tyr Glu Asp
245 250 255
Arg Arg Thr Asp Leu Thr Glu Pro Thr Lys Asp Met Gln Ala Leu Gln
260 265 270
Ala Glu Arg Tyr Thr Glu Leu Phe Lys Ile Leu Arg Glu Tyr Ser His
275 280 285
Val Ile Ser Ser Ile Thr Phe Trp Gly Ala Ala Asp Asp Tyr Thr Trp
290 295 300
Leu Asp Asp Phe Pro Val Lys Gly Arg Lys Asn Trp Pro Phe Val Phe
305 310 315 320
Asp Glu Asn Gln Glu Pro Lys Glu Ser Phe Trp Asn Ile Ile Asp Phe

325 330 335

<210> 45
<211> 1137
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 45
atgaagatat cacgccgaca attacttgct atgggtggtg ccgctgcaac cctggcctct 60
gccaaattat tcgctgccga aaaagctgct gccgccaccg gattgaaaga tgcctataaa 120
aacgatttcc tgatcggtgc tgcattaaat acccaaattg ttgatggcaa agaccccaaa 180
cttactgcac tgatcaccaa agaatttaat tcaattaccg cagagaattg ccagaagtgg 240
gaaaggttgc gcaatgaaaa agatggtagc tgggaatgga aagatagcga tgcctttgtg 300
aatttcgggg ttgcccataa catgcatatt gtcgggcata cgttgggctg gcatagccaa 360
attcccgaca gcgtctttaa aaacaaagat ggcagttata tttccaaaga ggcactggca 420
aaaaaacaac aagagcacat caccacctta gtggatcgtt acaaaggcaa aattgccgca 480
tgggatgtgg ttaacgaagc catgggcgat gacaacaaga tgcgcgcaag ccattggtac 540
aacattatgg gtgatgactt tctcgtcaac gcctttaagc tcgcgcatga gactgacccc 600
aaagcacatt tgatgtacaa cgattacaac aacgagcgcc cggaaaagcg cgcagcaacg 660
gttgatatgc tcaagcgcct gttaaaactc ggggcgccga tccacggttt gggaatgcag 720
gcacatattg gcctggatgc ggatatgaaa aactttgaag acagtattgt cgcctattca 780
gaattaggct tgcgtattca ccttaccgaa ctggatatag atgtgttgcc ctcggtgtgg 840
aatttgccag tcgctgaagt atctacccgt tttgaataca aaccggagcg agatccttac 900
atcaaaggcc tgccaaaaga gatcgacgaa aaactcgcga aggcttatga atcgctattt 960
aaaattttgc ttaagcataa agacaaagta gatcgtgtga ccttctgggg tgtgagtgat 1020
gatgccagct ggctaaatgg cttcccgatc ccgggccgca ccaattatcc actgttattt 1080
gaccgtaagc agcaacctaa agcagcgtac ttccgcttac tggatttaaa gcgttaa 1137

<210> 46
<211> 378
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(25)

<400> 46
Met Lys Ile Ser Arg Arg Gln Leu Leu Ala Met Gly Gly Ala Ala Ala
1 5 10 15
Thr Leu Ala Ser Ala Lys Leu Phe Ala Ala Glu Lys Ala Ala Ala Ala
20 25 30
Thr Gly Leu Lys Asp Ala Tyr Lys Asn Asp Phe Leu Ile Gly Ala Ala
35 40 45
Leu Asn Thr Gln Ile Val Asp Gly Lys Asp Pro Lys Leu Thr Ala Leu
50 55 60
Ile Thr Lys Glu Phe Asn Ser Ile Thr Ala Glu Asn Cys Gln Lys Trp
65 70 75 80
Glu Arg Leu Arg Asn Glu Lys Asp Gly Ser Trp Glu Trp Lys Asp Ser
85 90 95
Asp Ala Phe Val Asn Phe Gly Val Ala His Asn Met His Ile Val Gly
100 105 110
His Thr Leu Gly Trp His Ser Gln Ile Pro Asp Ser Val Phe Lys Asn
115 120 125
Lys Asp Gly Ser Tyr Ile Ser Lys Glu Ala Leu Ala Lys Lys Gln Gln
130 135 140
Glu His Ile Thr Thr Leu Val Asp Arg Tyr Lys Gly Lys Ile Ala Ala
145 150 155 160
Trp Asp Val Val Asn Glu Ala Met Gly Asp Asp Asn Lys Met Arg Ala
165 170 175
Ser His Trp Tyr Asn Ile Met Gly Asp Asp Phe Leu Val Asn Ala Phe
180 185 190
Lys Leu Ala His Glu Thr Asp Pro Lys Ala His Leu Met Tyr Asn Asp
195 200 205

Tyr Asn Asn Glu Arg Pro Glu Lys Arg Ala Ala Thr Val Asp Met Leu
    210   215   220
Lys Arg Leu Leu Lys Leu Gly Ala Pro Ile His Gly Leu Gly Met Gln
225   230   235   240
Ala His Ile Gly Leu Asp Ala Asp Met Lys Asn Phe Glu Asp Ser Ile
                245   250   255
Val Ala Tyr Ser Glu Leu Gly Leu Arg Ile His Leu Thr Glu Leu Asp
            260   265   270
Ile Asp Val Leu Pro Ser Val Trp Asn Leu Pro Val Ala Glu Val Ser
        275   280   285
Thr Arg Phe Glu Tyr Lys Pro Glu Arg Asp Pro Tyr Ile Lys Gly Leu
    290   295   300
Pro Lys Glu Ile Asp Glu Lys Leu Ala Lys Ala Tyr Glu Ser Leu Phe
305   310   315   320
Lys Ile Leu Leu Lys His Lys Asp Lys Val Asp Arg Val Thr Phe Trp
                325   330   335
Gly Val Ser Asp Asp Ala Ser Trp Leu Asn Gly Phe Pro Ile Pro Gly
            340   345   350
Arg Thr Asn Tyr Pro Leu Leu Phe Asp Arg Lys Gln Gln Pro Lys Ala
        355   360   365
Ala Tyr Phe Arg Leu Leu Asp Leu Lys Arg
    370   375

<210> 47
<211> 1137
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 47
atgaaaagaa taaagattct gaattcgatt gtattagctt taatcctggc gatcatcctg 60
ccgggatgtt ccaatgcaca gaagagcgag ccggtgctga aagatgccct ttcgggaaaa 120
ttttacatcg ggctgctct caatacccc caaattacgg gccgggatac cttgtccatg 180
aaaatggtca ccagacattt taactccatc gtagctgaga actgcatgaa aagcggggag 240
atccagcgga ccgaagggga gtttgatttc agtcttgccg accagtttgt cgcgttcggc 300
gaaaaacaca acatgcacat tgtggggcat accctgatat ggcattcaca ggcgccgcgc 360
tggtttttca ccggtgcaga cggaaacgaa gtcagccggg aggtactgat tgagcgcatg 420
aagaaccata tttatacggt cgtggggcgt tacaaaggcc gtgtccacgg ctgggatgtg 480
gtcaacgaag ccattgaaga caacggctca tggcgcaaca gcaagtttta ccagatctta 540
ggtgacgagt ttgtggaact ggcctttaaa tttgccgcag aagccgaccc ggatgccgaa 600
ctttactata acgactactc catggcatta gaaggcagga gaaatggcgt tatcagaatg 660
gtgaagaacc ttcagtccaa gggactcaaa attgacggta tcggcatgca ggggcatctg 720
ctcatggact cgcccacgct ggaagcttat gaagaaagta tcctggccta ttccggactg 780
ggcgttaagg tgatgatcac ggaactcgat ttgtctgcgc tgccatggcc agcccgtcag 840
cagggagccg atattgccct gagggctgag tatgaggcac ggatgaatcc ttacaccgaa 900
ggtttaaccg attcagcttc cgtggcatgg aatcagcgga tgggcgattt cttctctctt 960
ttcctgaagc accaggacaa aatcagcagg gttacccttt ggggggtcac cgataaccaa 1020
tcctggaaaa ataactttcc gatgagagga aggacagact acccgttgct ttttgaccgg 1080
aattaccaac ccaaaccggt ggtggaaaga atcatcaaag aagcgaaagc aaaataa 1137

<210> 48
<211> 378
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(26)

<400> 48
Met Lys Arg Ile Lys Ile Leu Asn Ser Ile Val Leu Ala Leu Ile Leu
 1   5   10   15
Ala Ile Ile Leu Pro Gly Cys Ser Asn Ala Gln Lys Ser Glu Pro Val
            20   25   30
Leu Lys Asp Ala Leu Ser Gly Lys Phe Tyr Ile Gly Ala Ala Leu Asn

35 40 45
Thr Pro Gln Ile Thr Gly Arg Asp Thr Leu Ser Met Lys Met Val Thr
50 55 60
Arg His Phe Asn Ser Ile Val Ala Glu Asn Cys Met Lys Ser Gly Glu
65 70 75 80
Ile Gln Arg Thr Glu Gly Glu Phe Asp Phe Ser Leu Ala Asp Gln Phe
85 90 95
Val Ala Phe Gly Glu Lys His Asn Met His Ile Val Gly His Thr Leu
100 105 110
Ile Trp His Ser Gln Ala Pro Arg Trp Phe Phe Thr Gly Ala Asp Gly
115 120 125
Asn Glu Val Ser Arg Glu Val Leu Ile Glu Arg Met Lys Asn His Ile
130 135 140
Tyr Thr Val Val Gly Arg Tyr Lys Gly Arg Val His Gly Trp Asp Val
145 150 155 160
Val Asn Glu Ala Ile Glu Asp Asn Gly Ser Trp Arg Asn Ser Lys Phe
165 170 175
Tyr Gln Ile Leu Gly Asp Glu Phe Val Glu Leu Ala Phe Lys Phe Ala
180 185 190
Ala Glu Ala Asp Pro Asp Ala Glu Leu Tyr Tyr Asn Asp Tyr Ser Met
195 200 205
Ala Leu Glu Gly Arg Arg Asn Gly Val Ile Arg Met Val Lys Asn Leu
210 215 220
Gln Ser Lys Gly Leu Lys Ile Asp Gly Ile Gly Met Gln Gly His Leu
225 230 235 240
Leu Met Asp Ser Pro Thr Leu Glu Ala Tyr Glu Glu Ser Ile Leu Ala
245 250 255
Tyr Ser Gly Leu Gly Val Lys Val Met Ile Thr Glu Leu Asp Leu Ser
260 265 270
Ala Leu Pro Trp Pro Ala Arg Gln Gln Gly Ala Asp Ile Ala Leu Arg
275 280 285
Ala Glu Tyr Glu Ala Arg Met Asn Pro Tyr Thr Glu Gly Leu Thr Asp
290 295 300
Ser Ala Ser Val Ala Trp Asn Gln Arg Met Gly Asp Phe Phe Ser Leu
305 310 315 320
Phe Leu Lys His Gln Asp Lys Ile Ser Arg Val Thr Leu Trp Gly Val
325 330 335
Thr Asp Asn Gln Ser Trp Lys Asn Asn Phe Pro Met Arg Gly Arg Thr
340 345 350
Asp Tyr Pro Leu Leu Phe Asp Arg Asn Tyr Gln Pro Lys Pro Val Val
355 360 365
Glu Arg Ile Ile Lys Glu Ala Lys Ala Lys
370 375

<210> 49
<211> 996
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 49
atgaacagct ccctcccctc cctccgcgat gtattcgcga atgatttccg catcggggcg 60
gcggtcaatc ctgtgacgat cgagatgcaa aaacagttgt tgatcgatca tgtcaacagt 120
attacggcag agaaccatat gaagtttgag catcttcagc cggaagaagg gaaatttacc 180
tttcaggaag cggatcggat tgtggatttt gcttgttcgc accgaatggc ggttcgaggg 240
cacacacttg tatggcacaa ccagactccg gattgggtgt ttcaagatgg tcaaggccat 300
ttcgtcagtc gggatgtgtt gcttgagcgg atgaaatgtc acatttcaac tgttgtacgg 360
cgatacaagg gaaaaatata ttgttgggat gtcatcaacg aagcggtagc cgacgaagga 420
gacgaattgt tgaggccgtc gaagtggcga caaatcatcg gggacgattt tatggaacaa 480
gcatttctct acgcttatga agctgaccca gatgcactgc tttttacaa tgactataat 540
gaatgtttc cggaaaagag agaaaaaatt tttgcacttg tcaaatcgct gcgtgataaa 600
ggcattccga ttcatggcat cggcatgcag gcgcactgga gcctgacccg cccgtcgctt 660
gatgaaattc gtgcggcgat tgaacggtat gcgtcccttg gtgttgttct tcatattacg 720
gaactcgatg tatccatgtt tgaatttcac gatcgtcgaa ccgatttggc tgtcccgacg 780
aacgaaatga tcgaacagca agcagaacgg tatgggcaaa tttttgcttt gtttaaggag 840
tatcgcgatg ttattcaaag tgtcacattt tggggaattg ctgatgacca tacatggctc 900
gataactttc cagtgcacgg gagaaaaaac tggccgcttt tgttcgatga acagcataaa 960

ccgaaaccag ctttttggcg ggcagtgagt gtctga 996

<210> 50
<211> 331
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 50
Met Asn Ser Ser Leu Pro Ser Leu Arg Asp Val Phe Ala Asn Asp Phe
1   5   10   15
Arg Ile Gly Ala Ala Val Asn Pro Val Thr Ile Glu Met Gln Lys Gln
            20   25   30
Leu Leu Ile Asp His Val Asn Ser Ile Thr Ala Glu Asn His Met Lys
        35   40   45
Phe Glu His Leu Gln Pro Glu Glu Gly Lys Phe Thr Phe Gln Glu Ala
    50   55   60
Asp Arg Ile Val Asp Phe Ala Cys Ser His Arg Met Ala Val Arg Gly
65   70   75   80
His Thr Leu Val Trp His Asn Gln Thr Pro Asp Trp Val Phe Gln Asp
                85   90   95
Gly Gln Gly His Phe Val Ser Arg Asp Val Leu Leu Glu Arg Met Lys
            100   105   110
Cys His Ile Ser Thr Val Val Arg Arg Tyr Lys Gly Lys Ile Tyr Cys
        115   120   125
Trp Asp Val Ile Asn Glu Ala Val Ala Asp Glu Gly Asp Glu Leu Leu
    130   135   140
Arg Pro Ser Lys Trp Arg Gln Ile Ile Gly Asp Asp Phe Met Glu Gln
145   150   155   160
Ala Phe Leu Tyr Ala Tyr Glu Ala Asp Pro Asp Ala Leu Leu Phe Tyr
                165   170   175
Asn Asp Tyr Asn Glu Cys Phe Pro Glu Lys Arg Glu Lys Ile Phe Ala
            180   185   190
Leu Val Lys Ser Leu Arg Asp Lys Gly Ile Pro Ile His Gly Ile Gly
        195   200   205
Met Gln Ala His Trp Ser Leu Thr Arg Pro Ser Leu Asp Glu Ile Arg
    210   215   220
Ala Ala Ile Glu Arg Tyr Ala Ser Leu Gly Val Val Leu His Ile Thr
225   230   235   240
Glu Leu Asp Val Ser Met Phe Glu Phe His Asp Arg Arg Thr Asp Leu
                245   250   255
Ala Val Pro Thr Asn Glu Met Ile Glu Gln Gln Ala Glu Arg Tyr Gly
            260   265   270
Gln Ile Phe Ala Leu Phe Lys Glu Tyr Arg Asp Val Ile Gln Ser Val
        275   280   285
Thr Phe Trp Gly Ile Ala Asp Asp His Thr Trp Leu Asp Asn Phe Pro
    290   295   300
Val His Gly Arg Lys Asn Trp Pro Leu Leu Phe Asp Glu Gln His Lys
305   310   315   320
Pro Lys Pro Ala Phe Trp Arg Ala Val Ser Val
                325   330

<210> 51
<211> 3162
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 51
atgagaggga aaagcaaaaa gggatttctg aacatctcag aagctgtact tgttggaatt 60
ttagcaggct ttcttggagt tcttctcgca gctacggggg ttttgagttt tggtggaaca 120
gcgtcttcgt ctcttgaaac ggtgttcacc ttgagtttcg agggaacaac gcaaggtgtc 180
aatccctttg gaaaagaagt agttctcaca gcttctcaag atgtagcagc cgatggcgaa 240
tattcattga aagtagagaa tagaacttcc ggctgggatg gagttgagat cgatttaacg 300
gaaaaagtag aagcgaacaa agattatctg ttgtctttct acgtctatca aacatctgac 360

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tcaccccaac tttttgaagt ccttgcaaga acagaagacg ggaaaggtga aaaatacgaa    420
acccttaccg acaaggtggt agtatcgaac tactggaaag aaattcttgt gcccttttcc    480
ccgagtttcg agagtacccc aacaaaatgt tctttgatcg ttgtttcacc aaagaaccca    540
tcattcactt tctatattga caaggttcaa attctcaaac cgaagaagca aggtccacaa    600
gtcatttacg aaacatcctt tgagagtggg acgggaagct ggcaagccag agggtctgat    660
gtgaaaatca aagtgacatc gaaagttgct cattctggaa aaaggtctct ctatgtctcc    720
aacagacaaa aaggctggca tggtgtacaa cttgacgtga agagactctt gagacccggg    780
aaaacgtatg cttttgaagg atgggtttat caagactctg gacaggatca aacaattatt    840
ctgacgatgc agagaagata ttcttctgat tctagcacac aatatgagtg gatcaaggcg    900
gtaactgttc catcaggaca atggacgcag atctctggaa cttacacaat ccaaccaaga    960
gtaagcgtgg aggaactcat tgtttacttt gaagccaagg atcccactct tgccttctat   1020
gtggacgatt tcaaaataac ggataccaca actactgaca tcaagctcga gctgaagcct   1080
gaagaagaaa ttccagctct taaagaagtg cttggagatt acttcaaagt aggtgttgcc   1140
ttacctttca aagtttttgc caaaccagag gatattgctc tcattactaa acatttcaac   1200
agcatcactg ccgaaaacga aatgaaacct gagagtctct tggctggcgt agaaaatgga   1260
aagttgaagt tcaggtttga gacagcagac aaatacgtag aatttgcaca gcaaaacggt   1320
atggttgtga gaggtcacac tctggtgtgg cacaatcaaa caccggactg gttcttcaag   1380
gacgagaacg gaaatctgct ctccaaagaa gcaatgactg aaaggcttag ggaatacatc   1440
cacacagtcg tcggacactt caaaggcaaa gtttacgcgt gggacgtcgt taatgaggca   1500
gtagatccat cccaaccaga tggacttaga agatctatat ggtacgaaat catgggacct   1560
gactatatag aacttgcatt caagtttgca agagaagcgg accccaatgc aaagctcttc   1620
tacaacgact acaacaccta ccaggagaag aagagagaca tcatttacaa cctcgtcaaa   1680
tccctcaaag agaagggact cattgacggt atcggtatgc agtgtcatat cggtgttggg   1740
accagtgtca aagagattga agaggcaatc aaaaaattca gcaccattcc aggtatcgaa   1800
attcatatca cggaactaga tataagtgtg tacgaggatg cgacttccaa ttatccaaca   1860
cctccaaggg aggctctcat taaacaagca cacgtaatga gagaactctt tgccatcttc   1920
aaaaagtaca gcaacgtcat aacaaacgtt actttctggg gattgaaaga tgattattcc   1980
tggaagaatg cccgcagaaa cgactggccg ctacttttg ataaagacta ccaagccaaa    2040
cttgcctact gggccatagt cagtcctgag gctctaccgg tgcttccaaa gaaatggtct   2100
atcgctacag gtagtgcttt ggtagttgga atgatggatg actcctattt ggcttcttca   2160
cctatcaaaa ttctcgtcga tggccaagaa aaactcacag ccagagtcat ctgggaagaa   2220
aacaaactct tcgtctacgc agaggtctat gacaggacaa gagacaaagg aaaggacggt   2280
atcaccatct ttgtggatcc taaaaacttc aaggcacctt acttgcatga agatgctttc   2340
tacgttacca taaaaaccga ctggagtgtt gagaagagtc gtgatgacat agaagtccag   2400
agattcgtag gtccaagtgg agtaaggtac aacgttgaat gtgaaataac acttcctgaa   2460
aaactccagg aaggacagca aatcggattt gatatcgccg tccaggatgg cgataaggtc   2520
tacagctggt ctgatacatc caatcagcag aagctcgcaa ccatgaacta cggaactctc   2580
actctgcagg gtgcggtaat ggccacagct aagtatggca cacctgtgat cgatggtgaa   2640
atagatgaca tctggtacac cactgaagaa atctcaaccg atgttgttgt catgggttca   2700
ctcaagaacg caagggcaaa agtgagagtg ctctgggatg aagagcacct ctatgtgctt   2760
gccatcgtaa ccgatcctgt gctcaataag gacaacacca atccatggga acaagactct   2820
gtagaaatct tcatagacga aaacaacgcc aaaacaccgt actatcagga cgatgatgct   2880
caatatcgtg tcaactacct caacgaacaa tccttcggta caggtgcaag cagcaagaac   2940
ttcaagacag ccgtgaaact catcgatggt ggttatcttg ttgaggcagc ggttaaatgg   3000
aagaccatca aaccttcacc aaacacagtg ataggctttg atttccaggt gaacgatgca   3060
aatgctcaag gtaagagagt tggaatactt aagtggtgcg atccaacgga caacagctgg   3120
cagaatacct ccaagtttgg taatctcagg ttgataaaat ag                      3162
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<210> 52
<211> 1053
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(30)

<400> 52

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Met Arg Gly Lys Ser Lys Lys Gly Phe Leu Asn Ile Ser Glu Ala Val
 1               5                  10                  15
Leu Val Gly Ile Leu Ala Gly Phe Leu Gly Val Leu Leu Ala Ala Thr
            20                  25                  30
Gly Val Leu Ser Phe Gly Gly Thr Ala Ser Ser Ser Leu Glu Thr Val
        35                  40                  45
Phe Thr Leu Ser Phe Glu Gly Thr Thr Gln Gly Val Asn Pro Phe Gly
    50                  55                  60
Lys Glu Val Val Leu Thr Ala Ser Gln Asp Val Ala Ala Asp Gly Glu
```

65 70 75 80
Tyr Ser Leu Lys Val Glu Asn Arg Thr Ser Gly Trp Asp Gly Val Glu
85 90 95
Ile Asp Leu Thr Glu Lys Val Glu Ala Asn Lys Asp Tyr Leu Leu Ser
100 105 110
Phe Tyr Val Tyr Gln Thr Ser Asp Ser Pro Gln Leu Phe Glu Val Leu
115 120 125
Ala Arg Thr Glu Asp Gly Lys Gly Glu Lys Tyr Glu Thr Leu Thr Asp
130 135 140
Lys Val Val Val Ser Asn Tyr Trp Lys Glu Ile Leu Val Pro Phe Ser
145 150 155 160
Pro Ser Phe Glu Ser Thr Pro Thr Lys Cys Ser Leu Ile Val Val Ser
165 170 175
Pro Lys Asn Pro Ser Phe Thr Phe Tyr Ile Asp Lys Val Gln Ile Leu
180 185 190
Lys Pro Lys Lys Gln Gly Pro Gln Val Ile Tyr Glu Thr Ser Phe Glu
195 200 205
Ser Gly Thr Gly Ser Trp Gln Ala Arg Gly Ser Asp Val Lys Ile Lys
210 215 220
Val Thr Ser Lys Val Ala His Ser Gly Lys Arg Ser Leu Tyr Val Ser
225 230 235 240
Asn Arg Gln Lys Gly Trp His Gly Val Gln Leu Asp Val Lys Arg Leu
245 250 255
Leu Arg Pro Gly Lys Thr Tyr Ala Phe Glu Gly Trp Val Tyr Gln Asp
260 265 270
Ser Gly Gln Asp Gln Thr Ile Ile Leu Thr Met Gln Arg Arg Tyr Ser
275 280 285
Ser Asp Ser Ser Thr Gln Tyr Glu Trp Ile Lys Ala Val Thr Val Pro
290 295 300
Ser Gly Gln Trp Thr Gln Ile Ser Gly Thr Tyr Thr Ile Gln Pro Arg
305 310 315 320
Val Ser Val Glu Glu Leu Ile Val Tyr Phe Glu Ala Lys Asp Pro Thr
325 330 335
Leu Ala Phe Tyr Val Asp Asp Phe Lys Ile Thr Asp Thr Thr Thr Thr
340 345 350
Asp Ile Lys Leu Glu Leu Lys Pro Glu Glu Glu Ile Pro Ala Leu Lys
355 360 365
Glu Val Leu Gly Asp Tyr Phe Lys Val Gly Val Ala Leu Pro Phe Lys
370 375 380
Val Phe Ala Lys Pro Glu Asp Ile Ala Leu Ile Thr Lys His Phe Asn
385 390 395 400
Ser Ile Thr Ala Glu Asn Glu Met Lys Pro Glu Ser Leu Leu Ala Gly
405 410 415
Val Glu Asn Gly Lys Leu Lys Phe Arg Phe Glu Thr Ala Asp Lys Tyr
420 425 430
Val Glu Phe Ala Gln Gln Asn Gly Met Val Val Arg Gly His Thr Leu
435 440 445
Val Trp His Asn Gln Thr Pro Asp Trp Phe Phe Lys Asp Glu Asn Gly
450 455 460
Asn Leu Leu Ser Lys Glu Ala Met Thr Glu Arg Leu Arg Glu Tyr Ile
465 470 475 480
His Thr Val Val Gly His Phe Lys Gly Lys Val Tyr Ala Trp Asp Val
485 490 495
Val Asn Glu Ala Val Asp Pro Ser Gln Pro Asp Gly Leu Arg Arg Ser
500 505 510
Ile Trp Tyr Glu Ile Met Gly Pro Asp Tyr Ile Glu Leu Ala Phe Lys
515 520 525
Phe Ala Arg Glu Ala Asp Pro Asn Ala Lys Leu Phe Tyr Asn Asp Tyr
530 535 540
Asn Thr Tyr Gln Glu Lys Lys Arg Asp Ile Ile Tyr Asn Leu Val Lys
545 550 555 560
Ser Leu Lys Glu Lys Gly Leu Ile Asp Gly Ile Gly Met Gln Cys His
565 570 575
Ile Gly Val Gly Thr Ser Val Lys Glu Ile Glu Glu Ala Ile Lys Lys
580 585 590
Phe Ser Thr Ile Pro Gly Ile Glu Ile His Ile Thr Glu Leu Asp Ile
595 600 605
Ser Val Tyr Glu Asp Ala Thr Ser Asn Tyr Pro Thr Pro Pro Arg Glu
610 615 620

Ala Leu Ile Lys Gln Ala His Val Met Arg Glu Leu Phe Ala Ile Phe
625 630 635 640
Lys Lys Tyr Ser Asn Val Ile Thr Asn Val Thr Phe Trp Gly Leu Lys
645 650 655
Asp Asp Tyr Ser Trp Lys Asn Ala Arg Arg Asn Asp Trp Pro Leu Leu
660 665 670
Phe Asp Lys Asp Tyr Gln Ala Lys Leu Ala Tyr Trp Ala Ile Val Ser
675 680 685
Pro Glu Ala Leu Pro Val Leu Pro Lys Lys Trp Ser Ile Ala Thr Gly
690 695 700
Ser Ala Leu Val Val Gly Met Met Asp Asp Ser Tyr Leu Ala Ser Ser
705 710 715 720
Pro Ile Lys Ile Leu Val Asp Gly Gln Glu Lys Leu Thr Ala Arg Val
725 730 735
Ile Trp Glu Glu Asn Lys Leu Phe Val Tyr Ala Glu Val Tyr Asp Arg
740 745 750
Thr Arg Asp Lys Gly Lys Asp Gly Ile Thr Ile Phe Val Asp Pro Lys
755 760 765
Asn Phe Lys Ala Pro Tyr Leu His Glu Asp Ala Phe Tyr Val Thr Ile
770 775 780
Lys Thr Asp Trp Ser Val Glu Lys Ser Arg Asp Asp Ile Glu Val Gln
785 790 795 800
Arg Phe Val Gly Pro Ser Gly Val Arg Tyr Asn Val Glu Cys Glu Ile
805 810 815
Thr Leu Pro Glu Lys Leu Gln Glu Gly Gln Gln Ile Gly Phe Asp Ile
820 825 830
Ala Val Gln Asp Gly Asp Lys Val Tyr Ser Trp Ser Asp Thr Ser Asn
835 840 845
Gln Gln Lys Leu Ala Thr Met Asn Tyr Gly Thr Leu Thr Leu Gln Gly
850 855 860
Ala Val Met Ala Thr Ala Lys Tyr Gly Thr Pro Val Ile Asp Gly Glu
865 870 875 880
Ile Asp Asp Ile Trp Tyr Thr Thr Glu Glu Ile Ser Thr Asp Val Val
885 890 895
Val Met Gly Ser Leu Lys Asn Ala Arg Ala Lys Val Arg Val Leu Trp
900 905 910
Asp Glu Glu His Leu Tyr Val Leu Ala Ile Val Thr Asp Pro Val Leu
915 920 925
Asn Lys Asp Asn Thr Asn Pro Trp Glu Gln Asp Ser Val Glu Ile Phe
930 935 940
Ile Asp Glu Asn Asn Ala Lys Thr Pro Tyr Tyr Gln Asp Asp Asp Ala
945 950 955 960
Gln Tyr Arg Val Asn Tyr Leu Asn Glu Gln Ser Phe Gly Thr Gly Ala
965 970 975
Ser Ser Lys Asn Phe Lys Thr Ala Val Lys Leu Ile Asp Gly Gly Tyr
980 985 990
Leu Val Glu Ala Ala Val Lys Trp Lys Thr Ile Lys Pro Ser Pro Asn
995 1000 1005
Thr Val Ile Gly Phe Asp Phe Gln Val Asn Asp Ala Asn Ala Gln Gly
1010 1015 1020
Lys Arg Val Gly Ile Leu Lys Trp Cys Asp Pro Thr Asp Asn Ser Trp
1025 1030 1035 1040
Gln Asn Thr Ser Lys Phe Gly Asn Leu Arg Leu Ile Lys
1045 1050

<210> 53
<211> 2370
<212> DNA
<213> Bacteria

<400> 53
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gcggcggtgg tcgccggcgc cctgacgctc ctccccggct ccgccggcgc cgcgggcctg 120
ggtacgcacg cggcccccctc gggccggtac ttcggcacgg ccgtggccgc gggccgcctc 180
ggcgactcgg cgtacaccgc gatcgccgac cgggagttca acatgatcac cccggagaac 240
gagatgaagt gggacgccgt cgagccgtcc cgcggccgtt tcgacttcgg tcccgcggac 300
cggatcgtcg agcgtgccct ggcacgcggc cagcgcgtcc gcggccacac cacggtctgg 360
cactcgcagc tcccctcctg ggtgggctcc atccgcgaca cgaagacgct gcgcggcgtg 420
atgaaccacc acatcaccac ccagatgacc cactacaagg gcaagatcta cgcctgggac 480

gtggtcaacg aggccttcgc cgatggcggc agcggccggc tccgcgactc ggtcttccag 540
aaggtgctgg gcgacggctt catcgaggag gcgttccgca ccgcccgcgc ggccgacccc 600
tcggccaagc tctgctacaa cgactacaac atcgagaact ggtcggacgc caagacccag 660
ggcgtctacc gcctggtgaa ggacttcacg tcccgaggcg ttcccatcga ctgcgtcggc 720
ttccagagcc acttcggcgc gggcggcccg ccggcgagct tcaagacgac cctggccaac 780
ttcgccgccc tgggcgtcga cgtccagatc accgagctgg acatcgccca ggcatcacct 840
gcccactacg cgagtgcggt cagcacctgt ctgtccgtgg cccggtgcac cggcatcacg 900
gtgtggggcg tccgtgacag cgactcctgg cggagcgccg aaagcccgct gctgttcgac 960
cggaacggca agcccaagcc cgcgtacgcc gccgtcatga acgccctcgg ctccggctcg 1020
ggtcccaccc cgagcaagcc ggccgacggt acggggagcg gtacggggga gatcaagggc 1080
gtggcctccg gccgctgtct ggacgtcccc gcctccacca ccgccaacgg cacccgggcg 1140
cagctgtggg actgtagcgg ccaggccaac cagcgctgga cccacaccgc cggcaagcag 1200
ctgaagatcc acggcgacaa gtgcctggac gccaagggca agggcaccgc caacggcacc 1260
gcggtggtcg tctgggactg caacggcggc accaaccagc agtggaacgt ccacaccgac 1320
ggcacgatca ccggcgtcca gtccggtctg tgcctcgatg ccgtcggcgc ggccaccgcc 1380
aacggcaccc cgatccagct gcacgcctgt gggggtgtcg gcaaccagaa gtggtccgcc 1440
ccgtccggat cgggcggcgg cacgtgcgtg cttccgtcga cgtacaagtg gagctcgacg 1500
ggtgccctgg cgcagcccaa ggccgggtgg gcctcgctga aggacttcac ccatgtggtg 1560
ctgggcggca agcacctggt ctacgggtcg aacttcaacg gatcgacgta cggctcgatg 1620
acgttcagcc ccttcaccac ctggtcggac atggcgtccg caggacagaa ggcgatgaag 1680
cagcccgcgg tcgcacccac cctgttctac ttcgcaccca agaagatctg ggtgctggcg 1740
taccagtggg gcaggaccgc gttctcctac cggacgtcga ccgaccccac caacccgaac 1800
ggctggtcgg cggagcagga gctcttctcc ggaagcatca ccggctcggg cacgggcccc 1860
atcgaccaga cgctcatcgg cgacgggacg aacatgtacc tgttcttcgc cggtgacaac 1920
ggcaagatct accgggccag catgccgatc gggaacttcc cgggcagctt cggctcctcg 1980
tacacgacgg tcatgagcga caccgcgaag aacctgttcg aggcgccgca ggtgtacaag 2040
gtcaaggacc agaaccagta cctcatgatc gtcgaggccc ggggcgcggg cgagcgccgc 2100
tacttccgct cgttcacggc ctccagcctg agcggtgcgt ggaccccgca ggccgcgacc 2160
gagagcaacc ccttcgcggg caaggccaac agcggcgcca cctggaccga cgacatcagc 2220
cacggtgatc tgatccgcac caaccccgat cagaccatga ccatcgaccc ctgcaacctt 2280
cagctgctct accagggcaa gtccccgcag gcgggcggac cctacgacca gctgccgtac 2340
cggccgggcg tcctcaccct gcagcgctga 2370

<210> 54
<211> 787
<212> PRT
<213> Bacteria

<220>
<221> SIGNAL
<222> (1)...(37)

<400> 54
Met Lys Gly Leu His Arg Leu Arg Arg Arg Arg Arg Thr Trp Val Ala
1 5 10 15
Gly Leu Ser Ala Ala Ala Val Val Ala Gly Ala Leu Thr Leu Leu Pro
20 25 30
Gly Ser Ala Gly Ala Ala Gly Leu Gly Thr His Ala Ala Pro Ser Gly
35 40 45
Arg Tyr Phe Gly Thr Ala Val Ala Ala Gly Arg Leu Gly Asp Ser Ala
50 55 60
Tyr Thr Ala Ile Ala Asp Arg Glu Phe Asn Met Ile Thr Pro Glu Asn
65 70 75 80
Glu Met Lys Trp Asp Ala Val Glu Pro Ser Arg Gly Arg Phe Asp Phe
85 90 95
Gly Pro Ala Asp Arg Ile Val Glu Arg Ala Leu Ala Arg Gly Gln Arg
100 105 110
Val Arg Gly His Thr Thr Val Trp His Ser Gln Leu Pro Ser Trp Val
115 120 125
Gly Ser Ile Arg Asp Thr Lys Thr Leu Arg Gly Val Met Asn His His
130 135 140
Ile Thr Thr Gln Met Thr His Tyr Lys Gly Lys Ile Tyr Ala Trp Asp
145 150 155 160
Val Val Asn Glu Ala Phe Ala Asp Gly Gly Ser Gly Arg Leu Arg Asp
165 170 175
Ser Val Phe Gln Lys Val Leu Gly Asp Gly Phe Ile Glu Glu Ala Phe
180 185 190
Arg Thr Ala Arg Ala Ala Asp Pro Ser Ala Lys Leu Cys Tyr Asn Asp
195 200 205

Tyr Asn Ile Glu Asn Trp Ser Asp Ala Lys Thr Gln Gly Val Tyr Arg
210 215 220
Leu Val Lys Asp Phe Thr Ser Arg Gly Val Pro Ile Asp Cys Val Gly
225 230 235 240
Phe Gln Ser His Phe Gly Ala Gly Gly Pro Pro Ala Ser Phe Lys Thr
245 250 255
Thr Leu Ala Asn Phe Ala Ala Leu Gly Val Asp Val Gln Ile Thr Glu
260 265 270
Leu Asp Ile Ala Gln Ala Ser Pro Ala His Tyr Ala Ser Ala Val Ser
275 280 285
Thr Cys Leu Ser Val Ala Arg Cys Thr Gly Ile Thr Val Trp Gly Val
290 295 300
Arg Asp Ser Asp Ser Trp Arg Ser Ala Glu Ser Pro Leu Leu Phe Asp
305 310 315 320
Arg Asn Gly Lys Pro Lys Pro Ala Tyr Ala Ala Val Met Asn Ala Leu
325 330 335
Gly Ser Gly Ser Gly Pro Thr Pro Ser Lys Pro Ala Asp Gly Thr Gly
340 345 350
Ser Gly Thr Gly Glu Ile Lys Gly Val Ala Ser Gly Arg Cys Leu Asp
355 360 365
Val Pro Ala Ser Thr Thr Ala Asn Gly Thr Arg Ala Gln Leu Trp Asp
370 375 380
Cys Ser Gly Gln Ala Asn Gln Arg Trp Thr His Thr Ala Gly Lys Gln
385 390 395 400
Leu Lys Ile His Gly Asp Lys Cys Leu Asp Ala Lys Gly Lys Gly Thr
405 410 415
Ala Asn Gly Thr Ala Val Val Val Trp Asp Cys Asn Gly Gly Thr Asn
420 425 430
Gln Gln Trp Asn Val His Thr Asp Gly Thr Ile Thr Gly Val Gln Ser
435 440 445
Gly Leu Cys Leu Asp Ala Val Gly Ala Ala Thr Ala Asn Gly Thr Pro
450 455 460
Ile Gln Leu His Ala Cys Gly Gly Val Gly Asn Gln Lys Trp Ser Ala
465 470 475 480
Pro Ser Gly Ser Gly Gly Gly Thr Cys Val Leu Pro Ser Thr Tyr Lys
485 490 495
Trp Ser Ser Thr Gly Ala Leu Ala Gln Pro Lys Ala Gly Trp Ala Ser
500 505 510
Leu Lys Asp Phe Thr His Val Val Leu Gly Gly Lys His Leu Val Tyr
515 520 525
Gly Ser Asn Phe Asn Gly Ser Thr Tyr Gly Ser Met Thr Phe Ser Pro
530 535 540
Phe Thr Thr Trp Ser Asp Met Ala Ser Ala Gly Gln Lys Ala Met Lys
545 550 555 560
Gln Pro Ala Val Ala Pro Thr Leu Phe Tyr Phe Ala Pro Lys Lys Ile
565 570 575
Trp Val Leu Ala Tyr Gln Trp Gly Arg Thr Ala Phe Ser Tyr Arg Thr
580 585 590
Ser Thr Asp Pro Thr Asn Pro Asn Gly Trp Ser Ala Glu Gln Glu Leu
595 600 605
Phe Ser Gly Ser Ile Thr Gly Ser Gly Thr Gly Pro Ile Asp Gln Thr
610 615 620
Leu Ile Gly Asp Gly Thr Asn Met Tyr Leu Phe Phe Ala Gly Asp Asn
625 630 635 640
Gly Lys Ile Tyr Arg Ala Ser Met Pro Ile Gly Asn Phe Pro Gly Ser
645 650 655
Phe Gly Ser Ser Tyr Thr Thr Val Met Ser Asp Thr Ala Lys Asn Leu
660 665 670
Phe Glu Ala Pro Gln Val Tyr Lys Val Lys Asp Gln Asn Gln Tyr Leu
675 680 685
Met Ile Val Glu Ala Arg Gly Ala Gly Glu Arg Arg Tyr Phe Arg Ser
690 695 700
Phe Thr Ala Ser Ser Leu Ser Gly Ala Trp Thr Pro Gln Ala Ala Thr
705 710 715 720
Glu Ser Asn Pro Phe Ala Gly Lys Ala Asn Ser Gly Ala Thr Trp Thr
725 730 735
Asp Asp Ile Ser His Gly Asp Leu Ile Arg Thr Asn Pro Asp Gln Thr
740 745 750
Met Thr Ile Asp Pro Cys Asn Leu Gln Leu Leu Tyr Gln Gly Lys Ser

755 760 765
Pro Gln Ala Gly Gly Pro Tyr Asp Gln Leu Pro Tyr Arg Pro Gly Val
770 775 780
Leu Thr Leu
785

<210> 55
<211> 1143
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 55
atgaaaaaaa cgattgcaca tttcacctta tggatagcgt tttttctctt cacttcctgt 60
gctgttacgg cgcagaagaa tactaagaat gcaagagtaa agcccactac tctaaaagag 120
gcttaccaag gtaaattcta tatcggtaca gcgatgaatc tgagacagat tcacggagat 180
gatcccccagt ctgaaaatat tatcaaaaaa cagttcaatt ccattgttgc tgaaaactgc 240
atgaagagta tgtatcttca gccggaggaa ggaaaatttt tcttcgatga tgcggataag 300
tttgtggatt ttggtcttca gaacaatatg tttattatcg ggcattgtct gatttggcat 360
tcgcaggcgc caaaatggtt tttcaccgac gagaatggga aaacggtctc cccagaagtt 420
cttaaacaaa ggatgaaagc tcatatcacc gccgtcgttt ctcgctacaa agggaaaatc 480
aaaggatggg atgtggtgaa cgaagccatt atggaagatg gttcttaccg caaaagcaaa 540
ttttacgaga ttttgggaga agaatttatt ccgttggcat ttcagtatgc gcatgaagca 600
gatcctgatg cagaactcta ttacaacgat tataacgaat ggtatcccgg aaaaagagct 660
acggtgacca aaataatccg agatttcaaa tctagaggaa tccgcattga tgccattgga 720
atgcaggctc atttcgggat ggattcaccc actatagaag agtatgaaca aactattcag 780
ggctatataa aagaaggcgt gaaagtcaat attacggaac tcgatttgag tccacttcct 840
tccccttggg gaacttccgc caacgttgcc gatacgcagc agtatcagga aaaaatgaat 900
ccttacacca aaggacttcc cacagaggtg gaaaaagctt gggaaaaccg ttatctcgat 960
tttttcaaac tattcctaaa atatcatcag catatcgagc gtgttacgtt ttggggcgtt 1020
agcgatatcg attcctggaa gaacgatttt ccagtgagag gacgtaccga ttatccgtta 1080
ccctttgacc gacagtatca ggcaaaacct ttggttcaga aattaataga cttaacgaaa 1140
tag 1143

<210> 56
<211> 380
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(24)

<400> 56
Met Lys Lys Thr Ile Ala His Phe Thr Leu Trp Ile Ala Phe Phe Leu
1 5 10 15
Phe Thr Ser Cys Ala Val Thr Ala Gln Lys Asn Thr Lys Asn Ala Arg
20 25 30
Val Lys Pro Thr Thr Leu Lys Glu Ala Tyr Gln Gly Lys Phe Tyr Ile
35 40 45
Gly Thr Ala Met Asn Leu Arg Gln Ile His Gly Asp Asp Pro Gln Ser
50 55 60
Glu Asn Ile Ile Lys Lys Gln Phe Asn Ser Ile Val Ala Glu Asn Cys
65 70 75 80
Met Lys Ser Met Tyr Leu Gln Pro Glu Glu Gly Lys Phe Phe Phe Asp
85 90 95
Asp Ala Asp Lys Phe Val Asp Phe Gly Leu Gln Asn Asn Met Phe Ile
100 105 110
Ile Gly His Cys Leu Ile Trp His Ser Gln Ala Pro Lys Trp Phe Phe
115 120 125
Thr Asp Glu Asn Gly Lys Thr Val Ser Pro Glu Val Leu Lys Gln Arg
130 135 140
Met Lys Ala His Ile Thr Ala Val Val Ser Arg Tyr Lys Gly Lys Ile
145 150 155 160
Lys Gly Trp Asp Val Val Asn Glu Ala Ile Met Glu Asp Gly Ser Tyr

165 170 175
Arg Lys Ser Lys Phe Tyr Glu Ile Leu Gly Glu Glu Phe Ile Pro Leu
180 185 190
Ala Phe Gln Tyr Ala His Glu Ala Asp Pro Asp Ala Glu Leu Tyr Tyr
195 200 205
Asn Asp Tyr Asn Glu Trp Tyr Pro Gly Lys Arg Ala Thr Val Thr Lys
210 215 220
Ile Ile Arg Asp Phe Lys Ser Arg Gly Ile Arg Ile Asp Ala Ile Gly
225 230 235 240
Met Gln Ala His Phe Gly Met Asp Ser Pro Thr Ile Glu Glu Tyr Glu
245 250 255
Gln Thr Ile Gln Gly Tyr Ile Lys Glu Gly Val Lys Val Asn Ile Thr
260 265 270
Glu Leu Asp Leu Ser Pro Leu Pro Ser Pro Trp Gly Thr Ser Ala Asn
275 280 285
Val Ala Asp Thr Gln Gln Tyr Gln Glu Lys Met Asn Pro Tyr Thr Lys
290 295 300
Gly Leu Pro Thr Glu Val Glu Lys Ala Trp Glu Asn Arg Tyr Leu Asp
305 310 315 320
Phe Phe Lys Leu Phe Leu Lys Tyr His Gln His Ile Glu Arg Val Thr
325 330 335
Phe Trp Gly Val Ser Asp Ile Asp Ser Trp Lys Asn Asp Phe Pro Val
340 345 350
Arg Gly Arg Thr Asp Tyr Pro Leu Pro Phe Asp Arg Gln Tyr Gln Ala
355 360 365
Lys Pro Leu Val Gln Lys Leu Ile Asp Leu Thr Lys
370 375 380

<210> 57
<211> 1578
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 57
atgaaaagaa tgatcggttt gctgctggcc atttgcctgg tgatgacgct ggctggggcc 60
tgggctgcct cggatacgct ggtctatgca tccagtttcg cagcgggcga tgacgactgg 120
tttgcaaggg gcgcttcccg ggtttaccat accacggagg cgacgctgcg gacggaaggc 180
cggagcgaca actggaattc tccgggacgc tattttgaac tggtgccgga taatgaatat 240
acgctgagcg tggaggtcta ccaggacgga gcggacagcg cgaacttcat gatttccctg 300
gaaaaggttg cggatgggat caccggatgg gaaaacctgg tgcggggaac cgtgaaaaag 360
ggtgaatgga cgacgctgtc cggaacctat acttttgcag actatgaaag ctatgtgctg 420
tatgtggaga cctccgacgc gccgacgctg gactttgaga tccggaattt ccgggtggaa 480
agccccaatg ggatcccgga gccgaaggct accgaggcgc cggcagtggt ttcggaagcc 540
acggatattc cgagcctgaa ggacgcttac gcggattact tcgactttgg cgcggccgtg 600
ccgcagtctg ctttcaccag cagagataat attcagctga tggagctgat gaaaaaccag 660
ttcagcatcc tgacgcctga aaatgagctg aagccggaca gtgtattgga tgtaagcgcc 720
agcaagcagc tggccaaaga ggatgaaacc gcggtagtgg tgcggtttaa cggggcaaag 780
tcattgctgc ggtttgccca gcaaaacggc atcaaggtgc acgggcatgt gctggtctgg 840
cacagccaga cgccggaagc ctttttccat gaaggatatg atcccaagaa cccgctggtg 900
agccgggaag tgatgctggg acggctggaa aactatatcc gggaagtgct gacccagacg 960
gaagaactgt atccgggcgt gatcgtcagc tgggacgtgg tgaacgaagc gattgacgac 1020
ggaaccaact ggatccggaa gggatcgggc tggtaccgga ccatcgggga agactatgtg 1080
gagaaggctt ttgagtttgc ccggaagtat gccccggaag gcgtgctgct gtactacaac 1140
gattacaaca cggcatacgc cggaaaactg aatgggatta tcaaactgat caaacccatg 1200
atcgagcagg gaacgatcga cggatacggc ttccagatgc accatacgac cgggcagccc 1260
agcaaccaga tgatcaccac ggcggtggag aagatcgcgg ccctgggaat caagctgcgg 1320
gtcagcgaga tggacatcgg gattacaaag tatacagaga cgagcctgca ggcacaaaag 1380
gacaagtaca aggcgatgat ggaactgatg ctgcggttcg cggaccagac ggaagcagtg 1440
caggtctggg ggattacgga tacgatgagc tggcggagct ccagctatcc gctgctgttt 1500
gaccggagca ggaatccgaa gccggcgttc tatggcgtga ttgaagcggt tgaagactgg 1560
acagggaaaa gtgaatag 1578

<210> 58
<211> 525
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<400> 58
Met Lys Arg Met Ile Gly Leu Leu Leu Ala Ile Cys Leu Val Met Thr
 1   5   10   15
Leu Ala Gly Ala Trp Ala Ala Ser Asp Thr Leu Val Tyr Ala Ser Ser
            20   25   30
Phe Ala Ala Gly Asp Asp Asp Trp Phe Ala Arg Gly Ala Ser Arg Val
        35   40   45
Tyr His Thr Thr Glu Ala Thr Leu Arg Thr Glu Gly Arg Ser Asp Asn
    50   55   60
Trp Asn Ser Pro Gly Arg Tyr Phe Glu Leu Val Pro Asp Asn Glu Tyr
65   70   75   80
Thr Leu Ser Val Glu Val Tyr Gln Asp Gly Ala Asp Ser Ala Asn Phe
                85   90   95
Met Ile Ser Leu Glu Lys Val Ala Asp Gly Ile Thr Gly Trp Glu Asn
            100   105   110
Leu Val Arg Gly Thr Val Lys Lys Gly Glu Trp Thr Thr Leu Ser Gly
        115   120   125
Thr Tyr Thr Phe Ala Asp Tyr Glu Ser Tyr Val Leu Tyr Val Glu Thr
    130   135   140
Ser Asp Ala Pro Thr Leu Asp Phe Glu Ile Arg Asn Phe Arg Val Glu
145   150   155   160
Ser Pro Asn Gly Ile Pro Glu Pro Lys Ala Thr Glu Ala Pro Ala Val
                165   170   175
Val Ser Glu Ala Thr Asp Ile Pro Ser Leu Lys Asp Ala Tyr Ala Asp
            180   185   190
Tyr Phe Asp Phe Gly Ala Ala Val Pro Gln Ser Ala Phe Thr Ser Arg
        195   200   205
Asp Asn Ile Gln Leu Met Glu Leu Met Lys Asn Gln Phe Ser Ile Leu
    210   215   220
Thr Pro Glu Asn Glu Leu Lys Pro Asp Ser Val Leu Asp Val Ser Ala
225   230   235   240
Ser Lys Gln Leu Ala Lys Glu Asp Glu Thr Ala Val Val Val Arg Phe
                245   250   255
Asn Gly Ala Lys Ser Leu Leu Arg Phe Ala Gln Gln Asn Gly Ile Lys
            260   265   270
Val His Gly His Val Leu Val Trp His Ser Gln Thr Pro Glu Ala Phe
        275   280   285
Phe His Glu Gly Tyr Asp Pro Lys Asn Pro Leu Val Ser Arg Glu Val
    290   295   300
Met Leu Gly Arg Leu Glu Asn Tyr Ile Arg Glu Val Leu Thr Gln Thr
305   310   315   320
Glu Glu Leu Tyr Pro Gly Val Ile Val Ser Trp Asp Val Val Asn Glu
                325   330   335
Ala Ile Asp Asp Gly Thr Asn Trp Ile Arg Lys Gly Ser Gly Trp Tyr
            340   345   350
Arg Thr Ile Gly Glu Asp Tyr Val Glu Lys Ala Phe Glu Phe Ala Arg
        355   360   365
Lys Tyr Ala Pro Glu Gly Val Leu Leu Tyr Tyr Asn Asp Tyr Asn Thr
    370   375   380
Ala Tyr Ala Gly Lys Leu Asn Gly Ile Ile Lys Leu Ile Lys Pro Met
385   390   395   400
Ile Glu Gln Gly Thr Ile Asp Gly Tyr Gly Phe Gln Met His His Thr
                405   410   415
Thr Gly Gln Pro Ser Asn Gln Met Ile Thr Thr Ala Val Glu Lys Ile
            420   425   430
Ala Ala Leu Gly Ile Lys Leu Arg Val Ser Glu Met Asp Ile Gly Ile
        435   440   445
Thr Lys Tyr Thr Glu Thr Ser Leu Gln Ala Gln Lys Asp Lys Tyr Lys
    450   455   460
Ala Met Met Glu Leu Met Leu Arg Phe Ala Asp Gln Thr Glu Ala Val
465   470   475   480
Gln Val Trp Gly Ile Thr Asp Thr Met Ser Trp Arg Ser Ser Ser Tyr

```
                485                 490                 495
Pro Leu Leu Phe Asp Arg Ser Arg Asn Pro Lys Pro Ala Phe Tyr Gly
            500                 505                 510
Val Ile Glu Ala Val Glu Asp Trp Thr Gly Lys Ser Glu
        515                 520                 525
```

<210> 59
<211> 1104
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 59

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atgcttgcca gtagtgccgg tttggtagca tcccaactca agctgtccgc gttagctgca      60
gctaaaaatg ctggattaaa agatgtatat aaggatcgct ttctgattgg tgcagcaatt     120
aatacctcga ttgcgagcgg ccagcaacct gatattacag aaattatcaa gcgtgatttt     180
tcgtcgttaa cacctgaaaa tgcaatgaag tgggaatctg tcaggactgc tgatggcgga     240
tggaaatggg cagatgccga tcaattcgtt acgtttgcaa cagaacacaa aatacacgct     300
gttggccaca cccttgcctg gcatagccag attcccgatt ccgtattcaa aaatgaaaaa     360
ggcgaataca taaaatccac cgagctatca aaaaaaatgg aagaacatat cactacgatt     420
gtaggtagat ataaaggcaa actcgatgcc tgggatgtag ttaatgaggc tgttggtgat     480
gataatcaaa tgcgcaaaag ccattattac aatattctcg gcgaagattt tattgataag     540
gcatttcacc ttgcgcatga ggtcgatccc aaagcgcatt taatgtataa cgactacaac     600
attgaaaaag atggcaagcg tgaagctacc cttgaaatgt taaagcgttt acaaaaacgc     660
ggtgtaccga ttcatgggct cggcatccag ggacatattg ccgttgatgg ccccagcatt     720
gcggatattg aaaaaagtat tttggcttat gcggatttgg gtttgcgtgt acatttcacc     780
gagttggata ttgatgtatt gccgcaaatc tggaacttac cggttgcaga aatttctaca     840
cgcttcgaat acaaacctga gcgagatcct ttcaaaaatg gtttatcaaa agaaatgaac     900
gataaactca gtgcacgcta tgaagaatta ttcacattat ttattaaaca caaagataaa     960
attgatcgta ttactttgtg ggtgtcagc gatgatgcaa cctggctaaa tgatttcccc    1020
atcaaaggca gaaccagtta tccattattg tttgatcgca agcatcaacc aaaagatgct    1080
tattataaca ttctggcgtt gtga                                            1104
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<210> 60
<211> 367
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(21)

<400> 60

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Met Leu Ala Ser Ser Ala Gly Leu Val Ala Ser Gln Leu Lys Leu Ser
 1               5                  10                  15
Ala Leu Ala Ala Ala Lys Asn Ala Gly Leu Lys Asp Val Tyr Lys Asp
            20                  25                  30
Arg Phe Leu Ile Gly Ala Ala Ile Asn Thr Ser Ile Ala Ser Gly Gln
        35                  40                  45
Gln Pro Asp Ile Thr Glu Ile Ile Lys Arg Asp Phe Ser Ser Leu Thr
    50                  55                  60
Pro Glu Asn Ala Met Lys Trp Glu Ser Val Arg Thr Ala Asp Gly Gly
65                  70                  75                  80
Trp Lys Trp Ala Asp Ala Asp Gln Phe Val Thr Phe Ala Thr Glu His
                85                  90                  95
Lys Ile His Ala Val Gly His Thr Leu Ala Trp His Ser Gln Ile Pro
            100                 105                 110
Asp Ser Val Phe Lys Asn Glu Lys Gly Glu Tyr Ile Lys Ser Thr Glu
        115                 120                 125
Leu Ser Lys Lys Met Glu Glu His Ile Thr Thr Ile Val Gly Arg Tyr
    130                 135                 140
Lys Gly Lys Leu Asp Ala Trp Asp Val Val Asn Glu Ala Val Gly Asp
145                 150                 155                 160
Asp Asn Gln Met Arg Lys Ser His Tyr Tyr Asn Ile Leu Gly Glu Asp
                165                 170                 175
```

Phe Ile Asp Lys Ala Phe His Leu Ala His Glu Val Asp Pro Lys Ala
180 185 190
His Leu Met Tyr Asn Asp Tyr Asn Ile Glu Lys Asp Gly Lys Arg Glu
195 200 205
Ala Thr Leu Glu Met Leu Lys Arg Leu Gln Lys Arg Gly Val Pro Ile
210 215 220
His Gly Leu Gly Ile Gln Gly His Ile Ala Val Asp Gly Pro Ser Ile
225 230 235 240
Ala Asp Ile Glu Lys Ser Ile Leu Ala Tyr Ala Asp Leu Gly Leu Arg
245 250 255
Val His Phe Thr Glu Leu Asp Ile Asp Val Leu Pro Gln Ile Trp Asn
260 265 270
Leu Pro Val Ala Glu Ile Ser Thr Arg Phe Glu Tyr Lys Pro Glu Arg
275 280 285
Asp Pro Phe Lys Asn Gly Leu Ser Lys Glu Met Asn Asp Lys Leu Ser
290 295 300
Ala Arg Tyr Glu Glu Leu Phe Thr Leu Phe Ile Lys His Lys Asp Lys
305 310 315 320
Ile Asp Arg Ile Thr Leu Trp Gly Val Ser Asp Asp Ala Thr Trp Leu
325 330 335
Asn Asp Phe Pro Ile Lys Gly Arg Thr Ser Tyr Pro Leu Leu Phe Asp
340 345 350
Arg Lys His Gln Pro Lys Asp Ala Tyr Tyr Asn Ile Leu Ala Leu
355 360 365

<210> 61
<211> 1041
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 61
atgagaagaa gcatggaaag gctgcccaag ctccatgaag cttacggcaa tagtttcaag 60
atcggcgctg ccgtgaatcc aattacgatg gtgacccaaa aggaattgtt gtcacaccac 120
ttcaacagcg ttacggcaga aaatgaaatg aaattcgagc gattgcaccc atcggaagag 180
gtgtatacat tcgagcaagc cgaccagatc gtatcgtttg ccaaatcgaa cggaatgtcg 240
gtgagaggac ataccctcgt atggcataat cagacgccgg aatgggtgtt tcaagacagt 300
tccggtggga cagccggccg cgagctgctg ctcgctcgga tgaaatcgca catcgatgag 360
gtcgttggcc gttatcgcgg agatatctat gcttgggatg tcgtaaacga agccattgcc 420
gacagtggaa gcgatctgct tcgttcctcc ccgtggcttg cgtcgatcgg ggaggatttt 480
atcgccaagg ctttcgaata tgcgcacgaa gcagacccgc aagcgctgct gttttataac 540
gattacaacg aatccgtgcc cgagaagcgg gagaagattt acacgctcct taaatcgtta 600
aaggagcagg atgtgccgat tcacggcgtc gggcttcagg cccattggaa tttggagttt 660
ccatcgcttg acgatatccg cagggcaatc gaaaggtatg caagccttgg catgatcttg 720
catatcacgg agcttgacgt atccgtattc gcgcatgagg ataagcggac cgatctggcg 780
gcgccgaccg aagaaatgct tgagcgccag gcggagcgtt acggtcaatt gttccgtctg 840
cttaaagagt acagcggcag cgtcacttcc gtgaccttct ggggagcggc ggacgattat 900
acctggctgg atcattttcc ggtaaggggc cgcaaaaatt ggccgttcgt cttcgacgag 960
aaccatcttc cgaaggaatc ctattggaac ctgttgaagg aagccaatcc cgaaagaaca 1020
ttccaagaga tacgttcgta a 1041

<210> 62
<211> 346
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 62
Met Arg Arg Ser Met Glu Arg Leu Pro Lys Leu His Glu Ala Tyr Gly
1 5 10 15
Asn Ser Phe Lys Ile Gly Ala Ala Val Asn Pro Ile Thr Met Val Thr
20 25 30
Gln Lys Glu Leu Leu Ser His His Phe Asn Ser Val Thr Ala Glu Asn
35 40 45
Glu Met Lys Phe Glu Arg Leu His Pro Ser Glu Glu Val Tyr Thr Phe

50 55 60
Glu Gln Ala Asp Gln Ile Val Ser Phe Ala Lys Ser Asn Gly Met Ser
65 70 75 80
Val Arg Gly His Thr Leu Val Trp His Asn Gln Thr Pro Glu Trp Val
85 90 95
Phe Gln Asp Ser Ser Gly Gly Thr Ala Gly Arg Glu Leu Leu Leu Ala
100 105 110
Arg Met Lys Ser His Ile Asp Glu Val Val Gly Arg Tyr Arg Gly Asp
115 120 125
Ile Tyr Ala Trp Asp Val Val Asn Glu Ala Ile Ala Asp Ser Gly Ser
130 135 140
Asp Leu Leu Arg Ser Ser Pro Trp Leu Ala Ser Ile Gly Glu Asp Phe
145 150 155 160
Ile Ala Lys Ala Phe Glu Tyr Ala His Glu Ala Asp Pro Gln Ala Leu
165 170 175
Leu Phe Tyr Asn Asp Tyr Asn Glu Ser Val Pro Glu Lys Arg Glu Lys
180 185 190
Ile Tyr Thr Leu Leu Lys Ser Leu Lys Glu Gln Asp Val Pro Ile His
195 200 205
Gly Val Gly Leu Gln Ala His Trp Asn Leu Glu Phe Pro Ser Leu Asp
210 215 220
Asp Ile Arg Arg Ala Ile Glu Arg Tyr Ala Ser Leu Gly Met Ile Leu
225 230 235 240
His Ile Thr Glu Leu Asp Val Ser Val Phe Ala His Glu Asp Lys Arg
245 250 255
Thr Asp Leu Ala Ala Pro Thr Glu Glu Met Leu Glu Arg Gln Ala Glu
260 265 270
Arg Tyr Gly Gln Leu Phe Arg Leu Leu Lys Glu Tyr Ser Gly Ser Val
275 280 285
Thr Ser Val Thr Phe Trp Gly Ala Ala Asp Asp Tyr Thr Trp Leu Asp
290 295 300
His Phe Pro Val Arg Gly Arg Lys Asn Trp Pro Phe Val Phe Asp Glu
305 310 315 320
Asn His Leu Pro Lys Glu Ser Tyr Trp Asn Leu Leu Lys Glu Ala Asn
325 330 335
Pro Glu Arg Thr Phe Gln Glu Ile Arg Ser
340 345

<210> 63
<211> 1110
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 63
atgaaacgaa ttttaattgg tttggcggct cttaccgctt ccgggctgtc ggcgcagaaa 60
tccgacggta ctttaaaaaa agcatttcag gataaattct atatcgggac tgcgatgagt 120
cttcctcaga ttgatgggac agataaaaga gcggtagcca ttatcagaaa tcagttcagt 180
tctattgttg ctgaaaactg tatgaaatcg atgtttctgc aacctcagga aggaaagttc 240
ttctttgatg acgctgataa atttgttgat ttcgggatga aaaacaatat gttcgtcatc 300
ggacatacgc taatctggca ttcccagctt ccaaaatggt tttttacaga taaaaatgga 360
aaagatgttt ctccggaagt attgaaacag cgcatgaaaa accacattac aaccgtagtt 420
tcccgttaca aggaaaaagt aaaaggatgg gatgtggtga atgaagccat tcttgaagac 480
ggaacctata gaaaaagtaa attttacgaa attctgggtg aagattttat tcctttggcg 540
tttcagtatg cacaggaagc cgatcccaat gcagaattat attacaacga ttataatgaa 600
tggtatccgg aaaaggtaaa agcagtcatt acaatggttg aaaagcttaa atcaagagga 660
atccgtattg atggagtagg aatgcaggcc catgtcggaa tggatatccc ttccatcaat 720
gaatatgaaa aagcaattct ggcgtattcc aatgccggag ttaaagttaa tattacggag 780
ctggaaatta gtgcgctgcc ttctccgtgg ggaagctctg ccaatgtttc agataccgtt 840
gcctatcaga aagaaatgaa tccttacacc aaagggcttc ccaatgaagt agaagcgaaa 900
tgggaaaaac gttaccttga tttctttagc ttgtttttaa aacataaaga taaaataaga 960
agggtgacct tatggggagt tactgataag cagtcctgga aaaacgattt tccggtaaaa 1020
ggaagaacag attacccgtt gctgtttgac aggaaagatc aggagaaacc tgtagtacaa 1080
aaaataataa aattggcaga gaaaaattaa 1110

<210> 64
<211> 369

<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(20)

<400> 64
Met Lys Arg Ile Leu Ile Gly Leu Ala Ala Leu Thr Ala Ser Gly Leu
1 5 10 15
Ser Ala Gln Lys Ser Asp Gly Thr Leu Lys Lys Ala Phe Gln Asp Lys
20 25 30
Phe Tyr Ile Gly Thr Ala Met Ser Leu Pro Gln Ile Asp Gly Thr Asp
35 40 45
Lys Arg Ala Val Ala Ile Ile Arg Asn Gln Phe Ser Ser Ile Val Ala
50 55 60
Glu Asn Cys Met Lys Ser Met Phe Leu Gln Pro Gln Glu Gly Lys Phe
65 70 75 80
Phe Phe Asp Asp Ala Asp Lys Phe Val Asp Phe Gly Met Lys Asn Asn
85 90 95
Met Phe Val Ile Gly His Thr Leu Ile Trp His Ser Gln Leu Pro Lys
100 105 110
Trp Phe Phe Thr Asp Lys Asn Gly Lys Asp Val Ser Pro Glu Val Leu
115 120 125
Lys Gln Arg Met Lys Asn His Ile Thr Thr Val Val Ser Arg Tyr Lys
130 135 140
Gly Lys Val Lys Gly Trp Asp Val Val Asn Glu Ala Ile Leu Glu Asp
145 150 155 160
Gly Thr Tyr Arg Lys Ser Lys Phe Tyr Glu Ile Leu Gly Glu Asp Phe
165 170 175
Ile Pro Leu Ala Phe Gln Tyr Ala Gln Glu Ala Asp Pro Asn Ala Glu
180 185 190
Leu Tyr Tyr Asn Asp Tyr Asn Glu Trp Tyr Pro Glu Lys Val Lys Ala
195 200 205
Val Ile Thr Met Val Glu Lys Leu Lys Ser Arg Gly Ile Arg Ile Asp
210 215 220
Gly Val Gly Met Gln Ala His Val Gly Met Asp Ile Pro Ser Ile Asn
225 230 235 240
Glu Tyr Glu Lys Ala Ile Leu Ala Tyr Ser Asn Ala Gly Val Lys Val
245 250 255
Asn Ile Thr Glu Leu Glu Ile Ser Ala Leu Pro Ser Pro Trp Gly Ser
260 265 270
Ser Ala Asn Val Ser Asp Thr Val Ala Tyr Gln Lys Glu Met Asn Pro
275 280 285
Tyr Thr Lys Gly Leu Pro Asn Glu Val Glu Ala Lys Trp Glu Lys Arg
290 295 300
Tyr Leu Asp Phe Phe Ser Leu Phe Leu Lys His Lys Asp Lys Ile Arg
305 310 315 320
Arg Val Thr Leu Trp Gly Val Thr Asp Lys Gln Ser Trp Lys Asn Asp
325 330 335
Phe Pro Val Lys Gly Arg Thr Asp Tyr Pro Leu Leu Phe Asp Arg Lys
340 345 350
Asp Gln Glu Lys Pro Val Val Gln Lys Ile Ile Lys Leu Ala Glu Lys
355 360 365
Asn

<210> 65
<211> 1557
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 65
atgaaaagaa tcggactgtt gctgctggct gtgatcatgc ttgtggctg tgtatattcc 60

gcggcggcgg aggatacgct ggtttatgct tccacttttg tggccggaac ggacggatgg 120
tacgcccgcg gagcgcagaa agtataccgc acaaccgagg agacactgcg gacggaaggc 180
cggaccagcg actggcattc cccgggccgt gattttgacc tggtggaagg cggcgtctat 240
gtcctgagcg tggaagtgtt ccaggacgaa gcggacaacg ccagcttcat gatttccatc 300
gcccacagca aggacggtac ggaaacctat gaaaacctgg ctcgcggaac cgccaaacgc 360
ggcgagtggg tcaccctgac cggaacatat accgccggca attttgaccg gaacgtcctg 420
tatgtggaaa cgaccggatc gccggaactg agctatgaaa tccggaattt ccgggttgaa 480
gcgccgaacg gagttccgga gccgaaggct acggagcccc cgatggtgat tgaggcggtg 540
gagaacctcc cgggcctgaa gaacgcgtat gcgggaaaat ttgatttcgg cgcggcggtt 600
ccgggatacg ctttcggcga tccgggcctg aaacagctga tgactgagca gttcagcatc 660
ctgacgcccg aaaacgaact gaaaccggac gctgtgctgg acgtggcggc gagcaagcgg 720
ctggcccagg aggatgaaac ggcggtggcg gttcattttg acggcgccat tccgctgctg 780
aactttgccc gggacaacgg catcagggtg cacggacatg tgctgatctg gcacagccag 840
acgccggaag cgttcttcca tgagggctat gacacctcca agcccctggt cagccgggaa 900
gtgatgctgg gccggatgga aaactatatc cgcgaggtgc tgacctggac gaacgagaat 960
tatccgggcg tgatcgtatc ctgggacgtg gtgaacgaag ccattgatga cggaacgaac 1020
tggctgcgga attccaactg gtacaagacg gtgggcggcg actttgtgaa ccgggctttt 1080
gaatttgccc gcatgtacgc ggcggacggc gtcctcctgt attacaatga ttacaatacc 1140
gcctatccgg ccaaacggaa gggaatcatc aagctgctgg gccagctgat tgaggaaggc 1200
aatattgacg gatacggctt ccagatgcat cacagcaccg gcgagccttc catggagatg 1260
atcaccgctt cggtggagga aatcgccgcg ctgggaataa aactgcgggt cagcgagctg 1320
gatgtgggca tgggcagcag catgacggaa gaagccctga tgaaacagaa ggacaaatac 1380
aaggcggtca tggaactgat gctgcggttt gccgaccaga cggaagcggt gcaggtatgg 1440
ggactgacgg acaatatgag ctggcggacc ggccagaatc cgctgctgtt tgaccggaac 1500
cggaacccga agccggcctt cttcggcgtc ctggaagcgg cggaagaaag caaataa 1557

<210> 66
<211> 518
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<400> 66
Met Lys Arg Ile Gly Leu Leu Leu Leu Ala Val Ile Met Leu Val Gly
1 5 10 15
Cys Val Tyr Ser Ala Ala Ala Glu Asp Thr Leu Val Tyr Ala Ser Thr
20 25 30
Phe Val Ala Gly Thr Asp Gly Trp Tyr Ala Arg Gly Ala Gln Lys Val
35 40 45
Tyr Arg Thr Thr Glu Glu Thr Leu Arg Thr Glu Gly Arg Thr Ser Asp
50 55 60
Trp His Ser Pro Gly Arg Asp Phe Asp Leu Val Glu Gly Gly Val Tyr
65 70 75 80
Val Leu Ser Val Glu Val Phe Gln Asp Glu Ala Asp Asn Ala Ser Phe
85 90 95
Met Ile Ser Ile Ala His Ser Lys Asp Gly Thr Glu Thr Tyr Glu Asn
100 105 110
Leu Ala Arg Gly Thr Ala Lys Arg Gly Glu Trp Val Thr Leu Thr Gly
115 120 125
Thr Tyr Thr Ala Gly Asn Phe Asp Arg Asn Val Leu Tyr Val Glu Thr
130 135 140
Thr Gly Ser Pro Glu Leu Ser Tyr Glu Ile Arg Asn Phe Arg Val Glu
145 150 155 160
Ala Pro Asn Gly Val Pro Glu Pro Lys Ala Thr Glu Pro Pro Met Val
165 170 175
Ile Glu Ala Val Glu Asn Leu Pro Gly Leu Lys Asn Ala Tyr Ala Gly
180 185 190
Lys Phe Asp Phe Gly Ala Ala Val Pro Gly Tyr Ala Phe Gly Asp Pro
195 200 205
Gly Leu Lys Gln Leu Met Thr Glu Gln Phe Ser Ile Leu Thr Pro Glu
210 215 220
Asn Glu Leu Lys Pro Asp Ala Val Leu Asp Val Ala Ala Ser Lys Arg
225 230 235 240
Leu Ala Gln Glu Asp Glu Thr Ala Val Ala Val His Phe Asp Gly Ala

```
                245                 250                 255
Ile Pro Leu Leu Asn Phe Ala Arg Asp Asn Gly Ile Arg Val His Gly
            260                 265                 270
His Val Leu Ile Trp His Ser Gln Thr Pro Glu Ala Phe Phe His Glu
        275                 280                 285
Gly Tyr Asp Thr Ser Lys Pro Leu Val Ser Arg Glu Val Met Leu Gly
    290                 295                 300
Arg Met Glu Asn Tyr Ile Arg Glu Val Leu Thr Trp Thr Asn Glu Asn
305                 310                 315                 320
Tyr Pro Gly Val Ile Val Ser Trp Asp Val Val Asn Glu Ala Ile Asp
                325                 330                 335
Asp Gly Thr Asn Trp Leu Arg Asn Ser Asn Trp Tyr Lys Thr Val Gly
            340                 345                 350
Gly Asp Phe Val Asn Arg Ala Phe Glu Phe Ala Arg Met Tyr Ala Ala
        355                 360                 365
Asp Gly Val Leu Leu Tyr Tyr Asn Asp Tyr Asn Thr Ala Tyr Pro Ala
    370                 375                 380
Lys Arg Lys Gly Ile Ile Lys Leu Leu Gly Gln Leu Ile Glu Glu Gly
385                 390                 395                 400
Asn Ile Asp Gly Tyr Gly Phe Gln Met His His Ser Thr Gly Glu Pro
                405                 410                 415
Ser Met Glu Met Ile Thr Ala Ser Val Glu Glu Ile Ala Ala Leu Gly
            420                 425                 430
Ile Lys Leu Arg Val Ser Glu Leu Asp Val Gly Met Gly Ser Ser Met
        435                 440                 445
Thr Glu Glu Ala Leu Met Lys Gln Lys Asp Lys Tyr Lys Ala Val Met
    450                 455                 460
Glu Leu Met Leu Arg Phe Ala Asp Gln Thr Glu Ala Val Gln Val Trp
465                 470                 475                 480
Gly Leu Thr Asp Asn Met Ser Trp Arg Thr Gly Gln Asn Pro Leu Leu
                485                 490                 495
Phe Asp Arg Asn Arg Asn Pro Lys Pro Ala Phe Phe Gly Val Leu Glu
            500                 505                 510
Ala Ala Glu Glu Ser Lys
        515
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<210> 67
<211> 1224
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 67

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atgcggaacg tcgtgcgtaa accattgaca atcggactcg ctttaacact attattgccc      60
atgggaatga cggcaacatc agcgaagaat gcagattcct atgcgaaaaa acctcacatc     120
agcgcattga atgccccaca attggatcaa cgctacaaaa acgagttcac gattggtgcg     180
gcagtagaac cttatcaact acaaaatgaa aaagacgtac aaatgctaaa gcgccacttc     240
aacagcattg ttgccgagaa cgtaatgaaa ccgatcagca ttcaacctga ggaaggaaaa     300
ttcaattttg aacaagcgga tcgaattgtg aagttcgcta aggcaaatgg catggatatt     360
cgcttccata cactcgtttg gcacagccaa gtacctcaat ggttctttct tgacaaggaa     420
ggcaagccaa tggttaatga aacagatcca gtgaaacgtg aacaaaataa acaactgctg     480
ttaaaacgac ttgaaactca tattaaaacg atcgtcgagc ggtacaaaga tgacattaag     540
tactgggacg ttgtaaatga ggttgtgggg gacgacggaa aactgcgcaa ctctccatgg     600
tatcaaatcg ccggcatcga ttatattaaa gtggcattcc aaacagcgag aaaatatggc     660
ggcaacaaga ttaaacttta tatcaatgat tacaataccg aagtggaacc aaagcgaagc     720
gctctttata acttggtgaa gcaattaaaa gaagagggcg ttcctattga cggcatcggc     780
catcaatccc acattcaaat cggctggcct tctgaagcag aaatcgagaa aacgattaac     840
atgttcgccg ctctcggctt agacaaccaa atcactgagc ttgatgtgag catgtacggt     900
tggccgccgc gcgcttaccc gacgtatgac gccattccaa aacaaaagtt tttggatcag     960
gcagcgcgct atgatcgttt gttcaaactg tatgaaaagt tgagcgataa aattagcaac    1020
gtcaccttct ggggcatcgc cgacaatcat acgtggctcg acagccgtgc ggatgtgtac    1080
tatgacgcca acgggaatgt tgtggttgac ccgaacgctc cgtacgcaaa agtggaaaaa    1140
gggaaaggaa aagatgcgcc gttcgttttt ggaccggatt acaaagtcaa acccgcatat    1200
tgggctatta tcgaccacaa atag                                           1224
```

<210> 68
<211> 407

<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<400> 68
Met Arg Asn Val Val Arg Lys Pro Leu Thr Ile Gly Leu Ala Leu Thr
1 5 10 15
Leu Leu Leu Pro Met Gly Met Thr Ala Thr Ser Ala Lys Asn Ala Asp
20 25 30
Ser Tyr Ala Lys Lys Pro His Ile Ser Ala Leu Asn Ala Pro Gln Leu
35 40 45
Asp Gln Arg Tyr Lys Asn Glu Phe Thr Ile Gly Ala Ala Val Glu Pro
50 55 60
Tyr Gln Leu Gln Asn Glu Lys Asp Val Gln Met Leu Lys Arg His Phe
65 70 75 80
Asn Ser Ile Val Ala Glu Asn Val Met Lys Pro Ile Ser Ile Gln Pro
85 90 95
Glu Glu Gly Lys Phe Asn Phe Glu Gln Ala Asp Arg Ile Val Lys Phe
100 105 110
Ala Lys Ala Asn Gly Met Asp Ile Arg Phe His Thr Leu Val Trp His
115 120 125
Ser Gln Val Pro Gln Trp Phe Phe Leu Asp Lys Glu Gly Lys Pro Met
130 135 140
Val Asn Glu Thr Asp Pro Val Lys Arg Glu Gln Asn Lys Gln Leu Leu
145 150 155 160
Leu Lys Arg Leu Glu Thr His Ile Lys Thr Ile Val Glu Arg Tyr Lys
165 170 175
Asp Asp Ile Lys Tyr Trp Asp Val Val Asn Glu Val Val Gly Asp Asp
180 185 190
Gly Lys Leu Arg Asn Ser Pro Trp Tyr Gln Ile Ala Gly Ile Asp Tyr
195 200 205
Ile Lys Val Ala Phe Gln Thr Ala Arg Lys Tyr Gly Gly Asn Lys Ile
210 215 220
Lys Leu Tyr Ile Asn Asp Tyr Asn Thr Glu Val Glu Pro Lys Arg Ser
225 230 235 240
Ala Leu Tyr Asn Leu Val Lys Gln Leu Lys Glu Glu Gly Val Pro Ile
245 250 255
Asp Gly Ile Gly His Gln Ser His Ile Gln Ile Gly Trp Pro Ser Glu
260 265 270
Ala Glu Ile Glu Lys Thr Ile Asn Met Phe Ala Ala Leu Gly Leu Asp
275 280 285
Asn Gln Ile Thr Glu Leu Asp Val Ser Met Tyr Gly Trp Pro Pro Arg
290 295 300
Ala Tyr Pro Thr Tyr Asp Ala Ile Pro Lys Gln Lys Phe Leu Asp Gln
305 310 315 320
Ala Ala Arg Tyr Asp Arg Leu Phe Lys Leu Tyr Glu Lys Leu Ser Asp
325 330 335
Lys Ile Ser Asn Val Thr Phe Trp Gly Ile Ala Asp Asn His Thr Trp
340 345 350
Leu Asp Ser Arg Ala Asp Val Tyr Tyr Asp Ala Asn Gly Asn Val Val
355 360 365
Val Asp Pro Asn Ala Pro Tyr Ala Lys Val Glu Lys Gly Lys Gly Lys
370 375 380
Asp Ala Pro Phe Val Phe Gly Pro Asp Tyr Lys Val Lys Pro Ala Tyr
385 390 395 400
Trp Ala Ile Ile Asp His Lys
405

<210> 69
<211> 1596
<212> DNA
<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 69
atggcgatgc atagatttaa gcaattaggg gccatcctac ttgtcctatg gttttgtgca 60
ttgccagtgc aggcgcaggc ttggcgtgcg gccgcagagc agcgtattga acagtaccgt 120
aaggggccac tgcgggttca ggtgaaggat cctgaaggac ggcccgtacc gaatgcccaa 180
gtgcacgttc gcatgacgcg tcacgctttt ggatttggta cggctgtcag ctttggcctg 240
gtcgtggggt cgggatacaa ccccacctat cgggccaagc tagaagacct gacgggcgac 300
ggccgcacat tcaacatggc tacgccagag aatgaattga agtggcctgc gtgggagtcg 360
gaatggccca tttcgaatcg tcgaaagatc gacgtcatca actggctgcg cgcaaaaggc 420
tacagcattc gaggacacaa cctgctatgg cctgactggc aatggatgcc ccgtgatatt 480
gagcaaaacc gcaacaatcc acagtacatc tacgatcgcg ttcgcaatca cattgcggcg 540
ttggctgggc atcgggacat tcggggcaaa ctgcgggact gggatgttct taacgaacca 600
gcccacctga ccgcattgcg cgatgtgttt aacggttggg gctcatatga gcgtggggaa 660
gacttctatg tggatgtctt taggtgggcc aaggcagcag actcgaccgc ccgtctatac 720
atcaacgagt acaacattat caacaactac gccaacgagc agcctacgcg caactattac 780
aagtggatca ttgcacgcct aatctcaaaa ggagcgccta tcgaagggat cggcattcag 840
gggcatattt cggcaccact gccaagcatg agtgaggtca aggcagccct agacgaaatg 900
gcagtttttg gattgccttt ggccatcaca gaatacgacg ttaccggcgt ttcggaagaa 960
gtcgaagcca actttatgcg ggactttttg accatggtct ttagtcatcc cgctgtggag 1020
agcttcgtca tgtggggttt ctggagcgga gcacactggc gtgacaatgc gccgctgttt 1080
cgggccgact ggagtctcaa gccttcggga caggtgttcc ttgatctggt ctttcggcgc 1140
tggtggaccg atactacggg ggtaaccggt ccagatggca gctggtctgt acgcggattt 1200
ttaggggatt acgttgtgga agtgcaggtg ggggaggttt cagtgaccaa gtccctgcgc 1260
ctcgaaagcc cgcaggatac aaccacgcta gaggtggtgg tcagtagcgt taaggtgggt 1320
gaaaagccta cagaagacgt gttgcgcgtg caagggtttg gaccagaccc ctttgtcgaa 1380
ggaacggcgc tgcgctactg gttagggcgg ccggccgatg ttgaactggc agtgtatgat 1440
gtgctgggcc gacaggtcta cgccgtgcaa aagcatcgcg tagctggttg gcatactgaa 1500
tgggtcgagg cttcccactg gcctgcagga ctttatctgt accgactcca agcaggtgat 1560
ctgttgcaca cgggtagaat ggtcaagatc caataa 1596

<210> 70
<211> 531
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(25)

<400> 70
Met Ala Met His Arg Phe Lys Gln Leu Gly Ala Ile Leu Leu Val Leu
1   5   10   15
Trp Phe Cys Ala Leu Pro Val Gln Ala Gln Ala Trp Arg Ala Ala Ala
            20   25   30
Glu Gln Arg Ile Glu Gln Tyr Arg Lys Gly Pro Leu Arg Val Gln Val
        35   40   45
Lys Asp Pro Glu Gly Arg Pro Val Pro Asn Ala Gln Val His Val Arg
    50   55   60
Met Thr Arg His Ala Phe Gly Phe Gly Thr Ala Val Ser Phe Gly Leu
65   70   75   80
Val Val Gly Ser Gly Tyr Asn Pro Thr Tyr Arg Ala Lys Leu Glu Asp
                85   90   95
Leu Thr Gly Asp Gly Arg Thr Phe Asn Met Ala Thr Pro Glu Asn Glu
            100   105   110
Leu Lys Trp Pro Ala Trp Glu Ser Glu Trp Pro Ile Ser Asn Arg Arg
        115   120   125
Lys Ile Asp Val Ile Asn Trp Leu Arg Ala Lys Gly Tyr Ser Ile Arg
    130   135   140
Gly His Asn Leu Leu Trp Pro Asp Trp Gln Trp Met Pro Arg Asp Ile
145   150   155   160
Glu Gln Asn Arg Asn Asn Pro Gln Tyr Ile Tyr Asp Arg Val Arg Asn
                165   170   175
His Ile Ala Ala Leu Ala Gly His Arg Asp Ile Arg Gly Lys Leu Arg
            180   185   190
Asp Trp Asp Val Leu Asn Glu Pro Ala His Leu Thr Ala Leu Arg Asp
        195   200   205

Val Phe Asn Gly Trp Gly Ser Tyr Glu Arg Gly Glu Asp Phe Tyr Val
210 215 220
Asp Val Phe Arg Trp Ala Lys Ala Ala Asp Ser Thr Ala Arg Leu Tyr
225 230 235 240
Ile Asn Glu Tyr Asn Ile Ile Asn Asn Tyr Ala Asn Glu Gln Pro Thr
245 250 255
Arg Asn Tyr Tyr Lys Trp Ile Ile Ala Arg Leu Ile Ser Lys Gly Ala
260 265 270
Pro Ile Glu Gly Ile Gly Ile Gln Gly His Ile Ser Ala Pro Leu Pro
275 280 285
Ser Met Ser Glu Val Lys Ala Ala Leu Asp Glu Met Ala Val Phe Gly
290 295 300
Leu Pro Leu Ala Ile Thr Glu Tyr Asp Val Thr Gly Val Ser Glu Glu
305 310 315 320
Val Glu Ala Asn Phe Met Arg Asp Phe Leu Thr Met Val Phe Ser His
325 330 335
Pro Ala Val Glu Ser Phe Val Met Trp Gly Phe Trp Ser Gly Ala His
340 345 350
Trp Arg Asp Asn Ala Pro Leu Phe Arg Ala Asp Trp Ser Leu Lys Pro
355 360 365
Ser Gly Gln Val Phe Leu Asp Leu Val Phe Arg Arg Trp Trp Thr Asp
370 375 380
Thr Thr Gly Val Thr Gly Pro Asp Gly Ser Trp Ser Val Arg Gly Phe
385 390 395 400
Leu Gly Asp Tyr Val Val Glu Val Gln Val Gly Glu Val Ser Val Thr
405 410 415
Lys Ser Leu Arg Leu Glu Ser Pro Gln Asp Thr Thr Thr Leu Glu Val
420 425 430
Val Val Ser Ser Val Lys Val Gly Glu Lys Pro Thr Glu Asp Val Leu
435 440 445
Arg Val Gln Gly Phe Gly Pro Asp Pro Phe Val Glu Gly Thr Ala Leu
450 455 460
Arg Tyr Trp Leu Gly Arg Pro Ala Asp Val Glu Leu Ala Val Tyr Asp
465 470 475 480
Val Leu Gly Arg Gln Val Tyr Ala Val Gln Lys His Arg Val Ala Gly
485 490 495
Trp His Thr Glu Trp Val Glu Ala Ser His Trp Pro Ala Gly Leu Tyr
500 505 510
Leu Tyr Arg Leu Gln Ala Gly Asp Leu Leu His Thr Gly Arg Met Val
515 520 525
Lys Ile Gln
530

<210> 71
<211> 1269
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 71
atgatttcca tcgcccattc agtgaacggg gcggagacct atgagaacct ggcgcacgga 60
actgccaaaa aaggcgaatg gactacgctg aaggggacat acaccgccgg cgcctatcag 120
cgcaacgtgc tctatgtgga aacggtttct gaaggcaccc ttgactttga gatccgtaat 180
tttgtcctga cggctccgaa cggactaccg gagcccaagc cgaccgagcc tccgatggtc 240
atcgaggaag ccgagaacgt gcccagtctc aaagagattt atgcagacaa attcgatttc 300
ggctccgccg cgccccagat ggtattccgt gaccccaaat ggctcaacct gatgaaggaa 360
cagttcagca ttctgacgcc ggaaaacgaa atgaaaccgg attccgttct ggatgtgggc 420
gcgagcaaag cgctggtgaa ggaaaccggt gatgagaccg ccgtcgccgt tcatttcgac 480
gctgccaaag cgctgctgaa ttttgccaag agcaacggga tcaaggttca cggccatgtg 540
ctgatctggc acagccagac gccggaagct ttcttccatc agggatatga ttccaagaag 600
cctttcgtta cacgggaagt gatgctgggc cgaatggaaa attacattaa gggtgttttt 660
gaatacctgg atgaaaatta tcccggcgtc gttgtctcct gggacgtgct gaatgaggcg 720
attgacgacg gaagcaactg gctgcggaac agcaactgga gaaagattgt cggcgaagac 780
tatccgaacc gggcatatga atatgcgcgc aaatatgcgc cggaaggtac gctgctgtat 840
tacaacgatt acaatacgtc gattcccggg aaactgaacg gcattgtgaa actgctgaac 900
agtctgattc cggaaggaaa tatcgacggt tacggcttcc agatgcacca tggcgtcggc 960
ttcccgtcca ttgatatgat ccagactgca gtggaacgga ttgccgcgct gaatatccgc 1020

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cttcgcgtca gcgaactgga tgtcacggtg gacaacaaca cggaagcgtc cttcaacaaa      1080
caggcaaagt attatgccga agtcatgaag attctgattg ctcacagcga ccagtttgag      1140
gctgtgcagg tctgggggct gacagacctg atgagctggc gcggcagtca gttcccgctg      1200
ctgtttgacg ggcaggcaa tccgaaaccg gcgttctggg ccgtcgcgga tccggattcc       1260
gtgaaataa                                                              1269
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<210> 72
<211> 422
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 72
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Met Ile Ser Ile Ala His Ser Val Asn Gly Ala Glu Thr Tyr Glu Asn
1               5                   10                  15
Leu Ala His Gly Thr Ala Lys Lys Gly Glu Trp Thr Thr Leu Lys Gly
            20                  25                  30
Thr Tyr Thr Ala Gly Ala Tyr Gln Arg Asn Val Leu Tyr Val Glu Thr
        35                  40                  45
Val Ser Glu Gly Thr Leu Asp Phe Glu Ile Arg Asn Phe Val Leu Thr
    50                  55                  60
Ala Pro Asn Gly Leu Pro Glu Pro Lys Pro Thr Glu Pro Pro Met Val
65                  70                  75                  80
Ile Glu Glu Ala Glu Asn Val Pro Ser Leu Lys Glu Ile Tyr Ala Asp
                85                  90                  95
Lys Phe Asp Phe Gly Ser Ala Ala Pro Gln Met Val Phe Arg Asp Pro
            100                 105                 110
Lys Trp Leu Asn Leu Met Lys Glu Gln Phe Ser Ile Leu Thr Pro Glu
        115                 120                 125
Asn Glu Met Lys Pro Asp Ser Val Leu Asp Val Gly Ala Ser Lys Ala
    130                 135                 140
Leu Val Lys Glu Thr Gly Asp Glu Thr Ala Val Ala Val His Phe Asp
145                 150                 155                 160
Ala Ala Lys Ala Leu Leu Asn Phe Ala Lys Ser Asn Gly Ile Lys Val
                165                 170                 175
His Gly His Val Leu Ile Trp His Ser Gln Thr Pro Glu Ala Phe Phe
            180                 185                 190
His Gln Gly Tyr Asp Ser Lys Lys Pro Phe Val Thr Arg Glu Val Met
        195                 200                 205
Leu Gly Arg Met Glu Asn Tyr Ile Lys Gly Val Phe Glu Tyr Leu Asp
    210                 215                 220
Glu Asn Tyr Pro Gly Val Val Val Ser Trp Asp Val Leu Asn Glu Ala
225                 230                 235                 240
Ile Asp Asp Gly Ser Asn Trp Leu Arg Asn Ser Asn Trp Arg Lys Ile
                245                 250                 255
Val Gly Glu Asp Tyr Pro Asn Arg Ala Tyr Glu Tyr Ala Arg Lys Tyr
            260                 265                 270
Ala Pro Glu Gly Thr Leu Leu Tyr Tyr Asn Asp Tyr Asn Thr Ser Ile
        275                 280                 285
Pro Gly Lys Leu Asn Gly Ile Val Lys Leu Leu Asn Ser Leu Ile Pro
    290                 295                 300
Glu Gly Asn Ile Asp Gly Tyr Gly Phe Gln Met His His Gly Val Gly
305                 310                 315                 320
Phe Pro Ser Ile Asp Met Ile Gln Thr Ala Val Glu Arg Ile Ala Ala
                325                 330                 335
Leu Asn Ile Arg Leu Arg Val Ser Glu Leu Asp Val Thr Val Asp Asn
            340                 345                 350
Asn Thr Glu Ala Ser Phe Asn Lys Gln Ala Lys Tyr Tyr Ala Glu Val
        355                 360                 365
Met Lys Ile Leu Ile Ala His Ser Asp Gln Phe Glu Ala Val Gln Val
    370                 375                 380
Trp Gly Leu Thr Asp Leu Met Ser Trp Arg Gly Ser Gln Phe Pro Leu
385                 390                 395                 400
Leu Phe Asp Gly Ala Gly Asn Pro Lys Pro Ala Phe Trp Ala Val Ala
                405                 410                 415
Asp Pro Asp Ser Val Lys
            420
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<210> 73
<211> 4455
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 73
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gttctactgt accatcgaat tgttgataat cctactaatc aatggacgga taccagcgtt 180
gaaacgttta aacagactat gcaatatcta aatgatagcg gttacaacac cttgtcagcc 240
gaacaatatg taaagatcat ggatggaacg gcaacggcgc ctgaaaaacc gattctatta 300
acgtttgacg atggtactcc agaatttatc accaatgctc ttccagtatt aaagcaatat 360
aacatgaaag ctgttctgtt tattgtcagt gactggatag gcggcggctt cagcatgtca 420
aaagaacagc tgcaaagttt ggctaatgaa ccatctttaa gcctcgaaaa tcatacgaaa 480
acccatgacg gtactatttg ggaacaaat ggcggtgtac gtagtacgat aacgaaagaa 540
caagctgagg accaaattat atcagcgaat acttatctta aaagtattac aggtaaagac 600
ccagtcctaa tggcataccc ttatggcagc tataatgata ttgcaaaact agtaaaccaa 660
gaaaatggta ttaagtacgc atttaaagtg ggatacccta atgaagataa ttatgctatg 720
ggccgtcact atgtaacaaa tcaaagtgtg gctcaaattg cccaaatgat tggcggccct 780
gtgccagaac caactccaga accaggaaac cagacagaaa ccgtctatca agaaaccttt 840
gccagtgata ttggtgtagc agttcaagcg ggtaacccac aagtaaccca cgtttctggt 900
atggtttttg caggcaatga cgatggaaaa gccatctctg ttagcggcag gacgaacaac 960
tgggacggcg tcgatatccc attcaacaat gtcggtatgg aaaacggcaa aacttatacg 1020
attacagtta ctggttatgt tgacgaaaat gcaactgttc cttctggcgc acaagcttta 1080
ctgcagaatg tagacagcta taacggtttg tatgttgccg cagattatgc agcgggacag 1140
gcttttactt taacgggtca gtataccgtg gatactagta aagatagagc cctacgtatc 1200
caatcaaatg atgctgggaa aactgttccg ttttacattg gaaacatctt gattacaacg 1260
aaaaaaacga ctgcgcctga aacagataga gtggtatttc acgaaacatt tggaaatggt 1320
gttggtgttg ctacacaagc gggaagtgcg aaattgactc ctgtttctga gcttgttttt 1380
gaaggcaata gcgatggaaa agcaatttct gttaatggca gatccaataa ctgggacgga 1440
gttgatatac cgttcagcag tgtcagcatg cagaacggca aagcctatac cattacagtc 1500
actggttttg tttatagcag tgtgagtgtt cctgaaggtg cacaagcttt gcttcagaat 1560
gtagacagct ataatggctt gtatgcagca gcagatgtta aggcaggtca aacatttact 1620
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gatgcaggga aaaccgttcc cttctatatc ggagatattc tcattaccga gaaggcagcc 1740
tctggtggtg gcggggacga tggaagacta cctgccgaac catttacagc aattaatttt 1800
gaagaccaaa atatgggtgg tttcgaggga agagctggta ccgaaacact aacagtaacc 1860
aatgaagcca atcatactga tggcggttcc tatgctttga aggttgaagg cagatcacaa 1920
gcttggcatg gaccagcatt acacgtagag aaatatgttg acaaggattc ggaatataaa 1980
atttctgcct gggtgaagct gatttcacca gcaacttcac agcttcagct ttctacacag 2040
gtcggcaatg gcggaactgc tagttacaat aatcttcaag gaaaaactat cagcactgaa 2100
gatggctggg ttaaacttga gggaacgtac cgttatagca gtgtaggcga tgagttttta 2160
accatttatg tagagagctc gaataatagc acagcctcct tttatatcga tgatattact 2220
tttgaatcga ctggttcggg tccgattgaa gttgaggatt tgacaccgat aaaagatgtt 2280
tatcaagacg atttcttaat tggaaacgct gtctcagctt ctgatcttga aggcaataga 2340
cttaagcttc tcaacatgca tcacaatgtt gtcacagcag agaatgcaat gaagccagat 2400
caagcgtata atgcggaaaa acaatttgac tttactgatg aaaatgcgct tgtcgacaag 2460
gttttggatc agggattgca gctgcatggt cacgtgcttg tatggcacca gcagacgcca 2520
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gatgataatc agagcaaagc cgaggccatt tatcagatgg tgaaagatat caatgaaaag 2880
tatgctaaag aacatgatgg ggatcttctc attgacggaa ttggaatgca agcgcactac 3000
aataaaaaca ctaatcctga aaatgttaaa ctctccctag agaagtttat tacattgggt 3000
gtagaagtca gtgtgactga acttgacatt accgctggaa ccaataatgt acttactgag 3060
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gcacagagtc cattgttgtt tgataaagat ttgcaagcaa aaccagctta ctatgctgtt 3240
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gcaaagacat cttccttcga agatggtgat ggacaatatc gagtaaactt tgacaatgaa 3600
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aatggctata ccgttgaagt aaagattccg ttcaaaacca ttacaccaga taacaatacg 3720
aaaatcggtt ttgatgttca gattaatgac ggtaaagatg gtgctcgtca aagtgctgca 3780
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aaacttcgtg cagaaagatt agcaaacggt aatggccgtg tttacaccat tacttatacg 4380
gccacagata aagctggtaa tgtgacaaca aaaagtgttg aagtttccgt tccacgcgac 4440
aattctaaaa aataa 4455

<210> 74
<211> 1484
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(21)

<400> 74
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Ala Ala Met Leu Ile Ile Pro Ser Gly Trp Ile Thr Gln Ala Ser Ala
20 25 30
Ala Glu Thr Asn Lys Asp Ile Pro Val Leu Leu Tyr His Arg Ile Val
35 40 45
Asp Asn Pro Thr Asn Gln Trp Thr Asp Thr Ser Val Glu Thr Phe Lys
50 55 60
Gln Thr Met Gln Tyr Leu Asn Asp Ser Gly Tyr Asn Thr Leu Ser Ala
65 70 75 80
Glu Gln Tyr Val Lys Ile Met Asp Gly Thr Ala Thr Ala Pro Glu Lys
85 90 95
Pro Ile Leu Leu Thr Phe Asp Asp Gly Thr Pro Glu Phe Ile Thr Asn
100 105 110
Ala Leu Pro Val Leu Lys Gln Tyr Asn Met Lys Ala Val Leu Phe Ile
115 120 125
Val Ser Asp Trp Ile Gly Gly Gly Phe Ser Met Ser Lys Glu Gln Leu
130 135 140
Gln Ser Leu Ala Asn Glu Pro Ser Leu Ser Leu Glu Asn His Thr Lys
145 150 155 160
Thr His Asp Gly Thr Ile Trp Gly Thr Asn Gly Gly Val Arg Ser Thr
165 170 175
Ile Thr Lys Glu Gln Ala Glu Asp Gln Ile Ile Ser Ala Asn Thr Tyr
180 185 190
Leu Lys Ser Ile Thr Gly Lys Asp Pro Val Leu Met Ala Tyr Pro Tyr
195 200 205
Gly Ser Tyr Asn Asp Ile Ala Lys Leu Val Asn Gln Glu Asn Gly Ile
210 215 220
Lys Tyr Ala Phe Lys Val Gly Tyr Pro Asn Glu Asp Asn Tyr Ala Met
225 230 235 240
Gly Arg His Tyr Val Thr Asn Gln Ser Val Ala Gln Ile Ala Gln Met
245 250 255
Ile Gly Gly Pro Val Pro Glu Pro Thr Pro Glu Pro Gly Asn Gln Thr
260 265 270
Glu Thr Val Tyr Gln Glu Thr Phe Ala Ser Asp Ile Gly Val Ala Val
275 280 285
Gln Ala Gly Asn Pro Gln Val Thr His Val Ser Gly Met Val Phe Ala
290 295 300
Gly Asn Asp Asp Gly Lys Ala Ile Ser Val Ser Gly Arg Thr Asn Asn
305 310 315 320

Trp Asp Gly Val Asp Ile Pro Phe Asn Asn Val Gly Met Glu Asn Gly
325 330 335
Lys Thr Tyr Thr Ile Thr Val Thr Gly Tyr Val Asp Glu Asn Ala Thr
340 345 350
Val Pro Ser Gly Ala Gln Ala Leu Leu Gln Asn Val Asp Ser Tyr Asn
355 360 365
Gly Leu Tyr Val Ala Ala Asp Tyr Ala Ala Gly Gln Ala Phe Thr Leu
370 375 380
Thr Gly Gln Tyr Thr Val Asp Thr Ser Lys Asp Arg Ala Leu Arg Ile
385 390 395 400
Gln Ser Asn Asp Ala Gly Lys Thr Val Pro Phe Tyr Ile Gly Asn Ile
405 410 415
Leu Ile Thr Thr Lys Lys Thr Thr Ala Pro Glu Thr Asp Arg Val Val
420 425 430
Phe His Glu Thr Phe Gly Asn Gly Val Gly Val Ala Thr Gln Ala Gly
435 440 445
Ser Ala Lys Leu Thr Pro Val Ser Glu Leu Val Phe Glu Gly Asn Ser
450 455 460
Asp Gly Lys Ala Ile Ser Val Asn Gly Arg Ser Asn Asn Trp Asp Gly
465 470 475 480
Val Asp Ile Pro Phe Ser Ser Val Ser Met Gln Asn Gly Lys Ala Tyr
485 490 495
Thr Ile Thr Val Thr Gly Phe Val Tyr Ser Ser Val Ser Val Pro Glu
500 505 510
Gly Ala Gln Ala Leu Leu Gln Asn Val Asp Ser Tyr Asn Gly Leu Tyr
515 520 525
Ala Ala Ala Asp Val Lys Ala Gly Gln Thr Phe Thr Leu Thr Gly Gln
530 535 540
Tyr Thr Val Asp Thr Ser Lys Asp Arg Ala Leu Arg Ile Gln Ser Asn
545 550 555 560
Asp Ala Gly Lys Thr Val Pro Phe Tyr Ile Gly Asp Ile Leu Ile Thr
565 570 575
Glu Lys Ala Ala Ser Gly Gly Gly Gly Asp Asp Gly Arg Leu Pro Ala
580 585 590
Glu Pro Phe Thr Ala Ile Asn Phe Glu Asp Gln Asn Met Gly Gly Phe
595 600 605
Glu Gly Arg Ala Gly Thr Glu Thr Leu Thr Val Thr Asn Glu Ala Asn
610 615 620
His Thr Asp Gly Gly Ser Tyr Ala Leu Lys Val Glu Gly Arg Ser Gln
625 630 635 640
Ala Trp His Gly Pro Ala Leu His Val Glu Lys Tyr Val Asp Lys Asp
645 650 655
Ser Glu Tyr Lys Ile Ser Ala Trp Val Lys Leu Ile Ser Pro Ala Thr
660 665 670
Ser Gln Leu Gln Leu Ser Thr Gln Val Gly Asn Gly Gly Thr Ala Ser
675 680 685
Tyr Asn Asn Leu Gln Gly Lys Thr Ile Ser Thr Glu Asp Gly Trp Val
690 695 700
Lys Leu Glu Gly Thr Tyr Arg Tyr Ser Ser Val Gly Asp Glu Phe Leu
705 710 715 720
Thr Ile Tyr Val Glu Ser Ser Asn Asn Ser Thr Ala Ser Phe Tyr Ile
725 730 735
Asp Asp Ile Thr Phe Glu Ser Thr Gly Ser Gly Pro Ile Glu Val Glu
740 745 750
Asp Leu Thr Pro Ile Lys Asp Val Tyr Gln Asp Asp Phe Leu Ile Gly
755 760 765
Asn Ala Val Ser Ala Ser Asp Leu Glu Gly Asn Arg Leu Lys Leu Leu
770 775 780
Asn Met His His Asn Val Val Thr Ala Glu Asn Ala Met Lys Pro Asp
785 790 795 800
Gln Ala Tyr Asn Ala Glu Lys Gln Phe Asp Phe Thr Asp Glu Asn Ala
805 810 815
Leu Val Asp Lys Val Leu Asp Gln Gly Leu Gln Leu His Gly His Val
820 825 830
Leu Val Trp His Gln Gln Thr Pro Glu Trp Leu Phe Thr Ala Glu Asn
835 840 845
Gly Ala Pro Leu Ser Arg Glu Ala Ala Leu Ala Asn Leu Arg Thr His
850 855 860
Val Lys Thr Val Val Glu Asn Tyr Gly Asn Lys Val Ile Ser Trp Asp

865 870 875 880
Val Val Asn Glu Ala Ile Ile Asp Asn Pro Pro Asn Pro Thr Asp Trp
885 890 895
Lys Ala Ser Leu Arg Lys Ser Gly Trp Tyr Lys Ser Ile Gly Pro Asp
900 905 910
Phe Val Glu Gln Ser Phe Leu Ala Ala Lys Glu Val Leu Asn Glu Lys
915 920 925
Gly Leu Asn Ile Lys Leu Tyr Tyr Asn Asp Tyr Asn Asp Asp Asn Gln
930 935 940
Ser Lys Ala Glu Ala Ile Tyr Gln Met Val Lys Asp Ile Asn Glu Lys
945 950 955 960
Tyr Ala Lys Glu His Asp Gly Asp Leu Leu Ile Asp Gly Ile Gly Met
965 970 975
Gln Ala His Tyr Asn Lys Asn Thr Asn Pro Glu Asn Val Lys Leu Ser
980 985 990
Leu Glu Lys Phe Ile Thr Leu Gly Val Glu Val Ser Val Thr Glu Leu
995 1000 1005
Asp Ile Thr Ala Gly Thr Asn Asn Val Leu Thr Glu Lys Glu Ala Ile
1010 1015 1020
Ala Gln Gly Tyr Leu Tyr Ala Gln Leu Phe Lys Ile Tyr Lys Glu His
1025 1030 1035 1040
Ala Glu His Ile Ser Arg Val Thr Phe Trp Gly Leu Asn Asp Ala Thr
1045 1050 1055
Ser Trp Arg Ala Ala Gln Ser Pro Leu Leu Phe Asp Lys Asp Leu Gln
1060 1065 1070
Ala Lys Pro Ala Tyr Tyr Ala Val Ile Asp Pro Asp Thr Phe Thr Val
1075 1080 1085
Glu Asn Gln Pro Glu Val Arg Glu Ala Asn Gln Gly Ser Ala Val Ser
1090 1095 1100
Gly Thr Pro Val Ile Asp Gly Thr Val Asp Gly Val Trp Ser Asn Ala
1105 1110 1115 1120
Thr Glu Leu Pro Ile Asn Arg Phe Gln Met Ala Trp Gln Gly Ala Asn
1125 1130 1135
Gly Val Ser Lys Val Leu Trp Asp Asn Glu Asn Leu Tyr Val Leu Ile
1140 1145 1150
Gln Val Ser Asp Ser Gln Leu Asp Lys Ser Ser Pro Asn Pro Trp Glu
1155 1160 1165
Gln Asp Ser Ile Glu Val Phe Val Asp Glu Asn Asn Ala Lys Thr Ser
1170 1175 1180
Ser Phe Glu Asp Gly Asp Gly Gln Tyr Arg Val Asn Phe Asp Asn Glu
1185 1190 1195 1200
Thr Ser Phe Asn Pro Val Arg Val Gly Glu Gly Phe Glu Ser Ala Thr
1205 1210 1215
Lys Ala Ser Gly Asn Gly Tyr Thr Val Glu Val Lys Ile Pro Phe Lys
1220 1225 1230
Thr Ile Thr Pro Asp Asn Asn Thr Lys Ile Gly Phe Asp Val Gln Ile
1235 1240 1245
Asn Asp Gly Lys Asp Gly Ala Arg Gln Ser Ala Ala Thr Trp Asn Asp
1250 1255 1260
Leu Thr Gly Leu Gly Tyr Gln Asp Thr Ser Val Phe Gly Val Leu Thr
1265 1270 1275 1280
Leu Met Lys Thr Asp Thr Thr Ala Pro Val Thr Thr Asp Asn Gly Pro
1285 1290 1295
Glu Asp Trp Val Asn Lys Asp Val Thr Ile Ala Phe Ser Ala Asn Asp
1300 1305 1310
Asn Asp Thr Gly Val Ala Ala Thr Tyr Tyr Ser Ile Asp Asn Gly Val
1315 1320 1325
Val Gln Asn Gly Asn Ser Val Thr Ile Ser Glu Glu Gly Val His Ile
1330 1335 1340
Leu Thr Tyr Trp Ser Val Asp Lys Ala Gly Asn Val Glu Gln Val His
1345 1350 1355 1360
Thr Lys Thr Ile Lys Leu Asp Lys Thr Gly Pro Ile Leu Asp Ile Lys
1365 1370 1375
Leu Asp Lys Thr Thr Leu Ser Pro Val Asn His Lys Met Val Pro Ile
1380 1385 1390
Ser Ala Ala Ile Ser Ala Ser Asp Ala Asp Ser Gly Ile His Ser Val
1395 1400 1405
Val Leu Thr Ser Ile Thr Ser Asn Glu Ser Ile Gln Pro Asp Asp Ile
1410 1415 1420

Gln Asn Ala Asn Tyr Asn Lys Pro Ile Thr Gly Thr Thr Asp Ser Phe
1425 1430 1435 1440
Lys Leu Arg Ala Glu Arg Leu Ala Asn Gly Asn Gly Arg Val Tyr Thr
1445 1450 1455
Ile Thr Tyr Thr Ala Thr Asp Lys Ala Gly Asn Val Thr Thr Lys Ser
1460 1465 1470
Val Glu Val Ser Val Pro Arg Asp Asn Ser Lys Lys
1475 1480

<210> 75
<211> 1122
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 75
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ctcaatgccg atcagattac gggggcggac tcggccagcc tcgacttgtc cttggctcac 180
ttcgattctc ttgtcgctga aaatgcgatg aagtgggggt cgctcaatcc tgagccgggg 240
gtttacgatt tccgggtggc tgacgccctg gtcgatttgg cggagcggga aggtttgttt 300
ttggttggcc acacactgct ctggcatcag cagacgccgg actgggtttt tctggacgag 360
aagggcgaga ccgccacgcg ggagctggtg ctcgctcgac tggagacgca catccgcacc 420
gtggtcggcc gctaccaggg ccgggtgcag ggctgggatg tggtcaacga agccttgaac 480
gaagacggtt cgttgcggga gtcgaaatgg ttgcagatca tcggcccgga ctacatcgaa 540
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aatgtgtcca agcccggcaa gcgaggtgga gtggtgcgcc tgcttggaga gctgcaggcg 660
aaaggagtta aggtcgatgc ggtcggcatc cagggccact acagtctcgg gcaccctgag 720
ctcgaccagc tcgaggccag catttctgcg ataacggagg ctggggctcc gatcatgata 780
accgagctcg atgtgtcggt cttgcccttt cccgacgcgg agcaaatggg ggcggacgtg 840
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gtttcgcagc agctagctga acgttacgcg gccatttttg aagtgttttt gcgccaccag 960
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tggccgatcg cgggcaggac cgactatccc ttgctgtttg atcgggagct caagcggaaa 1080
gcggccttcg aggcggtggt cgatttagcg gagggccgct ga 1122

<210> 76
<211> 373
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<400> 76
Met Lys Lys His Ile Val Leu Phe Ala Phe Leu Ser Val Ile Leu Leu
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Ala Ala Arg Ser Ser Ala Ser Glu Arg Phe Leu Lys Asp Val Phe Ser
20 25 30
Asp Ser Phe Lys Val Gly Val Ala Leu Asn Ala Asp Gln Ile Thr Gly
35 40 45
Ala Asp Ser Ala Ser Leu Asp Leu Ser Leu Ala His Phe Asp Ser Leu
50 55 60
Val Ala Glu Asn Ala Met Lys Trp Gly Ser Leu Asn Pro Glu Pro Gly
65 70 75 80
Val Tyr Asp Phe Arg Val Ala Asp Ala Leu Val Asp Leu Ala Glu Arg
85 90 95
Glu Gly Leu Phe Leu Val Gly His Thr Leu Leu Trp His Gln Gln Thr
100 105 110
Pro Asp Trp Val Phe Leu Asp Glu Lys Gly Glu Thr Ala Thr Arg Glu
115 120 125
Leu Val Leu Ala Arg Leu Glu Thr His Ile Arg Thr Val Val Gly Arg
130 135 140
Tyr Gln Gly Arg Val Gln Gly Trp Asp Val Val Asn Glu Ala Leu Asn

```
145                 150                 155                 160
Glu Asp Gly Ser Leu Arg Glu Ser Lys Trp Leu Gln Ile Ile Gly Pro
                165                 170                 175
Asp Tyr Ile Glu Leu Ala Phe Arg Met Ala Lys Glu Ala Asp Pro Asp
            180                 185                 190
Ala Glu Leu Tyr Tyr Asn Asp Tyr Asn Val Ser Lys Pro Gly Lys Arg
        195                 200                 205
Gly Gly Val Val Arg Leu Leu Gly Glu Leu Gln Ala Lys Gly Val Lys
    210                 215                 220
Val Asp Ala Val Gly Ile Gln Gly His Tyr Ser Leu Gly His Pro Glu
225                 230                 235                 240
Leu Asp Gln Leu Glu Ala Ser Ile Ser Ala Ile Thr Glu Ala Gly Ala
                245                 250                 255
Pro Ile Met Ile Thr Glu Leu Asp Val Ser Val Leu Pro Phe Pro Asp
            260                 265                 270
Ala Glu Gln Met Gly Ala Asp Val Ser Leu Ser Phe Glu Met Gln Asp
        275                 280                 285
His Leu Asn Pro Tyr Ala Asp Gly Leu Pro Glu Ala Val Ser Gln Gln
    290                 295                 300
Leu Ala Glu Arg Tyr Ala Ala Ile Phe Glu Val Phe Leu Arg His Gln
305                 310                 315                 320
Ser His Ile Asp Arg Val Thr Phe Trp Gly Val His Asp Gly Val Ser
                325                 330                 335
Trp Trp Asn Tyr Trp Pro Ile Ala Gly Arg Thr Asp Tyr Pro Leu Leu
            340                 345                 350
Phe Asp Arg Glu Leu Lys Arg Lys Ala Ala Phe Glu Ala Val Val Asp
        355                 360                 365
Leu Ala Glu Gly Arg
    370
```

<210> 77
<211> 1248
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 77

```
atgctaaaag ttttacgtaa acctatcgtt tctggattag ctctagcctt attattacct     60
ataggatcga cagttagtgc cgaaacaaat atttcaaata aaccaggtat tagcgggtta    120
acagcaccac aattggacca acgatataaa gattctttca ccataggtgc agcggttgag    180
ccaaatcaat tattagatgc aaaagactca caaatgttaa agcgccattt taatagcatt    240
gtagcagaaa atgtcatgaa gcctagcagt ttacagccag tagaagggca gtttaactgg    300
gaaccggcag ataaacttgt taagtttgcg aaagaaaatg gaatggacat gcgcggccat    360
acgcttgtct ggcatagcca agtaccagat tggttcttca aagatgcaaa tggaaattca    420
atggttgttt ggcagaatgg aaagcaagtg gttgcagatc cgtcaaatct tgaggctaac    480
aaaaagcttt tattaagccg tttagaaaca catgttaata cagtcgtttc tcgttataaa    540
aatgatatta aattttggga cgttgtcaat gaagtaatcg acgaatgggg cggacatcct    600
gaaggtttac gtcaatctcc atggttccta attaccggaa cggactatat taaagtcgct    660
tttgagacag caagacaata tgctgctcca gacgctaagc tttatatcaa tgattacaat    720
acagaagtaa caccaaaaag aacgtactta tacaacctag taaaaagttt aaaacagcaa    780
ggtgttccaa ttgatggtgt tgggcatcag tctcacattc aaatcggctg gccgtctgaa    840
aaagaaattg aagacacaat taacatgttt gctgaactgg ggttagacaa ccaaattact    900
gagcttgatg taagcatgta tggctggcca gtaagggcgt atcctaccta tgattctatt    960
ccagcacaga aatttataga tcaagcagac cgatatgatc gtttatttaa attatatgag   1020
aaattaggcg ataaaatcag caatgtgaca ttctggggaa ttgctgataa ccatacatgg   1080
ttaaatgacc gtgcagatgt ttactatgat gcagatggaa acgttgtaac attggcaaat   1140
gcaccatatg ctaaaatgga agctagatca ggtaaagatg caccatttgt atttgatcca   1200
gaatacaatg taaaaccagc ctattgggcg attatcgacc acaaataa                1248
```

<210> 78
<211> 415
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(27)

<400> 78
Met Leu Lys Val Leu Arg Lys Pro Ile Val Ser Gly Leu Ala Leu Ala
1   5   10   15
Leu Leu Leu Pro Ile Gly Ser Thr Val Ser Ala Glu Thr Asn Ile Ser
            20   25   30
Asn Lys Pro Gly Ile Ser Gly Leu Thr Ala Pro Gln Leu Asp Gln Arg
        35   40   45
Tyr Lys Asp Ser Phe Thr Ile Gly Ala Ala Val Glu Pro Asn Gln Leu
    50   55   60
Leu Asp Ala Lys Asp Ser Gln Met Leu Lys Arg His Phe Asn Ser Ile
65   70   75   80
Val Ala Glu Asn Val Met Lys Pro Ser Ser Leu Gln Pro Val Glu Gly
                85   90   95
Gln Phe Asn Trp Glu Pro Ala Asp Lys Leu Val Lys Phe Ala Lys Glu
            100   105   110
Asn Gly Met Asp Met Arg Gly His Thr Leu Val Trp His Ser Gln Val
        115   120   125
Pro Asp Trp Phe Phe Lys Asp Ala Asn Gly Asn Ser Met Val Val Trp
    130   135   140
Gln Asn Gly Lys Gln Val Val Ala Asp Pro Ser Asn Leu Glu Ala Asn
145   150   155   160
Lys Lys Leu Leu Leu Ser Arg Leu Glu Thr His Val Asn Thr Val Val
                165   170   175
Ser Arg Tyr Lys Asn Asp Ile Lys Phe Trp Asp Val Val Asn Glu Val
            180   185   190
Ile Asp Glu Trp Gly Gly His Pro Glu Gly Leu Arg Gln Ser Pro Trp
        195   200   205
Phe Leu Ile Thr Gly Thr Asp Tyr Ile Lys Val Ala Phe Glu Thr Ala
    210   215   220
Arg Gln Tyr Ala Ala Pro Asp Ala Lys Leu Tyr Ile Asn Asp Tyr Asn
225   230   235   240
Thr Glu Val Thr Pro Lys Arg Thr Tyr Leu Tyr Asn Leu Val Lys Ser
                245   250   255
Leu Lys Gln Gln Gly Val Pro Ile Asp Gly Val Gly His Gln Ser His
            260   265   270
Ile Gln Ile Gly Trp Pro Ser Glu Lys Glu Ile Glu Asp Thr Ile Asn
        275   280   285
Met Phe Ala Glu Leu Gly Leu Asp Asn Gln Ile Thr Glu Leu Asp Val
    290   295   300
Ser Met Tyr Gly Trp Pro Val Arg Ala Tyr Pro Thr Tyr Asp Ser Ile
305   310   315   320
Pro Ala Gln Lys Phe Ile Asp Gln Ala Asp Arg Tyr Asp Arg Leu Phe
                325   330   335
Lys Leu Tyr Glu Lys Leu Gly Asp Lys Ile Ser Asn Val Thr Phe Trp
            340   345   350
Gly Ile Ala Asp Asn His Thr Trp Leu Asn Asp Arg Ala Asp Val Tyr
        355   360   365
Tyr Asp Ala Asp Gly Asn Val Val Thr Leu Ala Asn Ala Pro Tyr Ala
    370   375   380
Lys Met Glu Ala Arg Ser Gly Lys Asp Ala Pro Phe Val Phe Asp Pro
385   390   395   400
Glu Tyr Asn Val Lys Pro Ala Tyr Trp Ala Ile Ile Asp His Lys
                405   410   415

<210> 79
<211> 1293
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 79
atgattggtc tggatttgat ttctggtggt cgtcgcaagg cctgtctggc tgcctgtctg 60
gcgcttgccg cgctgtcatt gccggtatcg gctcaaatgg ctgcggggaa ggaaaagttc 120
gtgggtaacg tgatcgctgg ttatgtgccc ggtgattacg gcaatctctg gaatcaggtg 180

acgccggaga attccaccaa gtggggagcg gttgagtcta cgcgtaatgt catgaactgg 240
acgcaggctg atctggccta caactacgcc aagtccaagg gcttcaagtt caagatgcac 300
acgctggtat ggggctcgca agagccggcc tgggtcaaga atctggatgc gacttcccag 360
cgtgtcgagg tcgaacagtg gatgcgtctg agctgcgaac gctaccccga ttcctgggct 420
atcgatgtgg tgaatgaacc cctgcatgcc gtgccctcgt acaagaacgc actgggtggc 480
gatggtgcca ccggctggga ttgggtcatc acctcgttcc gtctggcgcg tcagtactgt 540
ccgcgcgcca agctgctgct caatgagtac gccaccgagc tggatgccag caagcgcgcc 600
aagatcaaga ccattgcctc gctgctcaag agtcgcggtc tgattgatgg tgttggcctg 660
caggcccatt tcttcacgct ggattacatg aatgccagcc agatgaaggc ggcactggat 720
gattacgcca cgctgggtgt ggatatctac atttccgagc tggatctgaa gggcagtgcc 780
aataccgacg ccagccagaa ggcgaagtac gaagagctgt tcccggtgat gtggaatcac 840
gccagcgtga agggcatcac cctgtggggc tacaaggtgg gtgaaacctg gtcgagcggc 900
accggcctgc tgaatgcgaa cggtagcgag cgtccggccc tgacctggct gaaaagctat 960
atgagcagcc gtcctgcagc atcgagcagc agttcttcga gtgtttcatc cagcaaatcc 1020
agttcgtctt cttctagcca gtccagtgcc tccagcagtg caggcagtgc gccggtcttg 1080
tccggcacca gtgattaccc gagcggtttc agcaagtgtg ccgatctggg cggcacttgc 1140
agcgtgtctt ccggcaccgg ctgggcggcc ttcgggcgca agggtaagtg ggttgccaaa 1200
tacgtcggtg tgggcaagag cattccctgc acggtggcgg cgtttggtcg tgacccgggg 1260
ggcaatccca acaagtgttc cttccagagg taa 1293

<210> 80
<211> 430
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(36)

<400> 80
Met Ile Gly Leu Asp Leu Ile Ser Gly Gly Arg Arg Lys Ala Cys Leu
1 5 10 15
Ala Ala Cys Leu Ala Leu Ala Ala Leu Ser Leu Pro Val Ser Ala Gln
20 25 30
Met Ala Ala Gly Lys Glu Lys Phe Val Gly Asn Val Ile Ala Gly Tyr
35 40 45
Val Pro Gly Asp Tyr Gly Asn Leu Trp Asn Gln Val Thr Pro Glu Asn
50 55 60
Ser Thr Lys Trp Gly Ala Val Glu Ser Thr Arg Asn Val Met Asn Trp
65 70 75 80
Thr Gln Ala Asp Leu Ala Tyr Asn Tyr Ala Lys Ser Lys Gly Phe Lys
85 90 95
Phe Lys Met His Thr Leu Val Trp Gly Ser Gln Glu Pro Ala Trp Val
100 105 110
Lys Asn Leu Asp Ala Thr Ser Gln Arg Val Glu Val Glu Gln Trp Met
115 120 125
Arg Leu Ser Cys Glu Arg Tyr Pro Asp Ser Trp Ala Ile Asp Val Val
130 135 140
Asn Glu Pro Leu His Ala Val Pro Ser Tyr Lys Asn Ala Leu Gly Gly
145 150 155 160
Asp Gly Ala Thr Gly Trp Asp Trp Val Ile Thr Ser Phe Arg Leu Ala
165 170 175
Arg Gln Tyr Cys Pro Arg Ala Lys Leu Leu Leu Asn Glu Tyr Ala Thr
180 185 190
Glu Leu Asp Ala Ser Lys Arg Ala Lys Ile Lys Thr Ile Ala Ser Leu
195 200 205
Leu Lys Ser Arg Gly Leu Ile Asp Gly Val Gly Leu Gln Ala His Phe
210 215 220
Phe Thr Leu Asp Tyr Met Asn Ala Ser Gln Met Lys Ala Ala Leu Asp
225 230 235 240
Asp Tyr Ala Thr Leu Gly Val Asp Ile Tyr Ile Ser Glu Leu Asp Leu
245 250 255
Lys Gly Ser Ala Asn Thr Asp Ala Ser Gln Lys Ala Lys Tyr Glu Glu
260 265 270
Leu Phe Pro Val Met Trp Asn His Ala Ser Val Lys Gly Ile Thr Leu
275 280 285
Trp Gly Tyr Lys Val Gly Glu Thr Trp Ser Ser Gly Thr Gly Leu Leu

```
            290                     295                     300
Asn Ala Asn Gly Ser Glu Arg Pro Ala Leu Thr Trp Leu Lys Ser Tyr
305                 310                     315                 320
Met Ser Ser Arg Pro Ala Ala Ser Ser Ser Ser Ser Ser Ser Val Ser
                325                     330                 335
Ser Ser Lys Ser Ser Ser Ser Ser Ser Ser Gln Ser Ser Ala Ser Ser
            340                     345                 350
Ser Ala Gly Ser Ala Pro Val Leu Ser Gly Thr Ser Asp Tyr Pro Ser
        355                 360                     365
Gly Phe Ser Lys Cys Ala Asp Leu Gly Gly Thr Cys Ser Val Ser Ser
    370                     375                     380
Gly Thr Gly Trp Ala Ala Phe Gly Arg Lys Gly Lys Trp Val Ala Lys
385                 390                     395                 400
Tyr Val Gly Val Gly Lys Ser Ile Pro Cys Thr Val Ala Ala Phe Gly
                405                     410                 415
Arg Asp Pro Gly Gly Asn Pro Asn Lys Cys Ser Phe Gln Arg
            420                     425                 430
```

<210> 81
<211> 1017
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 81

```
ttgaccacga gagctattcg cacggaggca gcgctgaagg agatgtttgc ggaggacttt      60
cagatcggag ccgctgttaa tccgatgact atacggacac aggaggagct gcttgcttat     120
cacttcaaca gtattacggc agagaatgaa atgaagtttg ccagtctgca gccggaggag     180
ggggcttatg cttttgacga ggcggatcga ttggcggcct tcgcccggaa gcatggcatg     240
gcgatgcggg gacacacttt agtgtggcat aaccagtcca caggctggct gttcgaagac     300
aagcagggaa atcctgtaga taaggcaact ctgctggaga ggctgaaatc gcacatccat     360
acggtagtag gacgttataa aaacgatatt tatgcttggg atgtggtaaa cgaggttata     420
gaggacgagg gagacggcct gctgcgccgg tcgaaatggc tggatattgc cggaccggaa     480
ttcattgccc gggcgttcga gtatgctcat gaggctgacc ctaatgcgct gctcttctat     540
aatgactaca acgagtccaa tccggcgaag cgagacaaga tccatgctct ggtgaagtcg     600
ctgctggagc aaggcgtgcc tattcatggc attggactgc aggcgcattg gaatttgtat     660
ggtccttctc tcggcgagat ccgagcggca ctggagaagt atgcttctct tggcctgcag     720
ctgcagctta cggagctgga tatgtcgctg tttcgttttg acgacaagcg tacggatata     780
accgagcctc cggcggaatt gcttgagctg caggctgagc ggtatgagga aattttcaag     840
ctgctgaggg aataccggga tgtaatcact tccgtgacct tctgggggc tgcggatgat      900
tatacgtggc tgaacgattt tcccgtccgg gggcggaaaa attggccttt cctgttcgat     960
gagcagcatc accccaaact ggcatttcat cgggtcgctg cactttcccg ccagtga       1017
```

<210> 82
<211> 338
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 82

```
Leu Thr Thr Arg Ala Ile Arg Thr Glu Ala Ala Leu Lys Glu Met Phe
1               5                   10                  15
Ala Glu Asp Phe Gln Ile Gly Ala Ala Val Asn Pro Met Thr Ile Arg
            20                  25                  30
Thr Gln Glu Glu Leu Leu Ala Tyr His Phe Asn Ser Ile Thr Ala Glu
        35                  40                  45
Asn Glu Met Lys Phe Ala Ser Leu Gln Pro Glu Glu Gly Ala Tyr Ala
    50                  55                  60
Phe Asp Glu Ala Asp Arg Leu Ala Ala Phe Ala Arg Lys His Gly Met
65                  70                  75                  80
Ala Met Arg Gly His Thr Leu Val Trp His Asn Gln Ser Thr Gly Trp
                85                  90                  95
Leu Phe Glu Asp Lys Gln Gly Asn Pro Val Asp Lys Ala Thr Leu Leu
            100                 105                 110
Glu Arg Leu Lys Ser His Ile His Thr Val Val Gly Arg Tyr Lys Asn
```

115 120 125
Asp Ile Tyr Ala Trp Asp Val Val Asn Glu Val Ile Glu Asp Glu Gly
130 135 140
Asp Gly Leu Leu Arg Arg Ser Lys Trp Leu Asp Ile Ala Gly Pro Glu
145 150 155 160
Phe Ile Ala Arg Ala Phe Glu Tyr Ala His Glu Ala Asp Pro Asn Ala
165 170 175
Leu Leu Phe Tyr Asn Asp Tyr Asn Glu Ser Asn Pro Ala Lys Arg Asp
180 185 190
Lys Ile His Ala Leu Val Lys Ser Leu Leu Glu Gln Gly Val Pro Ile
195 200 205
His Gly Ile Gly Leu Gln Ala His Trp Asn Leu Tyr Gly Pro Ser Leu
210 215 220
Gly Glu Ile Arg Ala Ala Leu Glu Lys Tyr Ala Ser Leu Gly Leu Gln
225 230 235 240
Leu Gln Leu Thr Glu Leu Asp Met Ser Leu Phe Arg Phe Asp Asp Lys
245 250 255
Arg Thr Asp Ile Thr Glu Pro Pro Ala Glu Leu Leu Glu Leu Gln Ala
260 265 270
Glu Arg Tyr Glu Glu Ile Phe Lys Leu Leu Arg Glu Tyr Arg Asp Val
275 280 285
Ile Thr Ser Val Thr Phe Trp Gly Ala Ala Asp Asp Tyr Thr Trp Leu
290 295 300
Asn Asp Phe Pro Val Arg Gly Arg Lys Asn Trp Pro Phe Leu Phe Asp
305 310 315 320
Glu Gln His His Pro Lys Leu Ala Phe His Arg Val Ala Ala Leu Ser
325 330 335
Arg Gln

<210> 83
<211> 3024
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 83
atgaaaacca aaaggtctat attcaggttg tctatcctgg ttgtcctggc tgtgctgctg 60
ttcagcgcaa tcaccttgac agccagcgcc gccgacacgc tcggcgcggc ggcggcccag 120
tcgggccggt acttcggcac ggcgatagct gccggcaagc tcggcgactc gacctacacg 180
accattgcca accgtgagtt caacatgatc acggctgaga atgagatgaa gatcgacgcc 240
accgagccga accagaacca attcaacttc accaacgccg accggatctt caactgggcg 300
gtgcagaatg ggaagcaggt gcgcgggcac acgctggcat ggcactcgca gcagccgggg 360
tggatgagca gcatgagcgg caccgcgctg cgcaatgcga tgatcaacca catcaatggg 420
gtgatggccc actacaaggg caggatctac gcctgggatg tggtgaacga ggctttcaac 480
gaggacggca gccgccgcaa ctcgaacctg cagcagaccg gcaacgactg gatcgaggtg 540
gccttccgga cagcccgcac cgccgacccg gccgccaagc tgtgctacaa cgactacaac 600
atcgaagcct ggagctatgc caagacgcag ggcgtttacc ggatggtcca ggacttcaag 660
tcccgcggcg tgccgatcga ctgtgtcggg ttccagagcc acttcaacag cggcacttcc 720
tacgtcaaca gcaacttccg gacgacgctg caaagcttcg ccgcgctggg cgtggacgtg 780
cagatcaccg agctggatgt cgagaatgcc gactcgcggc tcgattggtg gagaggcatc 840
gtcaatgact gcctggcggt cccgcgctgc aacggcatca cggtgtgggg cgtgcgcgac 900
agcgattcgt ggcgctcttc gcagaacccg ctgctgttca actccagcgg tggtaagaag 960
gcttcgtaca ccgccgtcct cgacgccctc aacgctgccc cgaccgtcac acctccggta 1020
acgacacctc cggtgacgac accgccagtg accacgcctc ctcccggcac tgtgtcgatt 1080
aacgcgggcg gctcggcgag cggcagcttc acggccgacc agtacttcag cggtggcagc 1140
acctacacca acaccgccac catcgacatg agtcagatca ccagcaaccc accgccggcg 1200
gcggtcttca acagcgagcg ttacggggcg atgacctaca ccatccccaa ccgctcgggt 1260
gctcagacgg tgacgctgta ctttgccgag acctacctca ccgcggcagg gcagcggtcg 1320
ttcaacgtgt cgattaatgg cgcagcggcg ctgtccaact tcgacatcta tgcctcggca 1380
ggtggcgcta accgggccat cgcccggacg ttcagcacca cggctaactc aagtggccag 1440
gtggtgatcc agttcacggc ggttaccgag aaccccaaga tcaacgctat cacggtaaca 1500
gcgggtggca cgcctccacc gacaacgcct ccgcccacca cgccgccacc gaccacccct 1560
ccggtgacga cacccccagt gacgacaccc ccagtgacga caccgccccc cggcagcgtg 1620
tcgatcaacg cgggcggctc ggccaccggc agcttcacgg gcgaccagta ctttagcggt 1680
ggcagcacct acaccaacac cgccaccatc gacatgagcc agatcaccag caacccacca 1740
ccggcggcgg tgttcaacag cgagcgctac ggggcgatga cctacaccat ccccggccgc 1800

tcgggggctc agacggtcac gctttacttt gccgaaacgt atgtcactgc ggcagggcag 1860
cgcgtcttta acgtgtctgt aaacggcgcg gcagcgctgt ccaacttcga catctatgcc 1920
agcgccggcg gccagaaccg ggccatcgct cgctccttca acaccacggc caactcaagc 1980
ggccaggtgg tgatccagtt cacggcggtc accgagaacc ccaagatcaa cgccatcact 2040
gtggcgggcg ggatcgggga cttccaaacc ctgaccgtca cgaagtccgg cacggggacg 2100
gtcacctcca acccggctgg tatcaactgc ggctcgacct gcaacgccag cttcgctacc 2160
ggcaccagcg tgaccctgac cgcctccggc gggaccttca ccggctggag cggagcctgc 2220
tccggcacct ccaccacctg caccgtctcc atgacccagg cccggtcggt caccgctact 2280
tttagcggcg gtggtgacac caggccgagc gcggggtgtg gtaagaaccg gacactgcag 2340
aatggcacaa tcaccatttc aagtggcggc gtcaaccgca cctacatcct acgcacgcct 2400
gacaactaca acaacacgca tgcataccgg ctgatcatgg cttatcactg gcttaacggc 2460
agcgcgcaga atgtggcgag cgagaactac taccggctgt tcccactctc caacaacagc 2520
accatcttcg tggcgcctca ggggctggat gccggatggg ctaacaccaa caaccgcgac 2580
ctgaacctca ccgatgccat actcacccag gtcgagaacg atctgtgcgt cgacttgaac 2640
cgggtctggg ccaccgggtt cagctacggc gcaggtatgt catacgccat cgcctgtgcc 2700
agggccaatg tgttccgggg cgtcgctctc tatgccggcg cgcagctcag cggttgcacc 2760
ggtggaacca cggccattgc gtacttcgca acgcacggca tcaacgacag tgtcctcaac 2820
atctcgcaag ggcggactct acgcgaccgc tttgtctcga acaacagctg cacggcgcag 2880
aaccctcccg agccttcctc gggcagcggg acgcacatct gcacgtccta ccagaactgc 2940
tcggcaggac atcctgtccg gtggtgcgcg ttcgacggcg accacacccc gaatcagacc 3000
gaccgcggcc agagcacaag ctaa 3024

<210> 84
<211> 1007
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(30)

<400> 84
Met Lys Thr Lys Arg Ser Ile Phe Arg Leu Ser Ile Leu Val Val Leu
1 5 10 15
Ala Val Leu Leu Phe Ser Ala Ile Thr Leu Thr Ala Ser Ala Ala Asp
20 25 30
Thr Leu Gly Ala Ala Ala Ala Gln Ser Gly Arg Tyr Phe Gly Thr Ala
35 40 45
Ile Ala Ala Gly Lys Leu Gly Asp Ser Thr Tyr Thr Thr Ile Ala Asn
50 55 60
Arg Glu Phe Asn Met Ile Thr Ala Glu Asn Glu Met Lys Ile Asp Ala
65 70 75 80
Thr Glu Pro Asn Gln Asn Gln Phe Asn Phe Thr Asn Ala Asp Arg Ile
85 90 95
Phe Asn Trp Ala Val Gln Asn Gly Lys Gln Val Arg Gly His Thr Leu
100 105 110
Ala Trp His Ser Gln Gln Pro Gly Trp Met Ser Ser Met Ser Gly Thr
115 120 125
Ala Leu Arg Asn Ala Met Ile Asn His Ile Asn Gly Val Met Ala His
130 135 140
Tyr Lys Gly Arg Ile Tyr Ala Trp Asp Val Val Asn Glu Ala Phe Asn
145 150 155 160
Glu Asp Gly Ser Arg Arg Asn Ser Asn Leu Gln Gln Thr Gly Asn Asp
165 170 175
Trp Ile Glu Val Ala Phe Arg Thr Ala Arg Thr Ala Asp Pro Ala Ala
180 185 190
Lys Leu Cys Tyr Asn Asp Tyr Asn Ile Glu Ala Trp Ser Tyr Ala Lys
195 200 205
Thr Gln Gly Val Tyr Arg Met Val Gln Asp Phe Lys Ser Arg Gly Val
210 215 220
Pro Ile Asp Cys Val Gly Phe Gln Ser His Phe Asn Ser Gly Thr Ser
225 230 235 240
Tyr Val Asn Ser Asn Phe Arg Thr Thr Leu Gln Ser Phe Ala Ala Leu
245 250 255
Gly Val Asp Val Gln Ile Thr Glu Leu Asp Val Glu Asn Ala Asp Ser
260 265 270
Arg Leu Asp Trp Trp Arg Gly Ile Val Asn Asp Cys Leu Ala Val Pro

275 280 285
Arg Cys Asn Gly Ile Thr Val Trp Gly Val Arg Asp Ser Asp Ser Trp
290 295 300
Arg Ser Ser Gln Asn Pro Leu Leu Phe Asn Ser Ser Gly Gly Lys Lys
305 310 315 320
Ala Ser Tyr Thr Ala Val Leu Asp Ala Leu Asn Ala Ala Pro Thr Val
325 330 335
Thr Pro Pro Val Thr Thr Pro Pro Val Thr Thr Pro Pro Val Thr Thr
340 345 350
Pro Pro Pro Gly Thr Val Ser Ile Asn Ala Gly Gly Ser Ala Ser Gly
355 360 365
Ser Phe Thr Ala Asp Gln Tyr Phe Ser Gly Gly Ser Thr Tyr Thr Asn
370 375 380
Thr Ala Thr Ile Asp Met Ser Gln Ile Thr Ser Asn Pro Pro Pro Ala
385 390 395 400
Ala Val Phe Asn Ser Glu Arg Tyr Gly Ala Met Thr Tyr Thr Ile Pro
405 410 415
Asn Arg Ser Gly Ala Gln Thr Val Thr Leu Tyr Phe Ala Glu Thr Tyr
420 425 430
Leu Thr Ala Ala Gly Gln Arg Ser Phe Asn Val Ser Ile Asn Gly Ala
435 440 445
Ala Ala Leu Ser Asn Phe Asp Ile Tyr Ala Ser Ala Gly Gly Ala Asn
450 455 460
Arg Ala Ile Ala Arg Thr Phe Ser Thr Thr Ala Asn Ser Ser Gly Gln
465 470 475 480
Val Val Ile Gln Phe Thr Ala Val Thr Glu Asn Pro Lys Ile Asn Ala
485 490 495
Ile Thr Val Thr Ala Gly Gly Thr Pro Pro Pro Thr Thr Pro Pro Pro
500 505 510
Thr Thr Pro Pro Pro Thr Thr Pro Pro Val Thr Thr Pro Pro Val Thr
515 520 525
Thr Pro Pro Val Thr Thr Pro Pro Pro Gly Ser Val Ser Ile Asn Ala
530 535 540
Gly Gly Ser Ala Thr Gly Ser Phe Thr Gly Asp Gln Tyr Phe Ser Gly
545 550 555 560
Gly Ser Thr Tyr Thr Asn Thr Ala Thr Ile Asp Met Ser Gln Ile Thr
565 570 575
Ser Asn Pro Pro Pro Ala Ala Val Phe Asn Ser Glu Arg Tyr Gly Ala
580 585 590
Met Thr Tyr Thr Ile Pro Gly Arg Ser Gly Ala Gln Thr Val Thr Leu
595 600 605
Tyr Phe Ala Glu Thr Tyr Val Thr Ala Ala Gly Gln Arg Val Phe Asn
610 615 620
Val Ser Val Asn Gly Ala Ala Ala Leu Ser Asn Phe Asp Ile Tyr Ala
625 630 635 640
Ser Ala Gly Gly Gln Asn Arg Ala Ile Ala Arg Ser Phe Asn Thr Thr
645 650 655
Ala Asn Ser Ser Gly Gln Val Val Ile Gln Phe Thr Ala Val Thr Glu
660 665 670
Asn Pro Lys Ile Asn Ala Ile Thr Val Ala Gly Gly Ile Gly Asp Phe
675 680 685
Gln Thr Leu Thr Val Thr Lys Ser Gly Thr Gly Thr Val Thr Ser Asn
690 695 700
Pro Ala Gly Ile Asn Cys Gly Ser Thr Cys Asn Ala Ser Phe Ala Thr
705 710 715 720
Gly Thr Ser Val Thr Leu Thr Ala Ser Gly Gly Thr Phe Thr Gly Trp
725 730 735
Ser Gly Ala Cys Ser Gly Thr Ser Thr Thr Cys Thr Val Ser Met Thr
740 745 750
Gln Ala Arg Ser Val Thr Ala Thr Phe Ser Gly Gly Gly Asp Thr Arg
755 760 765
Pro Ser Ala Gly Cys Gly Lys Asn Arg Thr Leu Gln Asn Gly Thr Ile
770 775 780
Thr Ile Ser Ser Gly Gly Val Asn Arg Thr Tyr Ile Leu Arg Thr Pro
785 790 795 800
Asp Asn Tyr Asn Asn Thr His Ala Tyr Arg Leu Ile Met Ala Tyr His
805 810 815
Trp Leu Asn Gly Ser Ala Gln Asn Val Ala Ser Glu Asn Tyr Tyr Arg
820 825 830

```
Leu Phe Pro Leu Ser Asn Asn Ser Thr Ile Phe Val Ala Pro Gln Gly
        835                 840                 845
Leu Asp Ala Gly Trp Ala Asn Thr Asn Asn Arg Asp Leu Asn Leu Thr
    850                 855                 860
Asp Ala Ile Leu Thr Gln Val Glu Asn Asp Leu Cys Val Asp Leu Asn
865                 870                 875                 880
Arg Val Trp Ala Thr Gly Phe Ser Tyr Gly Ala Gly Met Ser Tyr Ala
                885                 890                 895
Ile Ala Cys Ala Arg Ala Asn Val Phe Arg Gly Val Ala Leu Tyr Ala
            900                 905                 910
Gly Ala Gln Leu Ser Gly Cys Thr Gly Gly Thr Thr Ala Ile Ala Tyr
        915                 920                 925
Phe Ala Thr His Gly Ile Asn Asp Ser Val Leu Asn Ile Ser Gln Gly
    930                 935                 940
Arg Thr Leu Arg Asp Arg Phe Val Ser Asn Asn Ser Cys Thr Ala Gln
945                 950                 955                 960
Asn Pro Pro Glu Pro Ser Ser Gly Ser Gly Thr His Ile Cys Thr Ser
                965                 970                 975
Tyr Gln Asn Cys Ser Ala Gly His Pro Val Arg Trp Cys Ala Phe Asp
            980                 985                 990
Gly Asp His Thr Pro Asn Gln Thr Asp Arg Gly Gln Ser Thr Ser
        995                 1000                1005

<210> 85
<211> 1254
<212> DNA
<213> Bacteria

<400> 85
atgaccttga ttacgccaag ctcgaaatta accctcacta aagggaacaa aagctggagc      60
tcgcgcgcct gcaggtcgac actagtggat ctcacacttt acttcgagtc tcagaatccg     120
accctcgagt tctacgtgga cgatgtgaag gtagtggaca ccacctctgc tgagataaaa     180
ctcgagatga atccagaaga ggaaatacca gccctcaggg aagttctgaa agactacttc     240
agagtgggcg ttgctcttcc atccaaggta ttcatcaacc agaaggactt aacgctcatc     300
accaagcact tcaacagcat caccgcagaa aatgagatga aacctgatag tctgcttgca     360
ggcattgaga atggcaaact caagttcaga tttgaaacag cagacaaata catcgaattt     420
gcacagcaaa acggcatggt tgtgaggggc cacacactgg tatggcacaa tcagacgccc     480
gagtggttct tcaaagacga aaatggaaac ctcctctcca aagaagcgat gacagaaaga     540
ctcagagaat acatacacac cgtcgttgga cacttcaaag ggaaggtcta cgcatgggac     600
gttgtgaacg aagcggtcga tccgaaccag ccagatggac tgagaagatc cacctggtat     660
cagatcatgg ggcctgacta catagaactt gccttcaagt ttgcaaggga ggcagatccc     720
gatgcgaaac tcttctacaa cgactacaac accttcgaac ccaaaaagag agacatcatc     780
tacaaccttg tgaagagtct caaggaaaag ggtctcatcg atggaatcgg tatgcagtgt     840
cacatcagtc ttgcaacgga catcaggcag atcgaagagg ccatcaaaaa gttcagctcc     900
atccctggta tagaaatcca cataacagag ctcgatatga gcgtctacag agattctact     960
tccaactacc cagaggcacc gaggaacgca ctcattgaac aggctcacaa gatggctcaa    1020
ctctttgaaa tcttcaagaa atacagtaat gtgatcacaa acgtcacgtt ctggggtctc    1080
aaagacgact actcctggag agcaacaaga agaaatgact ggacattgat ctttgacaaa    1140
gattatcagg caaaactcgc ttactgggcg attgtcgctc ctgaagtgct accacctctt    1200
tcaaaagaaa gcaagatcca aagaattcaa aaagcttctc gagagtactt ctag          1254

<210> 86
<211> 417
<212> PRT
<213> Bacteria

<400> 86
Met Thr Leu Ile Thr Pro Ser Ser Lys Leu Thr Leu Thr Lys Gly Asn
1               5                   10                  15
Lys Ser Trp Ser Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Leu Thr
            20                  25                  30
Leu Tyr Phe Glu Ser Gln Asn Pro Thr Leu Glu Phe Tyr Val Asp Asp
        35                  40                  45
Val Lys Val Val Asp Thr Thr Ser Ala Glu Ile Lys Leu Glu Met Asn
    50                  55                  60
Pro Glu Glu Glu Ile Pro Ala Leu Arg Glu Val Leu Lys Asp Tyr Phe
65                  70                  75                  80
Arg Val Gly Val Ala Leu Pro Ser Lys Val Phe Ile Asn Gln Lys Asp
                85                  90                  95
```

Leu Thr Leu Ile Thr Lys His Phe Asn Ser Ile Thr Ala Glu Asn Glu
100 105 110
Met Lys Pro Asp Ser Leu Leu Ala Gly Ile Glu Asn Gly Lys Leu Lys
115 120 125
Phe Arg Phe Glu Thr Ala Asp Lys Tyr Ile Glu Phe Ala Gln Gln Asn
130 135 140
Gly Met Val Val Arg Gly His Thr Leu Val Trp His Asn Gln Thr Pro
145 150 155 160
Glu Trp Phe Phe Lys Asp Glu Asn Gly Asn Leu Leu Ser Lys Glu Ala
165 170 175
Met Thr Glu Arg Leu Arg Glu Tyr Ile His Thr Val Val Gly His Phe
180 185 190
Lys Gly Lys Val Tyr Ala Trp Asp Val Val Asn Glu Ala Val Asp Pro
195 200 205
Asn Gln Pro Asp Gly Leu Arg Arg Ser Thr Trp Tyr Gln Ile Met Gly
210 215 220
Pro Asp Tyr Ile Glu Leu Ala Phe Lys Phe Ala Arg Glu Ala Asp Pro
225 230 235 240
Asp Ala Lys Leu Phe Tyr Asn Asp Tyr Asn Thr Phe Glu Pro Lys Lys
245 250 255
Arg Asp Ile Ile Tyr Asn Leu Val Lys Ser Leu Lys Glu Lys Gly Leu
260 265 270
Ile Asp Gly Ile Gly Met Gln Cys His Ile Ser Leu Ala Thr Asp Ile
275 280 285
Arg Gln Ile Glu Glu Ala Ile Lys Lys Phe Ser Ser Ile Pro Gly Ile
290 295 300
Glu Ile His Ile Thr Glu Leu Asp Met Ser Val Tyr Arg Asp Ser Thr
305 310 315 320
Ser Asn Tyr Pro Glu Ala Pro Arg Asn Ala Leu Ile Glu Gln Ala His
325 330 335
Lys Met Ala Gln Leu Phe Glu Ile Phe Lys Lys Tyr Ser Asn Val Ile
340 345 350
Thr Asn Val Thr Phe Trp Gly Leu Lys Asp Asp Tyr Ser Trp Arg Ala
355 360 365
Thr Arg Arg Asn Asp Trp Thr Leu Ile Phe Asp Lys Asp Tyr Gln Ala
370 375 380
Lys Leu Ala Tyr Trp Ala Ile Val Ala Pro Glu Val Leu Pro Pro Leu
385 390 395 400
Ser Lys Glu Ser Lys Ile Gln Arg Ile Gln Lys Ala Ser Arg Glu Tyr
405 410 415
Phe

<210> 87
<211> 1089
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 87
ttgaagaaca gaattaaaaa ggttgtgggc gggctcgccc tggcgagtgt tctgctcacc 60
tcggtaatgg caggcaatgc cagcgcagca attaccaatg gatcgaagtt cctggggaat 120
atcattgccg gcagtgctcc aagtaacttc accacctact ggaatcaggt caccccggag 180
aacggcacca aatggggttc catcgaaggc aaccgcaacc agatgaactg ggaaacgcg 240
gacatgatct ataactacgc catcagcaaa aacatcccgt tcaaattcca tactctcgtc 300
tggggaagcc aggagcccaa ctgggtggcc ggcttgtcgg cagcggagca gaaggcggaa 360
atcagctcat tcattactca agcaggacag cgttattccg cgaagacagc ttttgtggat 420
gtagtcaatg aaccgctgca tgccaagcct tcgtaccgca atgccatcgg cggcgatggc 480
agcaccggct gggattgggt gatctggtct ttccagcaag cccgggccgc cttcccgaac 540
gccaagctgc acctcaatga ctacggcatt atcggtgacc ccagcgcggc cgataaatat 600
gtgaacatta tcaatatcct gaaatccaga ggactgatcg atggtattgg tattcagtgc 660
cactacttca atatggataa cgtaagtgtg agcaccatga atactgtact gggtaagctt 720
gctgcaacag gcctgccaat ctatgtctcc gagctggata ttaccggtga tgacaacacc 780
cagcttgcca gataccaaca gaaattccct gtgctctgga accatccttc cgtgaagggc 840
gtcaccctgt ggggctacat ccaaaatcag acctgggcat caggcaccca tctggtgaat 900
tccaacggca cagagcgccc tgccctgaag tggctgaagc aatacctggg cggctcgtca 960
gctctgatgg aaaccacaga cgcccaagac ctcactatca ctgacagtct gatccagccg 1020

gacagtgtgg ttgagccgga ccctcaactg gatctccagc cggtgcttga gcccgttccg 1080
gctgagtaa 1089

<210> 88
<211> 362
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(29)

<400> 88
Leu Lys Asn Arg Ile Lys Lys Val Val Gly Gly Leu Ala Leu Ala Ser
1 5 10 15
Val Leu Leu Thr Ser Val Met Ala Gly Asn Ala Ser Ala Ala Ile Thr
20 25 30
Asn Gly Ser Lys Phe Leu Gly Asn Ile Ile Ala Gly Ser Ala Pro Ser
35 40 45
Asn Phe Thr Thr Tyr Trp Asn Gln Val Thr Pro Glu Asn Gly Thr Lys
50 55 60
Trp Gly Ser Ile Glu Gly Asn Arg Asn Gln Met Asn Trp Gly Asn Ala
65 70 75 80
Asp Met Ile Tyr Asn Tyr Ala Ile Ser Lys Asn Ile Pro Phe Lys Phe
85 90 95
His Thr Leu Val Trp Gly Ser Gln Glu Pro Asn Trp Val Ala Gly Leu
100 105 110
Ser Ala Ala Glu Gln Lys Ala Glu Ile Ser Ser Phe Ile Thr Gln Ala
115 120 125
Gly Gln Arg Tyr Ser Ala Lys Thr Ala Phe Val Asp Val Val Asn Glu
130 135 140
Pro Leu His Ala Lys Pro Ser Tyr Arg Asn Ala Ile Gly Gly Asp Gly
145 150 155 160
Ser Thr Gly Trp Asp Trp Val Ile Trp Ser Phe Gln Gln Ala Arg Ala
165 170 175
Ala Phe Pro Asn Ala Lys Leu His Leu Asn Asp Tyr Gly Ile Ile Gly
180 185 190
Asp Pro Ser Ala Ala Asp Lys Tyr Val Asn Ile Ile Asn Ile Leu Lys
195 200 205
Ser Arg Gly Leu Ile Asp Gly Ile Gly Ile Gln Cys His Tyr Phe Asn
210 215 220
Met Asp Asn Val Ser Val Ser Thr Met Asn Thr Val Leu Gly Lys Leu
225 230 235 240
Ala Ala Thr Gly Leu Pro Ile Tyr Val Ser Glu Leu Asp Ile Thr Gly
245 250 255
Asp Asp Asn Thr Gln Leu Ala Arg Tyr Gln Gln Lys Phe Pro Val Leu
260 265 270
Trp Asn His Pro Ser Val Lys Gly Val Thr Leu Trp Gly Tyr Ile Gln
275 280 285
Asn Gln Thr Trp Ala Ser Gly Thr His Leu Val Asn Ser Asn Gly Thr
290 295 300
Glu Arg Pro Ala Leu Lys Trp Leu Lys Gln Tyr Leu Gly Gly Ser Ser
305 310 315 320
Ala Leu Met Glu Thr Thr Asp Ala Gln Asp Leu Thr Ile Thr Asp Ser
325 330 335
Leu Ile Gln Pro Asp Ser Val Val Glu Pro Asp Pro Gln Leu Asp Leu
340 345 350
Gln Pro Val Leu Glu Pro Val Pro Ala Glu
355 360

<210> 89
<211> 2541
<212> DNA
<213> Bacteria

<400> 89
atggatacat tgttcaatac aaccgatgag cgtggggcgt ccaagcgccg tggcatcgtc 60

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gcggcgcttg cggccgcagc catgctggtg ccgctggcgt tcgccccgac ggccatggcg      120
gccgaccccg actatccggg cggcatcaag ggcgaataca atccgctggg aatcaacgct      180
ggtgtcgcca tcgagacata caccctcaac caggacaagg agaaggccct ggtcgagaac      240
ttcgaccaga tcaccccgga gaactcgctg aagccggaag gctggtacga cgaccagcat      300
aatttccgca tgtcggatga cgcgcggaac ctgctgacgt tcgccagcga gaacggcatc      360
aaggtctacg gccatgttct ggtctggcac tcgcagacgc ccgactggtt cttccaggcc      420
gacgaatggt gccatgacac caacgacaac cccggcgtca ccagctgccc gcttgccgac      480
aaggccacga tgcaggaacg ccagcgcagg cacatcgaga acgtggcgga ggccatctcc      540
gacgaattcg gaaaattcgg cagcccgacc aatcccgtcg tcgcgttcga cgtggtcaac      600
gagaccgtga acgacagcga cgaccccgcc accaacggca tgcgcaattc gctgtggtat      660
cagacctatg gggcgagga ctacatctat gacgcgttcc ggaacgcgaa tacgtatctg      720
aacgacgtct acgccgccga cgacgcggag catccggtga cgttgttcat caacgattac      780
ggcaccgagc aggcgggcaa gcgttcccgc tacaaggcgc ttctggaacg catgatccag      840
caggggggttc cctttgacgg catcggtcac cagttccatg tgtcgttgac cacggcctcg      900
tcgaatctcg acgacgcgct gaccgatatg tcctcgctcg gcaagaagca ggccatcacc      960
gaactggacg tcgccaccgg aacgccggtt acggaggcga agctcatcga gcagggacgg     1020
tactactacg acgtcaacca gatcatccac aggcacgccg accagctgtt ctcggtttcg     1080
gtgtgggggc tgagcgacga ccagtcctgg cgcaacaagg agggcgcgcc gctgctgttc     1140
gacgacaacc tggagaagaa gccggcgtac atcggctaca tcggtgatag cgccaacctt     1200
cccgagccgt tgaagagcat gaacgcattc aaggatgacg ccgtgggcat cgactcggcg     1260
cttcccggta ccgtggccga gtccggcgcg tcctctccgt gggaacgtct ttcgctggtc     1320
gagatgaccc cgtctgcgta tgacgccgtt tccggctcgt tcaatgtcta ttggaaggac     1380
ggctctctgg tcgtctacgc ggatgtcgcc gatgccagcg cggcggatga cgacaccgtc     1440
accgtgcgtg tgggtgacgc cgagtatacg atcggccgca acggtgtgac cggcggcgag     1500
ggtgtgcagg ccaacgtcgt ttcgtctgat gccggatacg aagtcgtggc cgatatcccg     1560
tacaccggtg cagagaagga catcgtcgag atgaacgtca tcgcgacgga ttccgccacc     1620
acggagacca gcgcgtggag cacgaacgac actggcgccg tcacgctggc cgagccgctg     1680
agctacacgg aagccgtgaa ggttcccgcc gacgcccagg ctccggtcgt tgacgccgac     1740
ccgtcggatt ccgtctgggc ggaagccaac gaggttcccg tgggtaaggt gaccgccgcc     1800
acgccttccc ccgaggcgac cgctaccgcc aagaccctgt ggtcggacgg caagctgtat     1860
gtcctcatgg aagtgaccga cgcggacatc gatctgacca actcgaatcc gtgggagaag     1920
gactccgttg aggtgtacat cgaccgtggc aacaccaaga gcggccagta taccaacgac     1980
atccagcaga ttcgcgtgtc cgccgatggt gcggagctga gcttcggctc cggcgcgtcg     2040
gaggatgtcc agaagtccat ggtccagacc gccggcaagc tcgtcgatgg cggctatgtc     2100
gtcgagatgg ccatcgatct gggaacggct gaggccggca ccttcgaagg tgtcgacttc     2160
cagatcaacg acgcgaagaa cggtgctcga atcggcatcc gcaactgggc cgatccgacc     2220
ggtgccggct atcagacggc gtcccattgg ggcgtgctgc gtctgctggc cgatccctcc     2280
gaaaccgaga ccccgggtgg agaagatccc gagacccccg gtgacgagga gactcctggc     2340
gaggataccg agaagcctgg cgacgaggaa acccccggtg aggataccga gaagcctggc     2400
gacgagaagc cgcggccttc cgacgatgct gacaacgacg acaagatgcc gcagaccggt     2460
tccgcggtca tcggaatcgc cgtggtggcg ctgctgctgg ttgccgccgg atgcgggctg     2520
gtcatcgctc ggcgtcgatg a                                               2541
```

<210> 90
<211> 846
<212> PRT
<213> Bacteria

<220>
<221> SIGNAL
<222> (1)...(40)

<400> 90

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Met Asp Thr Leu Phe Asn Thr Thr Asp Glu Arg Gly Ala Ser Lys Arg
 1              5                   10                  15
Arg Gly Ile Val Ala Ala Leu Ala Ala Ala Ala Met Leu Val Pro Leu
            20                  25                  30
Ala Phe Ala Pro Thr Ala Met Ala Ala Asp Pro Asp Tyr Pro Gly Gly
        35                  40                  45
Ile Lys Gly Glu Tyr Asn Pro Leu Gly Ile Asn Ala Gly Val Ala Ile
    50                  55                  60
Glu Thr Tyr Thr Leu Asn Gln Asp Lys Glu Lys Ala Leu Val Glu Asn
65                  70                  75                  80
Phe Asp Gln Ile Thr Pro Glu Asn Ser Leu Lys Pro Glu Gly Trp Tyr
                85                  90                  95
Asp Asp Gln His Asn Phe Arg Met Ser Asp Asp Ala Arg Asn Leu Leu
            100                 105                 110
Thr Phe Ala Ser Glu Asn Gly Ile Lys Val Tyr Gly His Val Leu Val
        115                 120                 125
```

Trp His Ser Gln Thr Pro Asp Trp Phe Phe Gln Ala Asp Glu Trp Cys
130 135 140
His Asp Thr Asn Asp Asn Pro Gly Val Thr Ser Cys Pro Leu Ala Asp
145 150 155 160
Lys Ala Thr Met Gln Glu Arg Gln Arg Arg His Ile Glu Asn Val Ala
165 170 175
Glu Ala Ile Ser Asp Glu Phe Gly Lys Phe Gly Ser Pro Thr Asn Pro
180 185 190
Val Val Ala Phe Asp Val Val Asn Glu Thr Val Asn Asp Ser Asp Asp
195 200 205
Pro Ala Thr Asn Gly Met Arg Asn Ser Leu Trp Tyr Gln Thr Tyr Gly
210 215 220
Gly Glu Asp Tyr Ile Tyr Asp Ala Phe Arg Asn Ala Asn Thr Tyr Leu
225 230 235 240
Asn Asp Val Tyr Ala Ala Asp Asp Ala Glu His Pro Val Thr Leu Phe
245 250 255
Ile Asn Asp Tyr Gly Thr Glu Gln Ala Gly Lys Arg Ser Arg Tyr Lys
260 265 270
Ala Leu Leu Glu Arg Met Ile Gln Gln Gly Val Pro Phe Asp Gly Ile
275 280 285
Gly His Gln Phe His Val Ser Leu Thr Thr Ala Ser Ser Asn Leu Asp
290 295 300
Asp Ala Leu Thr Asp Met Ser Ser Leu Gly Lys Lys Gln Ala Ile Thr
305 310 315 320
Glu Leu Asp Val Ala Thr Gly Thr Pro Val Thr Glu Ala Lys Leu Ile
325 330 335
Glu Gln Gly Arg Tyr Tyr Tyr Asp Val Asn Gln Ile Ile His Arg His
340 345 350
Ala Asp Gln Leu Phe Ser Val Ser Val Trp Gly Leu Ser Asp Asp Gln
355 360 365
Ser Trp Arg Asn Lys Glu Gly Ala Pro Leu Leu Phe Asp Asp Asn Leu
370 375 380
Glu Lys Lys Pro Ala Tyr Ile Gly Tyr Ile Gly Asp Ser Ala Asn Leu
385 390 395 400
Pro Glu Pro Leu Lys Ser Met Asn Ala Phe Lys Asp Asp Ala Val Gly
405 410 415
Ile Asp Ser Ala Leu Pro Gly Thr Val Ala Glu Ser Gly Ala Ser Ser
420 425 430
Pro Trp Glu Arg Leu Ser Leu Val Glu Met Thr Pro Ser Ala Tyr Asp
435 440 445
Ala Val Ser Gly Ser Phe Asn Val Tyr Trp Lys Asp Gly Ser Leu Val
450 455 460
Val Tyr Ala Asp Val Ala Asp Ala Ser Ala Ala Asp Asp Asp Thr Val
465 470 475 480
Thr Val Arg Val Gly Asp Ala Glu Tyr Thr Ile Gly Arg Asn Gly Val
485 490 495
Thr Gly Gly Glu Gly Val Gln Ala Asn Val Val Ser Ser Asp Ala Gly
500 505 510
Tyr Glu Val Val Ala Asp Ile Pro Tyr Thr Gly Ala Glu Lys Asp Ile
515 520 525
Val Glu Met Asn Val Ile Ala Thr Asp Ser Ala Thr Thr Glu Thr Ser
530 535 540
Ala Trp Ser Thr Asn Asp Thr Gly Ala Val Thr Leu Ala Glu Pro Leu
545 550 555 560
Ser Tyr Thr Glu Ala Val Lys Val Pro Ala Asp Ala Gln Ala Pro Val
565 570 575
Val Asp Ala Asp Pro Ser Asp Ser Val Trp Ala Glu Ala Asn Glu Val
580 585 590
Pro Val Gly Lys Val Thr Ala Ala Thr Pro Ser Pro Glu Ala Thr Ala
595 600 605
Thr Ala Lys Thr Leu Trp Ser Asp Gly Lys Leu Tyr Val Leu Met Glu
610 615 620
Val Thr Asp Ala Asp Ile Asp Leu Thr Asn Ser Asn Pro Trp Glu Lys
625 630 635 640
Asp Ser Val Glu Val Tyr Ile Asp Arg Gly Asn Thr Lys Ser Gly Gln
645 650 655
Tyr Thr Asn Asp Ile Gln Gln Ile Arg Val Ser Ala Asp Gly Ala Glu
660 665 670
Leu Ser Phe Gly Ser Gly Ala Ser Glu Asp Val Gln Lys Ser Met Val

```
        675                 680                 685
Gln Thr Ala Gly Lys Leu Val Asp Gly Gly Tyr Val Val Glu Met Ala
    690                 695                 700
Ile Asp Leu Gly Thr Ala Glu Ala Gly Thr Phe Glu Gly Val Asp Phe
705                 710                 715                 720
Gln Ile Asn Asp Ala Lys Asn Gly Ala Arg Ile Gly Ile Arg Asn Trp
                725                 730                 735
Ala Asp Pro Thr Gly Ala Gly Tyr Gln Thr Ala Ser His Trp Gly Val
            740                 745                 750
Leu Arg Leu Leu Ala Asp Pro Ser Glu Thr Glu Thr Pro Gly Gly Glu
        755                 760                 765
Asp Pro Glu Thr Pro Gly Asp Glu Glu Thr Pro Gly Glu Asp Thr Glu
    770                 775                 780
Lys Pro Gly Asp Glu Glu Thr Pro Gly Glu Asp Thr Glu Lys Pro Gly
785                 790                 795                 800
Asp Glu Lys Pro Arg Pro Ser Asp Asp Ala Asp Asn Asp Asp Lys Met
                805                 810                 815
Pro Gln Thr Gly Ser Ala Val Ile Gly Ile Ala Val Val Ala Leu Leu
            820                 825                 830
Leu Val Ala Ala Gly Cys Gly Leu Val Ile Ala Arg Arg Arg
        835                 840                 845
```

<210> 91
<211> 1023
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 91

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atgaatgtat cggtaccggc cgagtccgca cttaaagaca tcttcgcgga agacttccat      60
ataggtgcgg cggtcagtag taatacgatc aagtcgcagg agagtctgct tacgcatcac     120
tttaacagca ttacggcgga aaacgaaatg aagttcgcca gcgtccatcc agaggaagag     180
ctttacacct tcgaggaagc ggatcagatc gtggacttcg cgcgcaaaca cgggatggct     240
gtccgcggac atacgctggt atggcataac cagaccaccg attggttgtt ccgcgacaag     300
cagaatcagc tcgtgagcaa agccgtgctt tatgaaagaa tccgttcgca tatccaaacg     360
gtagtaggca gatataaggg cgatatttac gcttgggacg ttgtgaacga ggtcattgcc     420
gatgacggcg atcagttgct gcgtacctcc agctggacgg aaatcgccgg ggacgaattc     480
atcgccaaag cgtttgaata cgcgcatgct gccgacccga atgcgctgtt gttctacaac     540
gactacaatg agtcccatcc aagcaaacgg gataaaattt ataccttggt caagtctctt     600
ctggaccggg gagtacctat tcacggcatt ggcctgcagg cacactggaa tctgttcaac     660
ccgtccttgg atgacatccg ggcagccatc gaaaaatatg cttcgctagg attgcagctc     720
cagctcacgg aactggatgt gtcggtattc cgtttcgaag ataagcgggc cgatctgacc     780
gagcctgaac cgggaatgct ggaacagcag gctgaattct acgaagccgt gttcaagctg     840
cttaaggaat acagcgatgt aattagcgcg gtgacgttct ggggagctgc ggacgaccac     900
acctggctca gcgatttttcc ggtacgtggg cgcaaaaact ggccgctgct gttcgatgag     960
cggcacaggc cgaagccggc atattatcgc ttagctgctc ttgccaatca tcttcggcgt    1020
tga                                                                  1023
```

<210> 92
<211> 340
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 92

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Met Asn Val Ser Val Pro Ala Glu Ser Ala Leu Lys Asp Ile Phe Ala
1               5                   10                  15
Glu Asp Phe His Ile Gly Ala Ala Val Ser Ser Asn Thr Ile Lys Ser
            20                  25                  30
Gln Glu Ser Leu Leu Thr His His Phe Asn Ser Ile Thr Ala Glu Asn
        35                  40                  45
Glu Met Lys Phe Ala Ser Val His Pro Glu Glu Glu Leu Tyr Thr Phe
    50                  55                  60
Glu Glu Ala Asp Gln Ile Val Asp Phe Ala Arg Lys His Gly Met Ala
65                  70                  75                  80
```

Val Arg Gly His Thr Leu Val Trp His Asn Gln Thr Thr Asp Trp Leu
85 90 95
Phe Arg Asp Lys Gln Asn Gln Leu Val Ser Lys Ala Val Leu Tyr Glu
100 105 110
Arg Ile Arg Ser His Ile Gln Thr Val Val Gly Arg Tyr Lys Gly Asp
115 120 125
Ile Tyr Ala Trp Asp Val Val Asn Glu Val Ile Ala Asp Asp Gly Asp
130 135 140
Gln Leu Leu Arg Thr Ser Ser Trp Thr Glu Ile Ala Gly Asp Glu Phe
145 150 155 160
Ile Ala Lys Ala Phe Glu Tyr Ala His Ala Ala Asp Pro Asn Ala Leu
165 170 175
Leu Phe Tyr Asn Asp Tyr Asn Glu Ser His Pro Ser Lys Arg Asp Lys
180 185 190
Ile Tyr Thr Leu Val Lys Ser Leu Leu Asp Arg Gly Val Pro Ile His
195 200 205
Gly Ile Gly Leu Gln Ala His Trp Asn Leu Phe Asn Pro Ser Leu Asp
210 215 220
Asp Ile Arg Ala Ala Ile Glu Lys Tyr Ala Ser Leu Gly Leu Gln Leu
225 230 235 240
Gln Leu Thr Glu Leu Asp Val Ser Val Phe Arg Phe Glu Asp Lys Arg
245 250 255
Ala Asp Leu Thr Glu Pro Glu Pro Gly Met Leu Glu Gln Gln Ala Glu
260 265 270
Phe Tyr Glu Ala Val Phe Lys Leu Leu Lys Glu Tyr Ser Asp Val Ile
275 280 285
Ser Ala Val Thr Phe Trp Gly Ala Ala Asp Asp His Thr Trp Leu Ser
290 295 300
Asp Phe Pro Val Arg Gly Arg Lys Asn Trp Pro Leu Leu Phe Asp Glu
305 310 315 320
Arg His Arg Pro Lys Pro Ala Tyr Tyr Arg Leu Ala Ala Leu Ala Asn
325 330 335
His Leu Arg Arg
340

<210> 93
<211> 1011
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 93
atgaatcaat cagtaaatga agcacaggtt cctgcattat cggatgtata tgaagattat 60
ttttcaatag gtgccgctgt taatccactt actttaggta cgcaaaaaaa gctgttaacc 120
aaacatttta atagtataac ggctgagaat gaaatgaaat ttgaagcatt acagcctaaa 180
ccagatcaat ttacatttga tacggcggat aaaatggttg cctttgccca agcacatgat 240
atgaagatgc gtggccatac attaatctgg cacaatcaaa caccagattg gatgtttttg 300
caaaaagacg gtacgacaat tgatcgtgaa acactcttgg agagaatgaa aaaacatatt 360
aagacggtgg tggaaagata taaaggcaaa atatattgtt gggacgttgt aaatgaagcg 420
gtagctgatg aaggcgaagc tattttaaga ccatcaaaat ggacggacat tattggcgac 480
tcgtttattg agtatgcttt taaatacgcc cacgaggccg atcccgatgc actgttgttt 540
tacaatgact acaatgcttg ccaccctcat aaaagagata agatttatca acttgtaaag 600
ggttaatag acaagggtgt gcccatacac ggtattggcc tacaagcaca ttggaacatt 660
gttgacccgt cttacgatga tattaaacga gccatcgaaa cttatgcatc attaggatta 720
agcatacact ttactgaaat ggatgtgtct gtttttgaat atcatgatcg aagaacagac 780
ttattggaac ctacaaaaga tatggtttca cgtcaagctg agcgttatca ggcatttttt 840
gaaatattta ggtcgtatgc tgatgtgatt gattccgtta cgttttgggg catggccgat 900
gattatacat ggcttgatga ttttccggtg acaggtcgaa aaaattggcc ctttgtattt 960
gatgcgagac atcagcctaa aacagcattc tggaacatcg ttgattttta a 1011

<210> 94
<211> 336
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 94
Met Asn Gln Ser Val Asn Glu Ala Gln Val Pro Ala Leu Ser Asp Val
1 5 10 15
Tyr Glu Asp Tyr Phe Ser Ile Gly Ala Ala Val Asn Pro Leu Thr Leu
20 25 30
Gly Thr Gln Lys Lys Leu Leu Thr Lys His Phe Asn Ser Ile Thr Ala
35 40 45
Glu Asn Glu Met Lys Phe Glu Ala Leu Gln Pro Lys Pro Asp Gln Phe
50 55 60
Thr Phe Asp Thr Ala Asp Lys Met Val Ala Phe Ala Gln Ala His Asp
65 70 75 80
Met Lys Met Arg Gly His Thr Leu Ile Trp His Asn Gln Thr Pro Asp
85 90 95
Trp Met Phe Leu Gln Lys Asp Gly Thr Thr Ile Asp Arg Glu Thr Leu
100 105 110
Leu Glu Arg Met Lys Lys His Ile Lys Thr Val Val Glu Arg Tyr Lys
115 120 125
Gly Lys Ile Tyr Cys Trp Asp Val Val Asn Glu Ala Val Ala Asp Glu
130 135 140
Gly Glu Ala Ile Leu Arg Pro Ser Lys Trp Thr Asp Ile Ile Gly Asp
145 150 155 160
Ser Phe Ile Glu Tyr Ala Phe Lys Tyr Ala His Glu Ala Asp Pro Asp
165 170 175
Ala Leu Leu Phe Tyr Asn Asp Tyr Asn Ala Cys His Pro His Lys Arg
180 185 190
Asp Lys Ile Tyr Gln Leu Val Lys Gly Leu Ile Asp Lys Gly Val Pro
195 200 205
Ile His Gly Ile Gly Leu Gln Ala His Trp Asn Ile Val Asp Pro Ser
210 215 220
Tyr Asp Asp Ile Lys Arg Ala Ile Glu Thr Tyr Ala Ser Leu Gly Leu
225 230 235 240
Ser Ile His Phe Thr Glu Met Asp Val Ser Val Phe Glu Tyr His Asp
245 250 255
Arg Arg Thr Asp Leu Leu Glu Pro Thr Lys Asp Met Val Ser Arg Gln
260 265 270
Ala Glu Arg Tyr Gln Ala Phe Phe Glu Ile Phe Arg Ser Tyr Ala Asp
275 280 285
Val Ile Asp Ser Val Thr Phe Trp Gly Met Ala Asp Asp Tyr Thr Trp
290 295 300
Leu Asp Asp Phe Pro Val Thr Gly Arg Lys Asn Trp Pro Phe Val Phe
305 310 315 320
Asp Ala Arg His Gln Pro Lys Thr Ala Phe Trp Asn Ile Val Asp Phe
325 330 335

<210> 95
<211> 1143
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 95
atgaaaaaaa cgattgcaca tttcacctta tggatagtgt tttttctctt cacttcctgt 60
gctgttacgg cgcagaagaa tgctaagaat acaagagtaa aactcactac cctaaaagag 120
gcttaccaag gtaaattcta tatcggtact gcgatgaatc tgagacagat tcacggagat 180
gatccccagt ctgaaaatat tatcaaaaaa cagttcaatt ccatagttgc cgaaaactgc 240
atgaagagta tgtatcttca gccggaggaa ggaaaatttt tcttcgatga tgcggacaag 300
tttgtggatt ttggtcttca gaacaatatg ttcatcatcg ggcattgtct gatttggcat 360
tcgcaggcgc caaaatggtt tttcaccgat gagaatggaa aaacggtttc cccagaagtt 420
cttaaacaaa ggatgaaagc ccatatcacc gctgtcgttt cccgctacaa agggaaaatc 480
aaaggttggg atgtggtgaa cgaagccatt atggaagatg gttcttaccg caaaagcaaa 540
ttttatgaga ttttgggaga agaatttatt ccgttggcat ttcagtatgc gcatgaagca 600
gatcctgatg cagaacttta ttacaacgat tataacgaat ggtatcccgg aaaaagagct 660
acggtgacca agataatccg cgatttcaaa tctagaggaa tccgcattga tgccatcgga 720
atgcaggctc atttcgggat ggattcgccc actttagaag agtatgaaca aaccattcag 780
ggctatataa aagaaggcgt gaaagtcaat attacggaac tcgatttgag tccgcttcct 840
tctccttggg gaacttccgc caatgttgcc gatacgcagc agtatcagga aaaaatgaat 900

```
ccttacacca aaggacttcc cgccgatgtg gaaaaagcat gggaaaaccg ctatctcgat    960
tttttcaaac tgttcctgaa atatcatcag catatcgagc gtgttacgtt ttggggcgtt   1020
agcgatatcg attcctggaa gaacgatttt ccagtaagag gacgtaccga ttatccacta   1080
ccgtttaacc gacagtatca ggcaaaacct ttggtgcaga aattaataga cttaacgaaa   1140
tag                                                                 1143
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<210> 96
<211> 380
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(24)

<400> 96

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Met Lys Lys Thr Ile Ala His Phe Thr Leu Trp Ile Val Phe Phe Leu
1               5                   10                  15
Phe Thr Ser Cys Ala Val Thr Ala Gln Lys Asn Ala Lys Asn Thr Arg
            20                  25                  30
Val Lys Leu Thr Thr Leu Lys Glu Ala Tyr Gln Gly Lys Phe Tyr Ile
        35                  40                  45
Gly Thr Ala Met Asn Leu Arg Gln Ile His Gly Asp Asp Pro Gln Ser
    50                  55                  60
Glu Asn Ile Ile Lys Lys Gln Phe Asn Ser Ile Val Ala Glu Asn Cys
65                  70                  75                  80
Met Lys Ser Met Tyr Leu Gln Pro Glu Glu Gly Lys Phe Phe Phe Asp
                85                  90                  95
Asp Ala Asp Lys Phe Val Asp Phe Gly Leu Gln Asn Asn Met Phe Ile
            100                 105                 110
Ile Gly His Cys Leu Ile Trp His Ser Gln Ala Pro Lys Trp Phe Phe
        115                 120                 125
Thr Asp Glu Asn Gly Lys Thr Val Ser Pro Glu Val Leu Lys Gln Arg
    130                 135                 140
Met Lys Ala His Ile Thr Ala Val Val Ser Arg Tyr Lys Gly Lys Ile
145                 150                 155                 160
Lys Gly Trp Asp Val Val Asn Glu Ala Ile Met Glu Asp Gly Ser Tyr
                165                 170                 175
Arg Lys Ser Lys Phe Tyr Glu Ile Leu Gly Glu Glu Phe Ile Pro Leu
            180                 185                 190
Ala Phe Gln Tyr Ala His Glu Ala Asp Pro Asp Ala Glu Leu Tyr Tyr
        195                 200                 205
Asn Asp Tyr Asn Glu Trp Tyr Pro Gly Lys Arg Ala Thr Val Thr Lys
    210                 215                 220
Ile Ile Arg Asp Phe Lys Ser Arg Gly Ile Arg Ile Asp Ala Ile Gly
225                 230                 235                 240
Met Gln Ala His Phe Gly Met Asp Ser Pro Thr Leu Glu Glu Tyr Glu
                245                 250                 255
Gln Thr Ile Gln Gly Tyr Ile Lys Glu Gly Val Lys Val Asn Ile Thr
            260                 265                 270
Glu Leu Asp Leu Ser Pro Leu Pro Ser Pro Trp Gly Thr Ser Ala Asn
        275                 280                 285
Val Ala Asp Thr Gln Gln Tyr Gln Glu Lys Met Asn Pro Tyr Thr Lys
    290                 295                 300
Gly Leu Pro Ala Asp Val Glu Lys Ala Trp Glu Asn Arg Tyr Leu Asp
305                 310                 315                 320
Phe Phe Lys Leu Phe Leu Lys Tyr His Gln His Ile Glu Arg Val Thr
                325                 330                 335
Phe Trp Gly Val Ser Asp Ile Asp Ser Trp Lys Asn Asp Phe Pro Val
            340                 345                 350
Arg Gly Arg Thr Asp Tyr Pro Leu Pro Phe Asn Arg Gln Tyr Gln Ala
        355                 360                 365
Lys Pro Leu Val Gln Lys Leu Ile Asp Leu Thr Lys
    370                 375                 380
```

<210> 97
<211> 1407

<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 97
atgaatgaaa cctcgcggaa ttggttggag agaggattgc ctttcgaacg ccaacggcgt 60
tccaacattc agcccagggt tggcgcttgc gcctaccctg ggttggaagc aatcgctcca 120
tcaaccctga aagggttgca gcggaggttt gcacaagacc gatacaaccc tttcaggatt 180
ggctttctcc cttttccacc cagggtagcg cctgcggcgc aaccctgggc tgatggatca 240
gaacgccgtt ggcgttcccg gaaacctgcg aagaaacaac tcgccttcct ggccatcacc 300
agtctcctct cgggtctgct gtggggcgcc gaagtgcaac cggcactgaa agacgtattc 360
cgccaggact tcctgctggg ggcggcgttg aacgcggagc aggtgctgga caccaaccgg 420
gtcgagtcgg tattgatcga aaagcatttc aacacgatca cgcccgagaa tgtgctgaag 480
tgggaacgag tccatcctca gcccaaccag tattcttttg aggacgcgga tcgctacgtc 540
gagttcggcc gcaaacacgg aatggtcatc atcggccaca cgctggtctg gcacagccag 600
acgcccggct gggtcttccg ggatgccgac ggaaagacgc tgacgcgcga agccctgctg 660
gagcggatgc gcgaccacat ccacaccgtg gtcgggcgct acaagggcaa gatccgcggc 720
tgggatgtgg tgaacgaggc gctgcgcgac gacggcgcgt ggcggaattc ccaatggcgg 780
cggatcatcg gcgacgatta cattttgaaa gccttccagt atgcccatga ggccgatccg 840
gatgcggagc tctattacaa cgattattcg ctggagaagc cggccaagcg caatggcgcc 900
gtggacctgg tgaagcagct ccaggccggc ggggcgaagc tggccggcgt cggcttgcag 960
ggcactaca acctcgactg gccggagacc gccgagatcg aaaacaccat cgcggcgttc 1020
gcggagctgg ggctcaaggt gatgatcacg gagctggacg tcaacgcgct gccgacgccc 1080
ggccagtcgg gcgaagccga tgtagggatg acgttcggcg gcaatttcgg cggcgataaa 1140
tggaatcctt tcacgaacgg actgccggcc gcagtggagc aacgcctcgc ggaccgctac 1200
gctgaaatct tcaggatctt cacgaagcac agccgtcgga tttcgcgcgt caccttctgg 1260
ggcgtcaccg accggacctc ctggctcaac aattttccca tccgcggccg gaccaattac 1320
ccgttgctct ttgatcgggc tggggagccc aaacccgcgt tccgatccgt cgtggcggtc 1380
cgtcagccgc gccagcccgt cgaatga 1407

<210> 98
<211> 468
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 98
Met Asn Glu Thr Ser Arg Asn Trp Leu Glu Arg Gly Leu Pro Phe Glu
1 5 10 15
Arg Gln Arg Arg Ser Asn Ile Gln Pro Arg Val Gly Ala Cys Ala Tyr
20 25 30
Pro Gly Leu Glu Ala Ile Ala Pro Ser Thr Leu Lys Gly Leu Gln Arg
35 40 45
Arg Phe Ala Gln Asp Arg Tyr Asn Pro Phe Arg Ile Gly Phe Leu Pro
50 55 60
Phe Pro Pro Arg Val Ala Pro Ala Ala Gln Pro Trp Ala Asp Gly Ser
65 70 75 80
Glu Arg Arg Trp Arg Ser Arg Lys Pro Ala Lys Lys Gln Leu Ala Phe
85 90 95
Leu Ala Ile Thr Ser Leu Leu Ser Gly Leu Leu Trp Gly Ala Glu Val
100 105 110
Gln Pro Ala Leu Lys Asp Val Phe Arg Gln Asp Phe Leu Leu Gly Ala
115 120 125
Ala Leu Asn Ala Glu Gln Val Leu Asp Thr Asn Arg Val Glu Ser Val
130 135 140
Leu Ile Glu Lys His Phe Asn Thr Ile Thr Pro Glu Asn Val Leu Lys
145 150 155 160
Trp Glu Arg Val His Pro Gln Pro Asn Gln Tyr Ser Phe Glu Asp Ala
165 170 175
Asp Arg Tyr Val Glu Phe Gly Arg Lys His Gly Met Val Ile Ile Gly
180 185 190
His Thr Leu Val Trp His Ser Gln Thr Pro Gly Trp Val Phe Arg Asp
195 200 205
Ala Asp Gly Lys Thr Leu Thr Arg Glu Ala Leu Leu Glu Arg Met Arg
210 215 220

```
Asp His Ile His Thr Val Val Gly Arg Tyr Lys Gly Lys Ile Arg Gly
225                 230                 235                 240
Trp Asp Val Val Asn Glu Ala Leu Arg Asp Asp Gly Ala Trp Arg Asn
                245                 250                 255
Ser Gln Trp Arg Arg Ile Ile Gly Asp Asp Tyr Ile Leu Lys Ala Phe
            260                 265                 270
Gln Tyr Ala His Glu Ala Asp Pro Asp Ala Glu Leu Tyr Tyr Asn Asp
        275                 280                 285
Tyr Ser Leu Glu Lys Pro Ala Lys Arg Asn Gly Ala Val Asp Leu Val
    290                 295                 300
Lys Gln Leu Gln Ala Gly Gly Ala Lys Leu Ala Gly Val Gly Leu Gln
305                 310                 315                 320
Gly His Tyr Asn Leu Asp Trp Pro Glu Thr Ala Glu Ile Glu Asn Thr
                325                 330                 335
Ile Ala Ala Phe Ala Glu Leu Gly Leu Lys Val Met Ile Thr Glu Leu
            340                 345                 350
Asp Val Asn Ala Leu Pro Thr Pro Gly Gln Ser Gly Glu Ala Asp Val
        355                 360                 365
Gly Met Thr Phe Gly Gly Asn Phe Gly Gly Asp Lys Trp Asn Pro Phe
    370                 375                 380
Thr Asn Gly Leu Pro Ala Ala Val Glu Gln Arg Leu Ala Asp Arg Tyr
385                 390                 395                 400
Ala Glu Ile Phe Arg Ile Phe Thr Lys His Ser Arg Arg Ile Ser Arg
                405                 410                 415
Val Thr Phe Trp Gly Val Thr Asp Arg Thr Ser Trp Leu Asn Asn Phe
            420                 425                 430
Pro Ile Arg Gly Arg Thr Asn Tyr Pro Leu Leu Phe Asp Arg Ala Gly
        435                 440                 445
Glu Pro Lys Pro Ala Phe Arg Ser Val Val Ala Val Arg Gln Pro Arg
    450                 455                 460
Gln Pro Val Glu
465
```

<210> 99
<211> 1074
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 99

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gtgcgctcaa gagctagcgc gtactggttc ggcgtggggt tggtggtggc gctgagcctg      60
gctcagaccc cttcccccca gtccctgcgc gcgctggccg agcgccaggg gctgctggtg     120
ggagccgcgg tggacctagc ggccctgtac gaccccctcg agcccgagta cgcccaactc     180
ctcgcccgcg agttcaacct ggtggtggcc gagaacgcca tgaagtgggc ctccctgagc     240
aacgcgcggg ggcagtacag cttcaccggc gctgacgccc tggtgcgctt cgcccgccag     300
cacggccagc gcttgcgcgg ccacaccctc atctggcacg agcaactgcc cgcgtgggtg     360
cgcagcggca ccttctcccg cgaggccatg ctggcggtga tgcaggagca cattcaggcg     420
gtggccgggc acttccgcgg ccaggtggcc tactgggacg tggtcaacga ggcggtgagt     480
gaccggggcg gcctgcgcga gacccccttt ctgcgggcgg tgggccccga ctacctcgag     540
cacgccttcc gcttcgcccg cgccgccgac cccaggccca agctcttcta caacgactac     600
ggcgccgacg gcatgggcgc taaatcggac gagatctacg ccctgctcaa agcgctcaag     660
gccaaggggg tacccgtcga cggggtgggc ttccaggccc acctcgacag caccttctcg     720
gtccagcagg cgcggatgcg ggagaaccta gagacgcttc gccgacctgg gcctcgaggt     780
gcacatcacc gagctggacg tgcagctaaa aggggcgggc tcgcgggagg aacggctgga     840
ggcgcaggcc cggatctacg ccgaggtgct ggcgacctgc cgcgcggtcc gcggctgcag     900
cgccgtgacg ctgtggggct tcaccgacgc ccactcctgg cgagccgccg ccgaacccct     960
gatcttcgac gcgctctacc ggcccaaacc ggcgtaccag gctctgctgc gggctctggg    1020
aggcaacccct tgagcctttt cagcccagtt ttgccaacga ggacagcact atga         1074
```

<210> 100
<211> 357
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(33)

<400> 100
Val Arg Ser Arg Ala Ser Ala Tyr Trp Phe Gly Val Gly Leu Val Val
1 5 10 15
Ala Leu Ser Leu Ala Gln Thr Pro Ser Pro Gln Ser Leu Arg Ala Leu
20 25 30
Ala Glu Arg Gln Gly Leu Leu Val Gly Ala Ala Val Asp Leu Ala Ala
35 40 45
Leu Tyr Asp Pro Leu Glu Pro Glu Tyr Ala Gln Leu Leu Ala Arg Glu
50 55 60
Phe Asn Leu Val Val Ala Glu Asn Ala Met Lys Trp Ala Ser Leu Ser
65 70 75 80
Asn Ala Arg Gly Gln Tyr Ser Phe Thr Gly Ala Asp Ala Leu Val Arg
85 90 95
Phe Ala Arg Gln His Gly Gln Arg Leu Arg Gly His Thr Leu Ile Trp
100 105 110
His Glu Gln Leu Pro Ala Trp Val Arg Ser Gly Thr Phe Ser Arg Glu
115 120 125
Ala Met Leu Ala Val Met Gln Glu His Ile Gln Ala Val Ala Gly His
130 135 140
Phe Arg Gly Gln Val Ala Tyr Trp Asp Val Val Asn Glu Ala Val Ser
145 150 155 160
Asp Arg Gly Gly Leu Arg Glu Thr Pro Phe Leu Arg Ala Val Gly Pro
165 170 175
Asp Tyr Leu Glu His Ala Phe Arg Phe Ala Arg Ala Ala Asp Pro Gln
180 185 190
Ala Lys Leu Phe Tyr Asn Asp Tyr Gly Ala Asp Gly Met Gly Ala Lys
195 200 205
Ser Asp Glu Ile Tyr Ala Leu Leu Lys Ala Leu Lys Ala Lys Gly Val
210 215 220
Pro Val Asp Gly Val Gly Phe Gln Ala His Leu Asp Ser Thr Phe Ser
225 230 235 240
Val Gln Gln Ala Arg Met Arg Glu Asn Leu Glu Thr Leu Arg Arg Pro
245 250 255
Gly Pro Arg Gly Ala His His Arg Ala Gly Arg Ala Ala Lys Arg Gly
260 265 270
Gly Leu Ala Gly Gly Thr Ala Gly Gly Ala Gly Pro Asp Leu Arg Arg
275 280 285
Gly Ala Gly Asp Leu Pro Arg Gly Pro Arg Leu Gln Arg Arg Asp Ala
290 295 300
Val Gly Leu His Arg Arg Pro Leu Leu Ala Ser Arg Arg Arg Thr Pro
305 310 315 320
Asp Leu Arg Arg Ala Leu Pro Ala Gln Thr Gly Val Pro Gly Ser Ala
325 330 335
Ala Gly Ser Gly Arg Gln Pro Leu Ser Leu Phe Ser Pro Val Leu Pro
340 345 350
Thr Arg Thr Ala Leu
355

<210> 101
<211> 1131
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 101
atgaagtatt ggcttacaac cctggtttta atgatagcgg gaataccctt ggcttttggt 60
tcttcagcaa agcaagataa atcaaagagt ttgaaagatg ctttcaaaaa caaattctat 120
atcggtgtgg ctttgaaccg gagtcaatat ctggaacaaa acgaacaggc ggataaagag 180
ataaaggcac agttcagctc tattgtagct gagaactgca tgaaaagcga aaatctggaa 240
cctaaagagg gaaaattctt ctttgacgat gccgatcgtt ttgtcgcttt tggagaaaaa 300
aatggaatgt acatcattgg acatacctta atttggcatt ctcaagtgcc aaaatggttt 360
ttcatagata atgaaggcaa agttgtttcc cgggaagttt tgattgaacg aatgaaaaac 420
tacatccata cagttgtcgg tcattataaa ggtcgagtta aaggttggga tgttgtcaat 480
gaggccattc tagatgatgg ctcatttaga caaagtaatt tctttaaaat actaggagcc 540

```
gattttatta aacttgcttt tcaatttgcc catgaagcag atcccaatgc tgagctttat      600
tacaacgatt attcgatgtc caatccgacc aaaagagacg gagtggttcg catggtgaag      660
tcattgcagc aacaaggtgt gagaatagac gctatcggaa tgcagggaca cgtagggatg      720
gattatccca agttggatga gtttgaaaat agtatcaaag ctttttcgtc tttaggaacc      780
aaagtgatga ttacggaact cgatttaagt gtcctaccaa ctcctaaagg aaaacaaggt      840
gctaatattt cggatgttgc cgcttatgag gaaaagataa atccttacaa aaatggtctg      900
ccggctgaag ttgaaaaggc ttgggaagac cggtatttgg atttttcaa attatttttg      960
aaatatcaac accaaatttc aagggttaca ttatgggggc ttagtgatca ggattcgtgg     1020
aaaaatgatt tcccagtcag agggagaacg gattatcctt tgcttttcga cagacaatac     1080
aaaccaaaac ctgtagttca gaaaattatt aaattagcat tgaaaaaata a              1131
```

<210> 102
<211> 376
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(23)

<400> 102
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Met Lys Tyr Trp Leu Thr Thr Leu Val Leu Met Ile Ala Gly Ile Pro
 1               5                  10                  15
Leu Ala Phe Gly Ser Ser Ala Lys Gln Asp Lys Ser Lys Ser Leu Lys
            20                  25                  30
Asp Ala Phe Lys Asn Lys Phe Tyr Ile Gly Val Ala Leu Asn Arg Ser
        35                  40                  45
Gln Tyr Leu Glu Gln Asn Glu Gln Ala Asp Lys Glu Ile Lys Ala Gln
    50                  55                  60
Phe Ser Ser Ile Val Ala Glu Asn Cys Met Lys Ser Glu Asn Leu Glu
65                  70                  75                  80
Pro Lys Glu Gly Lys Phe Phe Phe Asp Asp Ala Asp Arg Phe Val Ala
                85                  90                  95
Phe Gly Glu Lys Asn Gly Met Tyr Ile Ile Gly His Thr Leu Ile Trp
            100                 105                 110
His Ser Gln Val Pro Lys Trp Phe Phe Ile Asp Asn Glu Gly Lys Val
        115                 120                 125
Val Ser Arg Glu Val Leu Ile Glu Arg Met Lys Asn Tyr Ile His Thr
    130                 135                 140
Val Val Gly His Tyr Lys Gly Arg Val Lys Gly Trp Asp Val Val Asn
145                 150                 155                 160
Glu Ala Ile Leu Asp Asp Gly Ser Phe Arg Gln Ser Asn Phe Phe Lys
                165                 170                 175
Ile Leu Gly Ala Asp Phe Ile Lys Leu Ala Phe Gln Phe Ala His Glu
            180                 185                 190
Ala Asp Pro Asn Ala Glu Leu Tyr Tyr Asn Asp Tyr Ser Met Ser Asn
        195                 200                 205
Pro Thr Lys Arg Asp Gly Val Val Arg Met Val Lys Ser Leu Gln Gln
    210                 215                 220
Gln Gly Val Arg Ile Asp Ala Ile Gly Met Gln Gly His Val Gly Met
225                 230                 235                 240
Asp Tyr Pro Lys Leu Asp Glu Phe Glu Asn Ser Ile Lys Ala Phe Ser
                245                 250                 255
Ser Leu Gly Thr Lys Val Met Ile Thr Glu Leu Asp Leu Ser Val Leu
            260                 265                 270
Pro Thr Pro Lys Gly Lys Gln Gly Ala Asn Ile Ser Asp Val Ala Ala
        275                 280                 285
Tyr Glu Glu Lys Ile Asn Pro Tyr Lys Asn Gly Leu Pro Ala Glu Val
    290                 295                 300
Glu Lys Ala Trp Glu Asp Arg Tyr Leu Asp Phe Phe Lys Leu Phe Leu
305                 310                 315                 320
Lys Tyr Gln His Gln Ile Ser Arg Val Thr Leu Trp Gly Leu Ser Asp
                325                 330                 335
Gln Asp Ser Trp Lys Asn Asp Phe Pro Val Arg Gly Arg Thr Asp Tyr
            340                 345                 350
Pro Leu Leu Phe Asp Arg Gln Tyr Lys Pro Lys Pro Val Val Gln Lys
        355                 360                 365
```

```
Ile Ile Lys Leu Ala Leu Lys Lys
    370                 375

<210> 103
<211> 1449
<212> DNA
<213> Bacteria

<220>
<223> Obtained from an environmental sample

<400> 103
atgcgttcac attcccttcc cccgtccacc gtccgccgga aattgggcgg cctcggcgcg      60
gcgctgctcg tcggcgccgt cggcgccgcc accgtgctcg tggcgcccct cacctcgcac     120
gccgccgaga gcacgctcgg cgccgcggcg aagcagagcg gccggtactt cggcaccgcc     180
atcgcctcgg gcaggctcaa cgactcgacg tacacgacga tcgcgaaccg cgagttcaac     240
tcggtgaccg ccgagaacga gatgaagatc gacgccaccg aaccccagca gggccgcttc     300
gacttcaccg ccggcgaccg cgtctacaac tgggcggtgc agaacggcaa gcaggtacgg     360
ggccacaccc tggcctggca ctcccagcag cccgcctgga tgcagaacct cagcggcagc     420
gcgctgcgca cggcgatgac caaccacatc aacggcgtca tggcccacta caagggcaag     480
atcggccagt gggacgtcgt caacgaggcg ttcgcggacg gcagttcggg agcgcgccgg     540
gactccaacc tccagcggag cggcaacgac tggatcgagg tcgccttccg caccgcccgc     600
gccgccgacc cggccgccaa gctctgctac aacgactaca acgtcgagaa ctggacgtgg     660
gccaagaccc aggccatgta cgccatggtc aaggacttca agcagcgcgg cgtgcccatc     720
gactgcgtcg gcttccagtc gcacttcaac aacgacagcc cctacaacag caacttccgc     780
accaccctcc agagtttcgc cgccctcggc gtcgacgtgg ccatcaccga actcgacatc     840
cagggcgcct cgggcacgac ctacgccaac gtgaccaacg actgcctggc cgtcccgcgc     900
tgcctcggca tcaccgtctg gggtgtccgc gacaccgact cctggcgagc cgagcacact     960
ccgctgctct tcaacggcga cggcagcaag aagcccgcct actcctccgt cctcaacgcc    1020
ctcaactccg tctcccccaa ccccaacccc actccgaccc cctcccccgg cgccgggccg    1080
atcaagggag tcgcctcggg ccgctgcgtg gacgtacccg gagccggcac cgccgacggc    1140
acccaggtcc agctgtggga ctgcaacaac cgcaccaacc agcagtggac cctcaccgcc    1200
gccggtgagc tcagggtcta cggcgacaag tgcctggacg ccgccggcac cggcaacggc    1260
gccaaggtcc agatctacag ctgctggggc ggcgacaacc agaagtggcg cctcaactcc    1320
gacggttcca tcgtcggtgt ccagtccggc ctctgcctcg acgccgctgc cggcggcacc    1380
gccaacggca cgctgatcca gctctactcc tgctggaaca gcggcaacca gcgctggacc    1440
cgcacctga                                                            1449

<210> 104
<211> 482
<212> PRT
<213> Bacteria

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(41)

<400> 104
Met Arg Ser His Ser Leu Pro Pro Ser Thr Val Arg Arg Lys Leu Gly
 1               5                  10                  15
Gly Leu Gly Ala Ala Leu Leu Val Gly Ala Val Gly Ala Ala Thr Val
            20                  25                  30
Leu Val Ala Pro Leu Thr Ser His Ala Ala Glu Ser Thr Leu Gly Ala
        35                  40                  45
Ala Ala Lys Gln Ser Gly Arg Tyr Phe Gly Thr Ala Ile Ala Ser Gly
    50                  55                  60
Arg Leu Asn Asp Ser Thr Tyr Thr Thr Ile Ala Asn Arg Glu Phe Asn
65                  70                  75                  80
Ser Val Thr Ala Glu Asn Glu Met Lys Ile Asp Ala Thr Glu Pro Gln
                85                  90                  95
Gln Gly Arg Phe Asp Phe Thr Ala Gly Asp Arg Val Tyr Asn Trp Ala
            100                 105                 110
Val Gln Asn Gly Lys Gln Val Arg Gly His Thr Leu Ala Trp His Ser
        115                 120                 125
Gln Gln Pro Ala Trp Met Gln Asn Leu Ser Gly Ser Ala Leu Arg Thr
    130                 135                 140
Ala Met Thr Asn His Ile Asn Gly Val Met Ala His Tyr Lys Gly Lys
```

```
145                 150                 155                 160
Ile Gly Gln Trp Asp Val Val Asn Glu Ala Phe Ala Asp Gly Ser Ser
                165                 170                 175
Gly Ala Arg Arg Asp Ser Asn Leu Gln Arg Ser Gly Asn Asp Trp Ile
            180                 185                 190
Glu Val Ala Phe Arg Thr Ala Arg Ala Ala Asp Pro Ala Ala Lys Leu
        195                 200                 205
Cys Tyr Asn Asp Tyr Asn Val Glu Asn Trp Thr Trp Ala Lys Thr Gln
    210                 215                 220
Ala Met Tyr Ala Met Val Lys Asp Phe Lys Gln Arg Gly Val Pro Ile
225                 230                 235                 240
Asp Cys Val Gly Phe Gln Ser His Phe Asn Asn Asp Ser Pro Tyr Asn
                245                 250                 255
Ser Asn Phe Arg Thr Thr Leu Gln Ser Phe Ala Ala Leu Gly Val Asp
            260                 265                 270
Val Ala Ile Thr Glu Leu Asp Ile Gln Gly Ala Ser Gly Thr Thr Tyr
        275                 280                 285
Ala Asn Val Thr Asn Asp Cys Leu Ala Val Pro Arg Cys Leu Gly Ile
    290                 295                 300
Thr Val Trp Gly Val Arg Asp Thr Asp Ser Trp Arg Ala Glu His Thr
305                 310                 315                 320
Pro Leu Leu Phe Asn Gly Asp Gly Ser Lys Lys Pro Ala Tyr Ser Ser
                325                 330                 335
Val Leu Asn Ala Leu Asn Ser Val Ser Pro Asn Pro Asn Pro Thr Pro
            340                 345                 350
Thr Pro Ser Pro Gly Ala Gly Pro Ile Lys Gly Val Ala Ser Gly Arg
        355                 360                 365
Cys Val Asp Val Pro Gly Ala Gly Thr Ala Asp Gly Thr Gln Val Gln
    370                 375                 380
Leu Trp Asp Cys Asn Asn Arg Thr Asn Gln Gln Trp Thr Leu Thr Ala
385                 390                 395                 400
Ala Gly Glu Leu Arg Val Tyr Gly Asp Lys Cys Leu Asp Ala Ala Gly
                405                 410                 415
Thr Gly Asn Gly Ala Lys Val Gln Ile Tyr Ser Cys Trp Gly Gly Asp
            420                 425                 430
Asn Gln Lys Trp Arg Leu Asn Ser Asp Gly Ser Ile Val Gly Val Gln
        435                 440                 445
Ser Gly Leu Cys Leu Asp Ala Ala Ala Gly Gly Thr Ala Asn Gly Thr
    450                 455                 460
Leu Ile Gln Leu Tyr Ser Cys Trp Asn Ser Gly Asn Gln Arg Trp Thr
465                 470                 475                 480
Arg Thr
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<210> 105
<211> 2793
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 105

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atgaagttca ctttgatgcc gctgctgtgc gggttcgcct tgctgttggg ttgcgcggtg     60
caggcaaccc cagccgcttc gttacagcag gcttatcagc cgtatttcca tatcggtact    120
gccgtcagct tggcgcaact gcaagcatcg aaaaaccatg aacgagattt aatcgcccag    180
cactttaaca gtctgaccgc tgaaaacctg atgaaatggg aaaaaatcca accgactgaa    240
ggcaactttg atttacagc ggccgacaag ctcgtcgctt ttgctgaaca acatcggatg    300
tggctggtcg gccatacgat cctgtggcat gaacaaaccc cggactgggt atttcagggg    360
ccagatggca aaccggccag caagcaagtg ttactcggca gattaaaaaa gcatatccaa    420
actgtggtcg gtcgttacca aggtcgggta catggctggg atgtagtgaa tgaagcgctg    480
aatgaagatg gcagtctgcg cgatacgccg tggcgaaaaa ttctgggtga tgattacatt    540
gccaccactt ttgcgctggt gcatcaggtc gaccccaaag ccaaactcta ttacaacgac    600
tacaacctgt ataaaccaaa aaaacgcact ggcgtgctac ggatcatcca gcaactgcag    660
caacaacaag tgcccattca tgccattggc gaacaagcgc attatggtct cgattcgccg    720
aaattgcagg aagttgaaga ctcgatcaac gcctttgcag ccaccggcct cgacgtgatg    780
ctgaccgagt tggaaatttc ggtgctaccg tttccgcctg gcatgacacc aggcgccgat    840
atcagtcagc atcaggaact gcaacaacag ctgaatcctt accgcgaagg cttaccaaaa    900
accgtcgaac aggcctggca acaacgttat ctggatctgt tttcgctgtt attgcgccag    960
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catcaaaaat tacaccgggt gacgttttgg ggtttagatg atggccaaag ctggcgcaat 1020
aactttccaa tgcgcggtcg taccgattac ccgctactgt ttgaccgcaa gctgcaagcc 1080
aaaccgctat tgagcgcact gatcaaactg gcagaaactc aagcctcagc caagccgaaa 1140
gtaaatcagc tcggttttgc gccaaatgcg caaaaattgc tggtggtgcc ggggcggcag 1200
gcggtgtcgt ttcagatcat caatcaaagc aacggcaaaa cggtgttgca aggccaaagt 1260
tcggtggctc agttttggcc cgaatcgggc gagtgggtca gtatcgctga cttttcgacc 1320
ttaaccaccc aagggcgtta tcaggttgaa gcggctggat taactccgat caccgtcgag 1380
attactgctg aaccttatgc cgcgctgcat gatgcgtcca tcaaagccta ttattttaat 1440
cgcgcctcgc tggcgctgga gccaagtttt gccgggcctt gggcgcgcgc tgccggtcat 1500
ccggataaca aagtgttggt gcacacttcc gccgcttccg acaagcgacc agccggtttt 1560
gtgatcagcg ccgctaaagg ctggtatgac gccggtgact ataacaaata cgtggtcaat 1620
tccggtattt ccagttacac cctattgcaa gcctggcagg attttcctga gttttatcgc 1680
gacagaacat ggaatcttcc ggagtccagc aacaacctac cagacattct cgacgagacg 1740
ttatggaatt tacagtggct gagcaccatg caggacccaa gcgacggcgg cgtgtatcac 1800
aagctgactg aactgaattt ctctgctacc caaatgccgt cagaagtgac agcgccacgt 1860
tatgtggtgc aaaaaaccac ggcagcggca cttaatttcg cggcggtgct ggccaaagcc 1920
agtcgcattt ttacagaatt tgaaacgcaa ctgcccggcc tgtcacagca atatcgccag 1980
caagcattag cagcctggca atgggcgcaa aaaaatccac aacaaattta tcagcaacca 2040
gccgatgttc acaccggtgc ttatggcgac aaacagctgg ctgatgaatg ggcttgggct 2100
ggggcggagc tatatttatt aaccggtgag cagagttacc tgcagccgtt gttggcactt 2160
gagacgccaa tcaccgcagc ttcctgggcc aatgtggcgg cgttgggtta ttttgcgttg 2220
gcatccgctg aacagtttga gcctgcactt cgaaaaaaag tgcagcaaaa aatccaacaa 2280
gccgcggcgc aaattgtagc cgagcatcaa gcgtccgcct accaggtggc gatgactcaa 2340
aaagattttg tctggggcag taatgcggtg gcgatgaaca aaggcatgtt gttatatcaa 2400
gcgtggaaaa ttgacccaca accagagctg cgacaggcga tgcaagggct gctggattac 2460
gtcctcggtc gcaacccgct gcagctgtct tatgtcacag gttttggtgc gcaaagcccg 2520
caacatatcc atcaccgccc ctcggcggca gatcagatca aagcaccagt gccgggctgg 2580
ttagtgggtg gtgcacagcc gggtaagcaa gataaatgct cttattccgg tatttttgct 2640
accggcactt tacccgctgc cagcacttta cctgcaacga cttatctcga ccactggtgc 2700
agctacgcca ccaatgaagt ggcgattaac tggaatgcac ctttagtgta cgtgctggcc 2760
tggagccttt caccagactc catgaccaaa tga 2793

<210> 106
<211> 930
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<400> 106
Met Lys Phe Thr Leu Met Pro Leu Leu Cys Gly Phe Ala Leu Leu Leu
1 5 10 15
Gly Cys Ala Val Gln Ala Thr Pro Ala Ala Ser Leu Gln Gln Ala Tyr
20 25 30
Gln Pro Tyr Phe His Ile Gly Thr Ala Val Ser Leu Ala Gln Leu Gln
35 40 45
Ala Ser Lys Asn His Glu Arg Asp Leu Ile Ala Gln His Phe Asn Ser
50 55 60
Leu Thr Ala Glu Asn Leu Met Lys Trp Glu Lys Ile Gln Pro Thr Glu
65 70 75 80
Gly Asn Phe Asp Phe Thr Ala Ala Asp Lys Leu Val Ala Phe Ala Glu
85 90 95
Gln His Arg Met Trp Leu Val Gly His Thr Ile Leu Trp His Glu Gln
100 105 110
Thr Pro Asp Trp Val Phe Gln Gly Pro Asp Gly Lys Pro Ala Ser Lys
115 120 125
Gln Val Leu Leu Gly Arg Leu Lys Lys His Ile Gln Thr Val Val Gly
130 135 140
Arg Tyr Gln Gly Arg Val His Gly Trp Asp Val Val Asn Glu Ala Leu
145 150 155 160
Asn Glu Asp Gly Ser Leu Arg Asp Thr Pro Trp Arg Lys Ile Leu Gly
165 170 175
Asp Asp Tyr Ile Ala Thr Thr Phe Ala Leu Val His Gln Val Asp Pro
180 185 190
Lys Ala Lys Leu Tyr Tyr Asn Asp Tyr Asn Leu Tyr Lys Pro Lys Lys

```
                195                     200                     205
Arg Thr Gly Val Leu Arg Ile Ile Gln Gln Leu Gln Gln Gln Gln Val
    210                     215                     220
Pro Ile His Ala Ile Gly Glu Gln Ala His Tyr Gly Leu Asp Ser Pro
225                     230                     235                     240
Lys Leu Gln Glu Val Glu Asp Ser Ile Asn Ala Phe Ala Ala Thr Gly
                245                     250                     255
Leu Asp Val Met Leu Thr Glu Leu Glu Ile Ser Val Leu Pro Phe Pro
            260                     265                     270
Pro Gly Met Thr Pro Gly Ala Asp Ile Ser Gln His Gln Glu Leu Gln
        275                     280                     285
Gln Gln Leu Asn Pro Tyr Arg Glu Gly Leu Pro Lys Thr Val Glu Gln
    290                     295                     300
Ala Trp Gln Gln Arg Tyr Leu Asp Leu Phe Ser Leu Leu Leu Arg Gln
305                     310                     315                     320
His Gln Lys Leu His Arg Val Thr Phe Trp Gly Leu Asp Asp Gly Gln
                325                     330                     335
Ser Trp Arg Asn Asn Phe Pro Met Arg Gly Arg Thr Asp Tyr Pro Leu
            340                     345                     350
Leu Phe Asp Arg Lys Leu Gln Ala Lys Pro Leu Leu Ser Ala Leu Ile
        355                     360                     365
Lys Leu Ala Glu Thr Gln Ala Ser Ala Lys Pro Lys Val Asn Gln Leu
    370                     375                     380
Gly Phe Ala Pro Asn Ala Gln Lys Leu Leu Val Val Pro Gly Arg Gln
385                     390                     395                     400
Ala Val Ser Phe Gln Ile Ile Asn Gln Ser Asn Gly Lys Thr Val Leu
                405                     410                     415
Gln Gly Gln Ser Ser Val Ala Gln Phe Trp Pro Glu Ser Gly Glu Trp
            420                     425                     430
Val Ser Ile Ala Asp Phe Ser Thr Leu Thr Thr Gln Gly Arg Tyr Gln
        435                     440                     445
Val Glu Ala Ala Gly Leu Thr Pro Ile Thr Val Glu Ile Thr Ala Glu
    450                     455                     460
Pro Tyr Ala Ala Leu His Asp Ala Ser Ile Lys Ala Tyr Tyr Phe Asn
465                     470                     475                     480
Arg Ala Ser Leu Ala Leu Glu Pro Ser Phe Ala Gly Pro Trp Ala Arg
                485                     490                     495
Ala Ala Gly His Pro Asp Asn Lys Val Leu Val His Thr Ser Ala Ala
            500                     505                     510
Ser Asp Lys Arg Pro Ala Gly Phe Val Ile Ser Ala Ala Lys Gly Trp
        515                     520                     525
Tyr Asp Ala Gly Asp Tyr Asn Lys Tyr Val Val Asn Ser Gly Ile Ser
    530                     535                     540
Ser Tyr Thr Leu Leu Gln Ala Trp Gln Asp Phe Pro Glu Phe Tyr Arg
545                     550                     555                     560
Asp Arg Thr Trp Asn Leu Pro Glu Ser Ser Asn Asn Leu Pro Asp Ile
                565                     570                     575
Leu Asp Glu Thr Leu Trp Asn Leu Gln Trp Leu Ser Thr Met Gln Asp
            580                     585                     590
Pro Ser Asp Gly Gly Val Tyr His Lys Leu Thr Glu Leu Asn Phe Ser
        595                     600                     605
Ala Thr Gln Met Pro Ser Glu Val Thr Ala Pro Arg Tyr Val Val Gln
    610                     615                     620
Lys Thr Thr Ala Ala Ala Leu Asn Phe Ala Ala Val Leu Ala Lys Ala
625                     630                     635                     640
Ser Arg Ile Phe Thr Glu Phe Glu Thr Gln Leu Pro Gly Leu Ser Gln
                645                     650                     655
Gln Tyr Arg Gln Gln Ala Leu Ala Ala Trp Gln Trp Ala Gln Lys Asn
            660                     665                     670
Pro Gln Gln Ile Tyr Gln Gln Pro Ala Asp Val His Thr Gly Ala Tyr
        675                     680                     685
Gly Asp Lys Gln Leu Ala Asp Glu Trp Ala Trp Ala Gly Ala Glu Leu
    690                     695                     700
Tyr Leu Leu Thr Gly Glu Gln Ser Tyr Leu Gln Pro Leu Leu Ala Leu
705                     710                     715                     720
Glu Thr Pro Ile Thr Ala Ala Ser Trp Ala Asn Val Ala Ala Leu Gly
                725                     730                     735
Tyr Phe Ala Leu Ala Ser Ala Glu Gln Phe Glu Pro Ala Leu Arg Lys
            740                     745                     750
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Lys Val Gln Gln Lys Ile Gln Gln Ala Ala Ala Gln Ile Val Ala Glu
755 760 765
His Gln Ala Ser Ala Tyr Gln Val Ala Met Thr Gln Lys Asp Phe Val
770 775 780
Trp Gly Ser Asn Ala Val Ala Met Asn Lys Gly Met Leu Leu Tyr Gln
785 790 795 800
Ala Trp Lys Ile Asp Pro Gln Pro Glu Leu Arg Gln Ala Met Gln Gly
805 810 815
Leu Leu Asp Tyr Val Leu Gly Arg Asn Pro Leu Gln Leu Ser Tyr Val
820 825 830
Thr Gly Phe Gly Ala Gln Ser Pro Gln His Ile His His Arg Pro Ser
835 840 845
Ala Ala Asp Gln Ile Lys Ala Pro Val Pro Gly Trp Leu Val Gly Gly
850 855 860
Ala Gln Pro Gly Lys Gln Asp Lys Cys Ser Tyr Ser Gly Ile Phe Ala
865 870 875 880
Thr Gly Thr Leu Pro Ala Ala Ser Thr Leu Pro Ala Thr Thr Tyr Leu
885 890 895
Asp His Trp Cys Ser Tyr Ala Thr Asn Glu Val Ala Ile Asn Trp Asn
900 905 910
Ala Pro Leu Val Tyr Val Leu Ala Trp Ser Leu Ser Pro Asp Ser Met
915 920 925
Thr Lys
930

<210> 107
<211> 1725
<212> DNA
<213> Bacteria

<400> 107
gtgtggaagc ccggattgtg gaatttcctt caaatggcag atgaagccgg attgacgagg 60
gatggaaaca ctccggttcc gacacccagt ccaaagccgg ctaacacacg tattgaagcg 120
gaagattatg acggtattaa ttcttcaagt attgagataa taggtgttcc acctgaagga 180
ggcagaggaa taggttatat taccagtggt gattatctgg tatacaagag tatagacttt 240
ggaaacggag caacgtcgtt taaggccaag gttgcaaatg caaatacttc caatattgaa 300
cttagattaa acggtccgaa tggtactctc ataggcacac tctcggtaaa atccacagga 360
gattggaata catatgagga gcaaacttgc agcattagca aagtcaccgg aataaatgat 420
ttgtacttgg tattcaaagg ccctgtaaac atagactggt tcacttttgg cgttgaaagc 480
agttccacag gtctgggggga tttaaatggt gacggaaata ttaactcgtc ggaccttcag 540
gcgttaaaga ggcatttgct cggtatatca ccgcttacgg gagaggctct tttaagagcg 600
gatgtaaata ggagcggcaa agtggattct actgactatt cagtgctgaa aagatatata 660
ctccgcatta ttacagagtt ccccggacaa ggtgatgtac agacacccaa tccgtctgtt 720
actccgacac aaactcctat ccccacgatt tcgggaaatg ctcttaggga ttatgcggag 780
gcaaggggaa taaaaatcgg aacatgtgtc aactatccgt tttacaacaa ttcagatcca 840
acctacaaca gcattttgca aagagaattt tcaatggttg tatgtgaaaa tgaaatgaag 900
tttgatgctt tgcagccgag acaaaacgtt tttgattttt cgaaaggaga ccagttgctt 960
gcttttgcag aaagaaacgg tatgcagatg aggggacata cgttgatttg gcacaatcaa 1020
aacccgtcat ggcttacaaa cggtaactgg aaccgggatt cgctgcttgc ggtaatgaaa 1080
aatcacatta ccactgttat gacccattac aaaggtaaaa ttgttgagtg ggatgtggca 1140
aacgaatgta tggatgattc cggcaacggc ttaagaagca gcatatggag aaatgtaatc 1200
ggtcaggact accttgacta tgctttcagg tatgcaagag aagcagatcc cgatgcactt 1260
cttttctaca atgattataa tattgaagac ttgggtccaa agtccaatgc ggtatttaac 1320
atgattaaaa gtatgaagga aagaggtgtg ccgattgacg gagtaggatt ccaatgccac 1380
tttatcaatg gaatgagccc cgagtacctt gccagcattg atcaaaatat taagagatat 1440
gcggaaatag gcgttatagt atcctttacc gaaatagata tacgcatacc tcagtcggaa 1500
aacccggcaa ctgcattcca ggtacaggca aacaactata aggaacttat gaaaatttgt 1560
ctggcaaacc ccaattgcaa taccttttgta atgtggggat tcacagataa atacacatgg 1620
attccgggaa ctttcccagg atatggcaat ccattgattt atgacagcaa ttacaatccg 1680
aaaccggcat acaatgcaat aaaggaagct cttatgggct attga 1725

<210> 108
<211> 574
<212> PRT
<213> Bacteria

<400> 108
Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
1 5 10 15

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
20 25 30
Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
35 40 45
Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
50 55 60
Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
65 70 75 80
Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
85 90 95
Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
100 105 110
Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
115 120 125
Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
130 135 140
Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val Glu Ser
145 150 155 160
Ser Ser Thr Gly Leu Gly Asp Leu Asn Gly Asp Gly Asn Ile Asn Ser
165 170 175
Ser Asp Leu Gln Ala Leu Lys Arg His Leu Leu Gly Ile Ser Pro Leu
180 185 190
Thr Gly Glu Ala Leu Leu Arg Ala Asp Val Asn Arg Ser Gly Lys Val
195 200 205
Asp Ser Thr Asp Tyr Ser Val Leu Lys Arg Tyr Ile Leu Arg Ile Ile
210 215 220
Thr Glu Phe Pro Gly Gln Gly Asp Val Gln Thr Pro Asn Pro Ser Val
225 230 235 240
Thr Pro Thr Gln Thr Pro Ile Pro Thr Ile Ser Gly Asn Ala Leu Arg
245 250 255
Asp Tyr Ala Glu Ala Arg Gly Ile Lys Ile Gly Thr Cys Val Asn Tyr
260 265 270
Pro Phe Tyr Asn Asn Ser Asp Pro Thr Tyr Asn Ser Ile Leu Gln Arg
275 280 285
Glu Phe Ser Met Val Val Cys Glu Asn Glu Met Lys Phe Asp Ala Leu
290 295 300
Gln Pro Arg Gln Asn Val Phe Asp Phe Ser Lys Gly Asp Gln Leu Leu
305 310 315 320
Ala Phe Ala Glu Arg Asn Gly Met Gln Met Arg Gly His Thr Leu Ile
325 330 335
Trp His Asn Gln Asn Pro Ser Trp Leu Thr Asn Gly Asn Trp Asn Arg
340 345 350
Asp Ser Leu Leu Ala Val Met Lys Asn His Ile Thr Thr Val Met Thr
355 360 365
His Tyr Lys Gly Lys Ile Val Glu Trp Asp Val Ala Asn Glu Cys Met
370 375 380
Asp Asp Ser Gly Asn Gly Leu Arg Ser Ser Ile Trp Arg Asn Val Ile
385 390 395 400
Gly Gln Asp Tyr Leu Asp Tyr Ala Phe Arg Tyr Ala Arg Glu Ala Asp
405 410 415
Pro Asp Ala Leu Leu Phe Tyr Asn Asp Tyr Asn Ile Glu Asp Leu Gly
420 425 430
Pro Lys Ser Asn Ala Val Phe Asn Met Ile Lys Ser Met Lys Glu Arg
435 440 445
Gly Val Pro Ile Asp Gly Val Gly Phe Gln Cys His Phe Ile Asn Gly
450 455 460
Met Ser Pro Glu Tyr Leu Ala Ser Ile Asp Gln Asn Ile Lys Arg Tyr
465 470 475 480
Ala Glu Ile Gly Val Ile Val Ser Phe Thr Glu Ile Asp Ile Arg Ile
485 490 495
Pro Gln Ser Glu Asn Pro Ala Thr Ala Phe Gln Val Gln Ala Asn Asn
500 505 510
Tyr Lys Glu Leu Met Lys Ile Cys Leu Ala Asn Pro Asn Cys Asn Thr
515 520 525
Phe Val Met Trp Gly Phe Thr Asp Lys Tyr Thr Trp Ile Pro Gly Thr
530 535 540
Phe Pro Gly Tyr Gly Asn Pro Leu Ile Tyr Asp Ser Asn Tyr Asn Pro
545 550 555 560
Lys Pro Ala Tyr Asn Ala Ile Lys Glu Ala Leu Met Gly Tyr

565 570

<210> 109
<211> 1242
<212> DNA
<213> Unknown

<220>
<223> obtained from an environmental sample

<400> 109
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gcaggggcag ctggtgccga aactaatatt tcaaagaagc caaatataag tggattaacc   120
gcgccgcaat tagaccaaag atataaagat tctttcacca ttggtgctgc ggttgagccg   180
tatcaattat tagatgcaaa agattcacaa atgctaaagc ggcattttaa tagtatcgta   240
gcagagaatg tcatgaagcc tagtagttta cagccagtag aaggacaatt caattgggag   300
ccggccgata aacttgttca gtttgcgaag gaaaatggaa tggacatgcg cggacatacg   360
cttgtctggc atagccaggt accggattgg ttctttgaag atgcggcagg aaatccaatg   420
gttgtttggg aaaatggcag gcaagtggtt gccgatccag caaatcttca ggaaaacaaa   480
gagctcttac ttagccgatt acaaaatcat attcaggcag tcgtaacgcg ttataaagat   540
gatataaaat cttgggatgt tgttaatgaa gtaatcgatg aatggggcgg acattctgaa   600
gggctgcgtc aatctccatg gttcctcatc accggaacgg actatattaa agttgctttt   660
gaaactgcaa gagaatatgc agctccagac gctaagctgt atatcaatga ttacaataca   720
gaagtagaac caaaaaggac gcacctttat aacttagtaa aaagtttaaa agaagaacaa   780
aacgttccaa ttgatggtgt tgggcatcag tctcacattc aaattggctg gccttcagaa   840
aaagaaattg aagataccat taatatgttt gcagatcttg gtttagataa ccaaatcacc   900
gagcttgatg ttagtatgta tggctggcca gtaaggtcgt atccaactta tgatgcgatc   960
ccagaactta aattcatgga tcaagcagct cgttatgatc gtttatttaa gttatatgag  1020
aaattaggag ataaaatcag taatgtgaca ttctggggta ttgcggataa ccatacatgg  1080
ctgaatgacc gtgcagatgt ttactatgat gaaaatggaa atgttgtatt agatagagaa  1140
acaccaagag tagaaagagg agcaggaaaa gatgcgccat ttgtatttga tcctgaatac  1200
aatgtaaaac cagcttattg ggcaattatc gaccacaaat aa                      1242
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<210> 110
<211> 413
<212> PRT
<213> Unknown

<220>
<223> obtained from an environmental sample

<221> SIGNAL
<222> (1)...(26)

<400> 110
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Met Leu Lys Val Leu Arg Lys Pro Ile Ile Ser Gly Leu Ala Leu Ala
 1               5                  10                  15
Leu Leu Leu Pro Ala Gly Ala Ala Gly Ala Glu Thr Asn Ile Ser Lys
            20                  25                  30
Lys Pro Asn Ile Ser Gly Leu Thr Ala Pro Gln Leu Asp Gln Arg Tyr
        35                  40                  45
Lys Asp Ser Phe Thr Ile Gly Ala Ala Val Glu Pro Tyr Gln Leu Leu
    50                  55                  60
Asp Ala Lys Asp Ser Gln Met Leu Lys Arg His Phe Asn Ser Ile Val
65                  70                  75                  80
Ala Glu Asn Val Met Lys Pro Ser Ser Leu Gln Pro Val Glu Gly Gln
                85                  90                  95
Phe Asn Trp Glu Pro Ala Asp Lys Leu Val Gln Phe Ala Lys Glu Asn
            100                 105                 110
Gly Met Asp Met Arg Gly His Thr Leu Val Trp His Ser Gln Val Pro
        115                 120                 125
Asp Trp Phe Phe Glu Asp Ala Ala Gly Asn Pro Met Val Val Trp Glu
    130                 135                 140
Asn Gly Arg Gln Val Val Ala Asp Pro Ala Asn Leu Gln Glu Asn Lys
145                 150                 155                 160
Glu Leu Leu Leu Ser Arg Leu Gln Asn His Ile Gln Ala Val Val Thr
                165                 170                 175
Arg Tyr Lys Asp Asp Ile Lys Ser Trp Asp Val Val Asn Glu Val Ile
            180                 185                 190
```

Asp Glu Trp Gly Gly His Ser Glu Gly Leu Arg Gln Ser Pro Trp Phe
195 200 205
Leu Ile Thr Gly Thr Asp Tyr Ile Lys Val Ala Phe Glu Thr Ala Arg
210 215 220
Glu Tyr Ala Ala Pro Asp Ala Lys Leu Tyr Ile Asn Asp Tyr Asn Thr
225 230 235 240
Glu Val Glu Pro Lys Arg Thr His Leu Tyr Asn Leu Val Lys Ser Leu
245 250 255
Lys Glu Glu Gln Asn Val Pro Ile Asp Gly Val Gly His Gln Ser His
260 265 270
Ile Gln Ile Gly Trp Pro Ser Glu Lys Glu Ile Glu Asp Thr Ile Asn
275 280 285
Met Phe Ala Asp Leu Gly Leu Asp Asn Gln Ile Thr Glu Leu Asp Val
290 295 300
Ser Met Tyr Gly Trp Pro Val Arg Ser Tyr Pro Thr Tyr Asp Ala Ile
305 310 315 320
Pro Glu Leu Lys Phe Met Asp Gln Ala Ala Arg Tyr Asp Arg Leu Phe
325 330 335
Lys Leu Tyr Glu Lys Leu Gly Asp Lys Ile Ser Asn Val Thr Phe Trp
340 345 350
Gly Ile Ala Asp Asn His Thr Trp Leu Asn Asp Arg Ala Asp Val Tyr
355 360 365
Tyr Asp Glu Asn Gly Asn Val Val Leu Asp Arg Glu Thr Pro Arg Val
370 375 380
Glu Arg Gly Ala Gly Lys Asp Ala Pro Phe Val Phe Asp Pro Glu Tyr
385 390 395 400
Asn Val Lys Pro Ala Tyr Trp Ala Ile Ile Asp His Lys
405 410

<210> 111
<211> 1089
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 111
atgttgacga ccccgacaac tcaagatcat gtccccgtgc ttaaggacgc tttcaaaggc 60
aagttcctca ttggagccgt gctgggttat gacgcactcc agggaaagga tccggcgagt 120
gtggaaattg cgaccacgca cttcgatgct ctcactgcgg aaaacagcat gaagcccgct 180
ctggtgcaac ctaaagaggg cgaatttgac ttcgctgatg gagaccggct tcttgacatc 240
acacagcagt gcggtgcgac tgcgattggc cacactttgc tctggcacca acagacaccg 300
aaatggtttt tcgaggggcc agatgaccag cctactaacc gcgagttggc cctggcacgc 360
atgagaaagc acatcgccac tcttgttggc cgttacaaag gtcgcattaa gcaatgggat 420
gtggtgaatg aggcgattag cgatgcagag ggcgagtact tgagaccaaa tagtccatgg 480
ttcaaggctg ttggagaaga tcacattgcg caggctttcc gggcagcgca cgaagccgat 540
cctgacgcca tcctcatcta taacgattac aacatcgagc aggagtacaa gcgtcccaaa 600
gcgatacgac tgctgaggtc attacttgag caggacgttc cccttcatgc cgtgggcatc 660
cagggccact ggcgtatgga cactctgaat gttgccgaaa tcgaagaagc tatcaaagaa 720
tttgctgcgc tgggtctcaa ggtcatgatc accgagcttg acatcagcgt gctaccgaca 780
aagtatcagg gagccgatct ctctacccgc gaagaattga cgcctgaaat caatccctat 840
acggagggac tacccgagaa cgttgcccgg caacatgccg aatgttaccg ccaagtcttc 900
aaaatgttcc tgtgccacaa ggatgccatt ggccgtgtca cgctctgggg cgttcatgat 960
ggcagatcat ggttcaatga ctttcccgtc agagggcgca ccgattatcc tctgcttttc 1020
gaccggcagg gcaaacccaa gccagcattt tttgccgtct tgaaggctgc gcaagatcag 1080
ccacaatga 1089

<210> 112
<211> 362
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 112
Met Leu Thr Thr Pro Thr Thr Gln Asp His Val Pro Val Leu Lys Asp
1 5 10 15

Ala Phe Lys Gly Lys Phe Leu Ile Gly Ala Val Leu Gly Tyr Asp Ala
20 25 30
Leu Gln Gly Lys Asp Pro Ala Ser Val Glu Ile Ala Thr Thr His Phe
35 40 45
Asp Ala Leu Thr Ala Glu Asn Ser Met Lys Pro Ala Leu Val Gln Pro
50 55 60
Lys Glu Gly Glu Phe Asp Phe Ala Asp Gly Asp Arg Leu Leu Asp Ile
65 70 75 80
Thr Gln Gln Cys Gly Ala Thr Ala Ile Gly His Thr Leu Leu Trp His
85 90 95
Gln Gln Thr Pro Lys Trp Phe Phe Glu Gly Pro Asp Asp Gln Pro Thr
100 105 110
Asn Arg Glu Leu Ala Leu Ala Arg Met Arg Lys His Ile Ala Thr Leu
115 120 125
Val Gly Arg Tyr Lys Gly Arg Ile Lys Gln Trp Asp Val Val Asn Glu
130 135 140
Ala Ile Ser Asp Ala Glu Gly Glu Tyr Leu Arg Pro Asn Ser Pro Trp
145 150 155 160
Phe Lys Ala Val Gly Glu Asp His Ile Ala Gln Ala Phe Arg Ala Ala
165 170 175
His Glu Ala Asp Pro Asp Ala Ile Leu Ile Tyr Asn Asp Tyr Asn Ile
180 185 190
Glu Gln Glu Tyr Lys Arg Pro Lys Ala Ile Arg Leu Leu Arg Ser Leu
195 200 205
Leu Glu Gln Asp Val Pro Leu His Ala Val Gly Ile Gln Gly His Trp
210 215 220
Arg Met Asp Thr Leu Asn Val Ala Glu Ile Glu Glu Ala Ile Lys Glu
225 230 235 240
Phe Ala Ala Leu Gly Leu Lys Val Met Ile Thr Glu Leu Asp Ile Ser
245 250 255
Val Leu Pro Thr Lys Tyr Gln Gly Ala Asp Leu Ser Thr Arg Glu Glu
260 265 270
Leu Thr Pro Glu Ile Asn Pro Tyr Thr Glu Gly Leu Pro Glu Asn Val
275 280 285
Ala Arg Gln His Ala Glu Cys Tyr Arg Gln Val Phe Lys Met Phe Leu
290 295 300
Cys His Lys Asp Ala Ile Gly Arg Val Thr Leu Trp Gly Val His Asp
305 310 315 320
Gly Arg Ser Trp Phe Asn Asp Phe Pro Val Arg Gly Arg Thr Asp Tyr
325 330 335
Pro Leu Leu Phe Asp Arg Gln Gly Lys Pro Lys Pro Ala Phe Phe Ala
340 345 350
Val Leu Lys Ala Ala Gln Asp Gln Pro Gln
355 360

<210> 113
<211> 1155
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 113
atgttaaaag tattgcgtaa accacttttt tctggattag ctttagcgat agtattacct 60
accggattat ccagtgctta tgcagctgaa aatcaaccag ttagtgcatt agatgcagcg 120
gttgaacttg atgaaagata tgcagaatca ttcgatattg gtgcagccgt tgagccttct 180
atgcttcaag gaaaagatgc tgaagtatta aagcgtcatt ataacagcat tgtggccgaa 240
aatgtaatga aaccgattaa tatacagcct gaagaaggaa agttcacttt taaagaaatg 300
gataaaatcg ttaagtttgc gaaagaaaat aatatgaagc ttcgtggcca tacccttatt 360
tggcacagtc aagtaccgga gtggttcttc cttgataaag aaggaaataa gatggtggat 420
gaaacggatc caaagcagcg cgaaaaaaat aaaaggcttt tacttaagcg tttagaaacg 480
catattaaaa cgatcgtcaa gcgctataaa aatgatatta gctcctggga cgtggtcaac 540
gaggtagtgg atgataacgg gaaattacgt aattcacccct ggtatcaaat cacaggtact 600
gattatatca aggttgcttt tgaaacagcg gaccgttatg cagggaagaa cgctaagctt 660
tatatcaatg actacaacac ggaaatagac cctaaaagag aaaccctcta taatcttgtc 720
aaggaattag tgaaggaggg agtcccagtt gatggagtgg gacatcaagc tcatatccaa 780
atcggctggc caactatagc ggaaatcgag aaaaccatta atatgtttgc agaccttggc 840
ctagacaatc aaattacaga actagatgtt agcctttatg ggtggccgcc aaagcctgct 900

tacccaactt atgacgaaat cccggcaagt gaattcgaac gtcaagctgt tcgttacgat 960
caactatttg atttatacga gagattggga gataaaatta gcagtgtgac attctggggc 1020
gttgctgaca accatacatg gttaaatgac cgtgcagaac aatataatga cggggtaggc 1080
gtggacgcac catttgtttt cgataaggat tataatgtaa aaccagctta ttgggctatt 1140
atcgatcgcg attaa 1155

<210> 114
<211> 384
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<400> 114
Met Leu Lys Val Leu Arg Lys Pro Leu Phe Ser Gly Leu Ala Leu Ala
1 5 10 15
Ile Val Leu Pro Thr Gly Leu Ser Ser Ala Tyr Ala Ala Glu Asn Gln
20 25 30
Pro Val Ser Ala Leu Asp Ala Ala Val Glu Leu Asp Glu Arg Tyr Ala
35 40 45
Glu Ser Phe Asp Ile Gly Ala Ala Val Glu Pro Ser Met Leu Gln Gly
50 55 60
Lys Asp Ala Glu Val Leu Lys Arg His Tyr Asn Ser Ile Val Ala Glu
65 70 75 80
Asn Val Met Lys Pro Ile Asn Ile Gln Pro Glu Glu Gly Lys Phe Thr
85 90 95
Phe Lys Glu Met Asp Lys Ile Val Lys Phe Ala Lys Glu Asn Asn Met
100 105 110
Lys Leu Arg Gly His Thr Leu Ile Trp His Ser Gln Val Pro Glu Trp
115 120 125
Phe Phe Leu Asp Lys Glu Gly Asn Lys Met Val Asp Glu Thr Asp Pro
130 135 140
Lys Gln Arg Glu Lys Asn Lys Arg Leu Leu Leu Lys Arg Leu Glu Thr
145 150 155 160
His Ile Lys Thr Ile Val Lys Arg Tyr Lys Asn Asp Ile Ser Ser Trp
165 170 175
Asp Val Val Asn Glu Val Val Asp Asp Asn Gly Lys Leu Arg Asn Ser
180 185 190
Pro Trp Tyr Gln Ile Thr Gly Thr Asp Tyr Ile Lys Val Ala Phe Glu
195 200 205
Thr Ala Asp Arg Tyr Ala Gly Lys Asn Ala Lys Leu Tyr Ile Asn Asp
210 215 220
Tyr Asn Thr Glu Ile Asp Pro Lys Arg Glu Thr Leu Tyr Asn Leu Val
225 230 235 240
Lys Glu Leu Val Lys Glu Gly Val Pro Val Asp Gly Val Gly His Gln
245 250 255
Ala His Ile Gln Ile Gly Trp Pro Thr Ile Ala Glu Ile Glu Lys Thr
260 265 270
Ile Asn Met Phe Ala Asp Leu Gly Leu Asp Asn Gln Ile Thr Glu Leu
275 280 285
Asp Val Ser Leu Tyr Gly Trp Pro Pro Lys Pro Ala Tyr Pro Thr Tyr
290 295 300
Asp Glu Ile Pro Ala Ser Glu Phe Glu Arg Gln Ala Val Arg Tyr Asp
305 310 315 320
Gln Leu Phe Asp Leu Tyr Glu Arg Leu Gly Asp Lys Ile Ser Ser Val
325 330 335
Thr Phe Trp Gly Val Ala Asp Asn His Thr Trp Leu Asn Asp Arg Ala
340 345 350
Glu Gln Tyr Asn Asp Gly Val Gly Val Asp Ala Pro Phe Val Phe Asp
355 360 365
Lys Asp Tyr Asn Val Lys Pro Ala Tyr Trp Ala Ile Ile Asp Arg Asp
370 375 380

<210> 115
<211> 1362

<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 115
atgacgaacc gtaaatcgaa cgtgcaccgt tcattgaccg atgatttgct cgatggtgtc 60
ttcgccgagg caaaagcggg caaagttgag aagtaccgtg ccaccgggat ccttggaacg 120
ctattcggat tcactgtggc gtcctccatc atgttggcgg cttgcagcaa cgcacaagag 180
aatgttccac cagttgcttc atccaccgca cagagcaata tcacccagga gaacgttccg 240
ccgctcaaag atgcgtttaa gggcaagttc ttgattggca ccgcggtgag caatcgcttg 300
ctggagggac aagatccggc cacggaagcc ttggtgcgca ggcacttcga tgctctcacg 360
gcggaaaacg ccatgaagcc ggatgcactg caaccgcgcg aaggccagtt caacttcgtc 420
gccgccgacc gtctggtgga aatcgcccag caaagcggcg cgacagtggt cggccacacg 480
ctggtctggc actcccaaac gccaggctgg ttcttccagg gtccgaatgg ccagccagcg 540
agtcgagaac tggccctggc gcggatgcga acacacatca agacggtggt gggacgctac 600
aaagggcgca tcaagcagtg ggatgtggtc aacgaagcga tcaacgacgg ccctggcgtg 660
ctgcggcaaa gtccgtggct gcgtgccatc ggcgaagact acatcgccga agcgttccgc 720
gccgcgcacg aagccgatcc tgacgccatt ctggtctaca acgactacaa catcgaactc 780
aactacaagc gtcccaaggc gctggaactg ctaaagaagc tcatcgacca gaaggttccg 840
attcatggtg tgggcattca ggctcactgg cgcatgaccc cgccgctggc cgagaccgaa 900
gaagccatca aacagttcgc cgcgctgggc ctgaaggtga tgttcaccga actggacatc 960
ggtgtgctgc ccactcagta tcaggggggct gacatctcgg cgcgtgaaac catgacaccc 1020
gaacagcaag cggtgatgaa cccttacact cagggcttgc cggctgaagt ggcacagcaa 1080
catgccgagc gctaccgaca ggccttcgag ctgttcctgc gccacaagga tgtgattggt 1140
cgcgtcacgc tctggggcac gcatgatggc gaatcctggc tgaacggttt tccggtgcgg 1200
ggccgcaccg actatccctt gctcttcgac cgccggtatc agccaaaacc agccttcttc 1260
gccgtcaggc aggttgcaca ggcgcatact gtacaaacga ccggtgcgca aacccaagct 1320
acagcgaaga caattcaaaa agcttctcga gagtacttct ag 1362

<210> 116
<211> 453
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 116
Met Thr Asn Arg Lys Ser Asn Val His Arg Ser Leu Thr Asp Asp Leu
1 5 10 15
Leu Asp Gly Val Phe Ala Glu Ala Lys Ala Gly Lys Val Glu Lys Tyr
20 25 30
Arg Ala Thr Gly Ile Leu Gly Thr Leu Phe Gly Phe Thr Val Ala Ser
35 40 45
Ser Ile Met Leu Ala Ala Cys Ser Asn Ala Gln Glu Asn Val Pro Pro
50 55 60
Val Ala Ser Ser Thr Ala Gln Ser Asn Ile Thr Gln Glu Asn Val Pro
65 70 75 80
Pro Leu Lys Asp Ala Phe Lys Gly Lys Phe Leu Ile Gly Thr Ala Val
85 90 95
Ser Asn Arg Leu Leu Glu Gly Gln Asp Pro Ala Thr Glu Ala Leu Val
100 105 110
Arg Arg His Phe Asp Ala Leu Thr Ala Glu Asn Ala Met Lys Pro Asp
115 120 125
Ala Leu Gln Pro Arg Glu Gly Gln Phe Asn Phe Val Ala Ala Asp Arg
130 135 140
Leu Val Glu Ile Ala Gln Gln Ser Gly Ala Thr Val Val Gly His Thr
145 150 155 160
Leu Val Trp His Ser Gln Thr Pro Gly Trp Phe Phe Gln Gly Pro Asn
165 170 175
Gly Gln Pro Ala Ser Arg Glu Leu Ala Leu Ala Arg Met Arg Thr His
180 185 190
Ile Lys Thr Val Val Gly Arg Tyr Lys Gly Arg Ile Lys Gln Trp Asp
195 200 205
Val Val Asn Glu Ala Ile Asn Asp Gly Pro Gly Val Leu Arg Gln Ser
210 215 220
Pro Trp Leu Arg Ala Ile Gly Glu Asp Tyr Ile Ala Glu Ala Phe Arg

```
225                 230                 235                 240
Ala Ala His Glu Ala Asp Pro Asp Ala Ile Leu Val Tyr Asn Asp Tyr
                245                 250                 255
Asn Ile Glu Leu Asn Tyr Lys Arg Pro Lys Ala Leu Glu Leu Leu Lys
            260                 265                 270
Lys Leu Ile Asp Gln Lys Val Pro Ile His Gly Val Gly Ile Gln Ala
        275                 280                 285
His Trp Arg Met Thr Pro Pro Leu Ala Glu Thr Glu Glu Ala Ile Lys
    290                 295                 300
Gln Phe Ala Ala Leu Gly Leu Lys Val Met Phe Thr Glu Leu Asp Ile
305                 310                 315                 320
Gly Val Leu Pro Thr Gln Tyr Gln Gly Ala Asp Ile Ser Ala Arg Glu
                325                 330                 335
Thr Met Thr Pro Glu Gln Gln Ala Val Met Asn Pro Tyr Thr Gln Gly
            340                 345                 350
Leu Pro Ala Glu Val Ala Gln Gln His Ala Glu Arg Tyr Arg Gln Ala
        355                 360                 365
Phe Glu Leu Phe Leu Arg His Lys Asp Val Ile Gly Arg Val Thr Leu
    370                 375                 380
Trp Gly Thr His Asp Gly Glu Ser Trp Leu Asn Gly Phe Pro Val Arg
385                 390                 395                 400
Gly Arg Thr Asp Tyr Pro Leu Leu Phe Asp Arg Arg Tyr Gln Pro Lys
                405                 410                 415
Pro Ala Phe Phe Ala Val Arg Gln Val Ala Gln Ala His Thr Val Gln
            420                 425                 430
Thr Thr Gly Ala Gln Thr Gln Ala Thr Ala Lys Thr Ile Gln Lys Ala
        435                 440                 445
Ser Arg Glu Tyr Phe
    450
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<210> 117
<211> 1437
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 117

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atgacgaacc gtaaattgaa cgtgcaccgt tcattgagcg atgatttgct cgatggcgcc     60
ttcgccgagt caaaagcggg caaagttgag aaataccgtg ccacggggat ccttggaacg    120
ctattcggat tcactgtggc gtcctccatc atgttggcgg cttgcagcaa cgcacaagag    180
aatgctccac cagttgcttc atccaccgca caaagcaata tcacccagga gaacgttccg    240
ccgctcaagg atgcgtttaa gggcaagttc ttgattggca ccatcgcgag caatcgcttg    300
ctgcagggac aagatccagc cacagaagcc ctggtgcgca ggcacttcga cgccctcacg    360
gcggaaaatg ccatgaagcc tgatgccatg caacccagag agggtgagtt caactttgcc    420
gccgctgacc gcctggtgga aatcgcccag caaagcggcg ccacggtggt cggccacacc    480
ttggtctggc atagccaaac gccaagctgg ttcttccagg gtccagatgg ccaaccggcg    540
agtcgggaac tggccttggc acggatgcga acgcacatca agactgtggt gggacgctac    600
aaaggacgca tcaagcaatg ggatgtggtc aacgaagcga tcaacgacgg ccctggagtg    660
ctgcggccat cgccgtggtt gcgcgccatc ggcgaagact tcatcgccga agcgttccgc    720
gccgcgcacg aagctgatcc cgacgcgatt ctcgtctaca acgactacaa catcgagctc    780
aactacaagc gtcccaaggc gctggaacta ctgaagagac tcatcgagca gaaggttccg    840
attcatggtg tgggcattca ggctcactgg cgcatgaccc cgccgctggc cgagatggaa    900
gagaccatca agcagttttc ggctttgggc ttgaaggtaa tgatcaccga gttggacatt    960
ggtgtattgc caacacaata ccagggtgcc gacatctcgg ctcgcgagac catgacaccc   1020
gaacagcaag cggtgatgaa cccttacacg cagggcttgc cggctgaagt ggcgcagcaa   1080
catgccgagc gttatcgtca ggcgtttgag ctgttcatgc gttacaagga tgtgattggt   1140
cgcgttaccc tgtggggcac gcatgatggc gaatcttggc tgaacggttt tcccgttcgt   1200
ggccgcacgg attatcctct actgttcgac cgccggtatc agcctaagcc cgccttcttc   1260
gcggtgcaaa aggtcgcgca ggcgcagaac gcacaggcag caaccgatca agcaccactt   1320
gcacaaaacc cagttgcgca gaagaaatct gcaccaaggc aggcggctca aaatcagacc   1380
actcaaaagc cagtggtaca aaagcaaagt gcggcaagtc gggccgcaga aaagtaa      1437
```

<210> 118
<211> 478
<212> PRT
<213> Unknown

<220>
<223> obtained from an environmental sample

<400> 118
Met Thr Asn Arg Lys Leu Asn Val His Arg Ser Leu Ser Asp Asp Leu
1 5 10 15
Leu Asp Gly Ala Phe Ala Glu Ser Lys Ala Gly Lys Val Glu Lys Tyr
20 25 30
Arg Ala Thr Gly Ile Leu Gly Thr Leu Phe Gly Phe Thr Val Ala Ser
35 40 45
Ser Ile Met Leu Ala Ala Cys Ser Asn Ala Gln Glu Asn Ala Pro Pro
50 55 60
Val Ala Ser Ser Thr Ala Gln Ser Asn Ile Thr Gln Glu Asn Val Pro
65 70 75 80
Pro Leu Lys Asp Ala Phe Lys Gly Lys Phe Leu Ile Gly Thr Ile Ala
85 90 95
Ser Asn Arg Leu Leu Gln Gly Gln Asp Pro Ala Thr Glu Ala Leu Val
100 105 110
Arg Arg His Phe Asp Ala Leu Thr Ala Glu Asn Ala Met Lys Pro Asp
115 120 125
Ala Met Gln Pro Arg Glu Gly Glu Phe Asn Phe Ala Ala Ala Asp Arg
130 135 140
Leu Val Glu Ile Ala Gln Gln Ser Gly Ala Thr Val Val Gly His Thr
145 150 155 160
Leu Val Trp His Ser Gln Thr Pro Ser Trp Phe Phe Gln Gly Pro Asp
165 170 175
Gly Gln Pro Ala Ser Arg Glu Leu Ala Leu Ala Arg Met Arg Thr His
180 185 190
Ile Lys Thr Val Val Gly Arg Tyr Lys Gly Arg Ile Lys Gln Trp Asp
195 200 205
Val Val Asn Glu Ala Ile Asn Asp Gly Pro Gly Val Leu Arg Pro Ser
210 215 220
Pro Trp Leu Arg Ala Ile Gly Glu Asp Phe Ile Ala Glu Ala Phe Arg
225 230 235 240
Ala Ala His Glu Ala Asp Pro Asp Ala Ile Leu Val Tyr Asn Asp Tyr
245 250 255
Asn Ile Glu Leu Asn Tyr Lys Arg Pro Lys Ala Leu Glu Leu Leu Lys
260 265 270
Arg Leu Ile Glu Gln Lys Val Pro Ile His Gly Val Gly Ile Gln Ala
275 280 285
His Trp Arg Met Thr Pro Pro Leu Ala Glu Met Glu Glu Thr Ile Lys
290 295 300
Gln Phe Ser Ala Leu Gly Leu Lys Val Met Ile Thr Glu Leu Asp Ile
305 310 315 320
Gly Val Leu Pro Thr Gln Tyr Gln Gly Ala Asp Ile Ser Ala Arg Glu
325 330 335
Thr Met Thr Pro Glu Gln Gln Ala Val Met Asn Pro Tyr Thr Gln Gly
340 345 350
Leu Pro Ala Glu Val Ala Gln Gln His Ala Glu Arg Tyr Arg Gln Ala
355 360 365
Phe Glu Leu Phe Met Arg Tyr Lys Asp Val Ile Gly Arg Val Thr Leu
370 375 380
Trp Gly Thr His Asp Gly Glu Ser Trp Leu Asn Gly Phe Pro Val Arg
385 390 395 400
Gly Arg Thr Asp Tyr Pro Leu Leu Phe Asp Arg Arg Tyr Gln Pro Lys
405 410 415
Pro Ala Phe Phe Ala Val Gln Lys Val Ala Gln Ala Gln Asn Ala Gln
420 425 430
Ala Ala Thr Asp Gln Ala Pro Leu Ala Gln Asn Pro Val Ala Gln Lys
435 440 445
Lys Ser Ala Pro Arg Gln Ala Ala Gln Asn Gln Thr Thr Gln Lys Pro
450 455 460
Val Val Gln Lys Gln Ser Ala Ala Ser Arg Ala Ala Glu Lys
465 470 475

<210> 119
<211> 2559
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 119
atgaaaaaaa gattgttagc gttgatagtg acattagttt ttattatctc attgtttaat 60
cccatattca ccacaccttt aacaaatgta gcaaaggctc aaagtaacca aacaaattta 120
aaatttgact ttgaaaacgg tactcaaggt tggggagcaa gaggtgtttc aacaactatt 180
gcaaccgttt acgagcaagc ttatgaagga agttattctt taaaggtttc aggtagaagt 240
tcaacgtggg atggagcagt tgtggatatc acatcaagta tttcagcaaa tgtcacctat 300
acagtttctt tatttgttcg tcacagcgat gtaaaaccac aaagattttc tgtctatgta 360
tatgtcaaag ataacacagg cgaaaaatac atccaggttg cagacaaagt ggttatgcca 420
aacttttgga agcagctctt tgggaagttc acaatcacaa catcaaatcc aattcaaaaa 480
gtagaacttc ttgtatgtgt tccatctaac aaatctttag gattttatct tgacaatgta 540
gttattactt cagcacaacc agcttcctcg ggtgttgtta aatcttgcac atttgaaagc 600
ggtagcactg agggttttgt tcagagaggt tcagcttcat tgacagttgt cgacggtgta 660
tactatcatt ctccaacaaa agcattatat gtgacaggaa ggacagctac atggcagggt 720
gcacagatag atatgacaag tttgcttgag aagggcaagg attatcagtt tagcatatgg 780
gtatatcaaa atagtggaag tgatcagaag ataaccctta cgatgcaaag gaagaatgaa 840
gatggaacta cgagttatga ttctataaag tatcagcaaa cagttccatc tggtacatgg 900
acagaagtaa caggttcata cacagtgcct cagacagcaa cacagcttat attctatgtt 960
gaatcaccga atattaattt tgacttctac cttgatgact ttacagcggt tgacaaaaac 1020
ccacctgttg taaacccagg gcttgttaaa tcttgcacat ttgaaagcgg tagcactgag 1080
ggttttgttc agagaggttc agcttcattg acagttgtcg acggtgtata ctatcattct 1140
ccaacaaaag cattgtatgt gacaggaagg acagctacat ggcagggtgc acagatagat 1200
atgacaagtt tgcttgagaa gggcaaggat tatcagttta gcatatgggt atatcaaaat 1260
agtggaagtg atcagaagat aacccttacg atgcaaagga agaatgaaga tggaactacg 1320
agttatgatt ctataaagta tcagcaaaca gttccatctg gtacatggac agaagtaaca 1380
ggttcataca cagtgcctca gacagcaaca cagcttatat tctatgttga atcaccgaat 1440
attaattttg acttctacct tgatgacttt acagtaatag ataaaaatcc agtgacggta 1500
ccgattgcag caaaagaacc cgaatgggaa attccgtcac tttgtcagca atatagtcaa 1560
tatttctcaa taggtgttgc aataccgtat aaagtacttc aaaatcctgt tgaaagagca 1620
atggtgttaa aacacttcaa cagtataaca gctgaaaatg agatgaaacc tgacgctctg 1680
caaagaacag aagggaactt tacattcgat atagcagacc agtatgtaaa cttcgcacag 1740
caaaacggta ttggaattag agggcatact ctggtatggc acagccaagt acctaattgg 1800
ttcttccagc acagtgatgg aacttcactt gatccaagca atccagatga taagcaactt 1860
ttgagagata gattgaaaaa tcatattcaa actgttatgt caagatacaa agggaaagtc 1920
tatgcatggg atgttgtaaa cgaggcaata gatgaaagcc agcctgatgg atttagaaga 1980
agcgaatggt acagaatact tggtccaaca cctgagacaa atggtattcc agaatacatt 2040
gtgcttgctt tcaggtatgc aagagaggcg gatccggatg caaaactttt ctacaatgac 2100
tacaacacag agatatctaa aaaaagacag tttatatatg acatggtaaa aaagctacat 2160
gatatgggtt taattgatgg tgttggtttg caagggcata taaatgttga ttctccaaca 2220
gtaaaagata tagaagatac aatcaatctt ttctcaacaa ttcctggact tgagatacag 2280
gtaacagagc ttgacataag cgtttacaca agcagcagtc agcgttatga tacgcttcct 2340
caggatataa tgataaaaca agcaatgaag tttaaagaac tatttgaaat gttaaagaga 2400
catagtgata gagtcacaaa tgtgacactt tggggactta aggatgatta ttcatggctt 2460
tcaaaggata gaaataactg gccattgctt tttgacagca actaccaggc aaaatacagc 2520
tactgggcaa ttcaaaaagc ttctcgagag tacttctag 2559

<210> 120
<211> 852
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(33)

<400> 120
Met Lys Lys Arg Leu Leu Ala Leu Ile Val Thr Leu Val Phe Ile Ile
1   5   10   15
Ser Leu Phe Asn Pro Ile Phe Thr Thr Pro Leu Thr Asn Val Ala Lys
            20   25   30
Ala Gln Ser Asn Gln Thr Asn Leu Lys Phe Asp Phe Glu Asn Gly Thr
        35   40   45
Gln Gly Trp Gly Ala Arg Gly Val Ser Thr Thr Ile Ala Thr Val Tyr
    50   55   60

Glu Gln Ala Tyr Glu Gly Ser Tyr Ser Leu Lys Val Ser Gly Arg Ser
65 70 75 80
Ser Thr Trp Asp Gly Ala Val Val Asp Ile Thr Ser Ser Ile Ser Ala
85 90 95
Asn Val Thr Tyr Thr Val Ser Leu Phe Val Arg His Ser Asp Val Lys
100 105 110
Pro Gln Arg Phe Ser Val Tyr Val Tyr Val Lys Asp Asn Thr Gly Glu
115 120 125
Lys Tyr Ile Gln Val Ala Asp Lys Val Val Met Pro Asn Phe Trp Lys
130 135 140
Gln Leu Phe Gly Lys Phe Thr Ile Thr Thr Ser Asn Pro Ile Gln Lys
145 150 155 160
Val Glu Leu Leu Val Cys Val Pro Ser Asn Lys Ser Leu Gly Phe Tyr
165 170 175
Leu Asp Asn Val Val Ile Thr Ser Ala Gln Pro Ala Ser Ser Gly Val
180 185 190
Val Lys Ser Cys Thr Phe Glu Ser Gly Ser Thr Glu Gly Phe Val Gln
195 200 205
Arg Gly Ser Ala Ser Leu Thr Val Val Asp Gly Val Tyr Tyr His Ser
210 215 220
Pro Thr Lys Ala Leu Tyr Val Thr Gly Arg Thr Ala Thr Trp Gln Gly
225 230 235 240
Ala Gln Ile Asp Met Thr Ser Leu Leu Glu Lys Gly Lys Asp Tyr Gln
245 250 255
Phe Ser Ile Trp Val Tyr Gln Asn Ser Gly Ser Asp Gln Lys Ile Thr
260 265 270
Leu Thr Met Gln Arg Lys Asn Glu Asp Gly Thr Thr Ser Tyr Asp Ser
275 280 285
Ile Lys Tyr Gln Gln Thr Val Pro Ser Gly Thr Trp Thr Glu Val Thr
290 295 300
Gly Ser Tyr Thr Val Pro Gln Thr Ala Thr Gln Leu Ile Phe Tyr Val
305 310 315 320
Glu Ser Pro Asn Ile Asn Phe Asp Phe Tyr Leu Asp Asp Phe Thr Ala
325 330 335
Val Asp Lys Asn Pro Pro Val Val Asn Pro Gly Leu Val Lys Ser Cys
340 345 350
Thr Phe Glu Ser Gly Ser Thr Glu Gly Phe Val Gln Arg Gly Ser Ala
355 360 365
Ser Leu Thr Val Val Asp Gly Val Tyr Tyr His Ser Pro Thr Lys Ala
370 375 380
Leu Tyr Val Thr Gly Arg Thr Ala Thr Trp Gln Gly Ala Gln Ile Asp
385 390 395 400
Met Thr Ser Leu Leu Glu Lys Gly Lys Asp Tyr Gln Phe Ser Ile Trp
405 410 415
Val Tyr Gln Asn Ser Gly Ser Asp Gln Lys Ile Thr Leu Thr Met Gln
420 425 430
Arg Lys Asn Glu Asp Gly Thr Thr Ser Tyr Asp Ser Ile Lys Tyr Gln
435 440 445
Gln Thr Val Pro Ser Gly Thr Trp Thr Glu Val Thr Gly Ser Tyr Thr
450 455 460
Val Pro Gln Thr Ala Thr Gln Leu Ile Phe Tyr Val Glu Ser Pro Asn
465 470 475 480
Ile Asn Phe Asp Phe Tyr Leu Asp Asp Phe Thr Val Ile Asp Lys Asn
485 490 495
Pro Val Thr Val Pro Ile Ala Ala Lys Glu Pro Glu Trp Glu Ile Pro
500 505 510
Ser Leu Cys Gln Gln Tyr Ser Gln Tyr Phe Ser Ile Gly Val Ala Ile
515 520 525
Pro Tyr Lys Val Leu Gln Asn Pro Val Glu Arg Ala Met Val Leu Lys
530 535 540
His Phe Asn Ser Ile Thr Ala Glu Asn Glu Met Lys Pro Asp Ala Leu
545 550 555 560
Gln Arg Thr Glu Gly Asn Phe Thr Phe Asp Ile Ala Asp Gln Tyr Val
565 570 575
Asn Phe Ala Gln Gln Asn Gly Ile Gly Ile Arg Gly His Thr Leu Val
580 585 590
Trp His Ser Gln Val Pro Asn Trp Phe Phe Gln His Ser Asp Gly Thr
595 600 605
Ser Leu Asp Pro Ser Asn Pro Asp Asp Lys Gln Leu Leu Arg Asp Arg

610 615 620
Leu Lys Asn His Ile Gln Thr Val Met Ser Arg Tyr Lys Gly Lys Val
625 630 635 640
Tyr Ala Trp Asp Val Val Asn Glu Ala Ile Asp Glu Ser Gln Pro Asp
645 650 655
Gly Phe Arg Arg Ser Glu Trp Tyr Arg Ile Leu Gly Pro Thr Pro Glu
660 665 670
Thr Asn Gly Ile Pro Glu Tyr Ile Val Leu Ala Phe Arg Tyr Ala Arg
675 680 685
Glu Ala Asp Pro Asp Ala Lys Leu Phe Tyr Asn Asp Tyr Asn Thr Glu
690 695 700
Ile Ser Lys Lys Arg Gln Phe Ile Tyr Asp Met Val Lys Lys Leu His
705 710 715 720
Asp Met Gly Leu Ile Asp Gly Val Gly Leu Gln Gly His Ile Asn Val
725 730 735
Asp Ser Pro Thr Val Lys Asp Ile Glu Asp Thr Ile Asn Leu Phe Ser
740 745 750
Thr Ile Pro Gly Leu Glu Ile Gln Val Thr Glu Leu Asp Ile Ser Val
755 760 765
Tyr Thr Ser Ser Ser Gln Arg Tyr Asp Thr Leu Pro Gln Asp Ile Met
770 775 780
Ile Lys Gln Ala Met Lys Phe Lys Glu Leu Phe Glu Met Leu Lys Arg
785 790 795 800
His Ser Asp Arg Val Thr Asn Val Thr Leu Trp Gly Leu Lys Asp Asp
805 810 815
Tyr Ser Trp Leu Ser Lys Asp Arg Asn Asn Trp Pro Leu Leu Phe Asp
820 825 830
Ser Asn Tyr Gln Ala Lys Tyr Ser Tyr Trp Ala Ile Gln Lys Ala Ser
835 840 845
Arg Glu Tyr Phe
850

<210> 121
<211> 1905
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 121
atgaagcata tttttattgt attaattgtt tccctgctgt ttagcttcgg gggatatgct 60
caacaaacca ttagcagagc tccgcagggg tttgaccagc aacgtgccgg cattgcatcc 120
ggtaaagttg aaatcgtaac ctataaatcg aaaaccgtag gagtgaatcg ctctgcacgt 180
gtttatacac cagccggatt ctcaaaaaag aagaaatatc ctgtgcttta tttattacat 240
ggcattggag gcgacgaaga tgagtggtac aaaaacggcg ttcctcatat tattttcgac 300
aacctgattg ccgacggcaa aatggaaccg atgattgtgg tactgcccaa tggtcgcgcc 360
atgaaaaacg accgtgccga aggaaatatt ttcgacaaag agaaagttga agcctttgca 420
acattcgaaa aagacctttt aaacgattta ataccgttta tcgaaaaaaa ataccctgta 480
ttaaaaaccc gtgagtttcg cgccattgca ggattatcaa tgggcggcgg acaatcgctc 540
aattttggac tgggaaatct cgacaaattt gcatgggtag gcggcttttc atcggccccc 600
aataccaaaa tgcccgctga gttggttcca aacactcaaa aggcaacaga aatgcttaag 660
ttgctttatg tgtcttgtgg cgataaagac aatttaatgc aggttagtca gcgcacccac 720
gattatctga aagccaataa agtacctcat attttcaggg ttattcctga tggttaccac 780
gattttaatg tttggaaaga cgatttgtat cattacgtac aaatgctgtt taagcctgtg 840
gtaatgcccg tagcagcagc tactttaaaa gatgcttata aagggaaatt cttcattgga 900
actgccctta ataccсctca aattttgggt accgctgttg atgaagtgaa tattgttaaa 960
acccatttca actccattgt tgccgaaaac tgtatgaaga gtggcccgat gcaaccacaa 1020
gaagggaaat ttgagtttga cctggccgat aagtttgtag agtttggagt taaaaacaat 1080
atgcagatta ttggtcatac gcttatctgg cattcgcagg caccccgctg gtttttttacc 1140
gacagcgaag gcaaggacgt atcgcccgag gtgcttaccg agcgcatgaa aaaccatatc 1200
tatactgttg ttggccgtta caaaggcaag gtgcacggat gggatgtggt gaatgaagcc 1260
atagttgacg atggcagcta ccgaaacagt aaattctacc aaatactggg cgaagatttt 1320
atcaaactgg cattccagtt tgctcatgaa gccgaccccg atgcagaatt gtactacaac 1380
gattattccg aatttgttcc tgccaaaaga gaaggcattg cccgcatggt gaagaaactc 1440
aaagaccagg gcattagaat cgacggcgtt ggatttcagt gccatattgg cctcgattat 1500
ccaggcctgg atgaatacga aaaaaccatt caattaattg ccaacgaggg ggtaaaagta 1560
atgataaccg aaatggaaat atcggtatta cccatgcccg actggcgcgt tggtgctgag 1620
atttcggcca gtttcgaata tcaacagaaa ttaaatccct acaccgaagg attgcccgat 1680

tcagtgaatg ctcaattaga acagcgttat gtcgactttt tcacgctctt ccttaaatat 1740
cacgaagtga ttccaagagt tacggtttgg ggggttaacg atggcaactc atggaaaaac 1800
ggattcccgg tgcgtggaag aaccgactac ccattgttat tcgaccggaa aaatcagcct 1860
aaatcagctg ttgccaaatt aattgaactg gctaatacaa agtag 1905

<210> 122
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(20)

<400> 122
Met Lys His Ile Phe Ile Val Leu Ile Val Ser Leu Leu Phe Ser Phe
1 5 10 15
Gly Gly Tyr Ala Gln Gln Thr Ile Ser Arg Ala Pro Gln Gly Phe Asp
20 25 30
Gln Gln Arg Ala Gly Ile Ala Ser Gly Lys Val Glu Ile Val Thr Tyr
35 40 45
Lys Ser Lys Thr Val Gly Val Asn Arg Ser Ala Arg Val Tyr Thr Pro
50 55 60
Ala Gly Phe Ser Lys Lys Lys Lys Tyr Pro Val Leu Tyr Leu Leu His
65 70 75 80
Gly Ile Gly Gly Asp Glu Asp Glu Trp Tyr Lys Asn Gly Val Pro His
85 90 95
Ile Ile Phe Asp Asn Leu Ile Ala Asp Gly Lys Met Glu Pro Met Ile
100 105 110
Val Val Leu Pro Asn Gly Arg Ala Met Lys Asn Asp Arg Ala Glu Gly
115 120 125
Asn Ile Phe Asp Lys Glu Lys Val Glu Ala Phe Ala Thr Phe Glu Lys
130 135 140
Asp Leu Leu Asn Asp Leu Ile Pro Phe Ile Glu Lys Lys Tyr Pro Val
145 150 155 160
Leu Lys Thr Arg Glu Phe Arg Ala Ile Ala Gly Leu Ser Met Gly Gly
165 170 175
Gly Gln Ser Leu Asn Phe Gly Leu Gly Asn Leu Asp Lys Phe Ala Trp
180 185 190
Val Gly Gly Phe Ser Ser Ala Pro Asn Thr Lys Met Pro Ala Glu Leu
195 200 205
Val Pro Asn Thr Gln Lys Ala Thr Glu Met Leu Lys Leu Leu Tyr Val
210 215 220
Ser Cys Gly Asp Lys Asp Asn Leu Met Gln Val Ser Gln Arg Thr His
225 230 235 240
Asp Tyr Leu Lys Ala Asn Lys Val Pro His Ile Phe Arg Val Ile Pro
245 250 255
Asp Gly Tyr His Asp Phe Asn Val Trp Lys Asp Asp Leu Tyr His Tyr
260 265 270
Val Gln Met Leu Phe Lys Pro Val Val Met Pro Val Ala Ala Ala Thr
275 280 285
Leu Lys Asp Ala Tyr Lys Gly Lys Phe Phe Ile Gly Thr Ala Leu Asn
290 295 300
Thr Pro Gln Ile Leu Gly Thr Ala Val Asp Glu Val Asn Ile Val Lys
305 310 315 320
Thr His Phe Asn Ser Ile Val Ala Glu Asn Cys Met Lys Ser Gly Pro
325 330 335
Met Gln Pro Gln Glu Gly Lys Phe Glu Phe Asp Leu Ala Asp Lys Phe
340 345 350
Val Glu Phe Gly Val Lys Asn Asn Met Gln Ile Ile Gly His Thr Leu
355 360 365
Ile Trp His Ser Gln Ala Pro Arg Trp Phe Phe Thr Asp Ser Glu Gly
370 375 380
Lys Asp Val Ser Pro Glu Val Leu Thr Glu Arg Met Lys Asn His Ile
385 390 395 400
Tyr Thr Val Val Gly Arg Tyr Lys Gly Lys Val His Gly Trp Asp Val
405 410 415

Val Asn Glu Ala Ile Val Asp Asp Gly Ser Tyr Arg Asn Ser Lys Phe
420 425 430
Tyr Gln Ile Leu Gly Glu Asp Phe Ile Lys Leu Ala Phe Gln Phe Ala
435 440 445
His Glu Ala Asp Pro Asp Ala Glu Leu Tyr Tyr Asn Asp Tyr Ser Glu
450 455 460
Phe Val Pro Ala Lys Arg Glu Gly Ile Ala Arg Met Val Lys Lys Leu
465 470 475 480
Lys Asp Gln Gly Ile Arg Ile Asp Gly Val Gly Phe Gln Cys His Ile
485 490 495
Gly Leu Asp Tyr Pro Gly Leu Asp Glu Tyr Glu Lys Thr Ile Gln Leu
500 505 510
Ile Ala Asn Glu Gly Val Lys Val Met Ile Thr Glu Met Glu Ile Ser
515 520 525
Val Leu Pro Met Pro Asp Trp Arg Val Gly Ala Glu Ile Ser Ala Ser
530 535 540
Phe Glu Tyr Gln Gln Lys Leu Asn Pro Tyr Thr Glu Gly Leu Pro Asp
545 550 555 560
Ser Val Asn Ala Gln Leu Glu Gln Arg Tyr Val Asp Phe Phe Thr Leu
565 570 575
Phe Leu Lys Tyr His Glu Val Ile Pro Arg Val Thr Val Trp Gly Val
580 585 590
Asn Asp Gly Asn Ser Trp Lys Asn Gly Phe Pro Val Arg Gly Arg Thr
595 600 605
Asp Tyr Pro Leu Leu Phe Asp Arg Lys Asn Gln Pro Lys Ser Ala Val
610 615 620
Ala Lys Leu Ile Glu Leu Ala Asn Thr Lys
625 630

<210> 123
<211> 1200
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 123
atgatcgttg gattctcgtt tatgctgctg cttcctttag ggatgacgaa tgcattggca 60
aaaacggaac cagcgtacgc taaaaagccg cgaatcagcg cattgcacgc ccctcaattg 120
gatcagcgct acaaagattc cttcactatt ggggcggccg ttgaacctta tcagttgcaa 180
aacgaaaaag acgtccaaat gctgaaacgc cattttaaca gcattgtcgc tgagaacgtt 240
atgaaaccga tcaacatcca acccgaagaa ggaaagttca attttgctga ggcggatcaa 300
atcgtccgat ttgctaaaaa acatcatatg gatattcgtt tccatacact cgtttggcac 360
agccaagtac ctcaatggtt ctttcttgac aaggaaggca agccgatggt caatgaaacg 420
gatccggcaa agcgcgaaca aaataaacag ctgttactga aacggctcga aatccatatt 480
aaaacgattg tcgaacggta taaagacgac atcaaatatt gggacgtcgt gaacgaggta 540
gtcggggatg atggaaaatt gcgcaattcc ccgtggtatc aaatcgccgg catcgattat 600
atcaaggtag cattccaaac ggcgagaaca tatggcggca acaagattaa actgtacatc 660
aacgattaca ataccgaagt ggaaccgaag cgaagcgctc tttataactt agtgaaacaa 720
ttaaaagaag aaggcgttcc cattgacggg attggccacc agtcccacat ccaaattggc 780
tggccttctg aagaagaaat cgaaaaaacg atcaacatgt ttgccgatct agggttagac 840
aatcaaatta cggagctgga tgtgagcatg tacggctggc cgccgcgcgc ctacccgtcg 900
tatgacgcca ttccggaaca aaagtttttg gaccaagcgg ctcgctatga ccgattgttt 960
aagctgtacg aaaaacttgg cgataaaatc agcaacgtca ccttctgggg catcgccgac 1020
aaccatacgt ggctcgacag ccgtgcggat gtgtactatg acgccaacgg gaatgttgtg 1080
gttgacccga acgctccgta cgcaaaagtg gaaaaaggga aaggaaaaga tgcgccgttt 1140
ctgttcgacc ccgaatacca cgtaaaacct gcgtattggg ccattatcga tcataagtga 1200

<210> 124
<211> 399
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(20)

<400> 124
Met Ile Val Gly Phe Ser Phe Met Leu Leu Leu Pro Leu Gly Met Thr
1 5 10 15
Asn Ala Leu Ala Lys Thr Glu Pro Ala Tyr Ala Lys Lys Pro Arg Ile
20 25 30
Ser Ala Leu His Ala Pro Gln Leu Asp Gln Arg Tyr Lys Asp Ser Phe
35 40 45
Thr Ile Gly Ala Ala Val Glu Pro Tyr Gln Leu Gln Asn Glu Lys Asp
50 55 60
Val Gln Met Leu Lys Arg His Phe Asn Ser Ile Val Ala Glu Asn Val
65 70 75 80
Met Lys Pro Ile Asn Ile Gln Pro Glu Glu Gly Lys Phe Asn Phe Ala
85 90 95
Glu Ala Asp Gln Ile Val Arg Phe Ala Lys Lys His His Met Asp Ile
100 105 110
Arg Phe His Thr Leu Val Trp His Ser Gln Val Pro Gln Trp Phe Phe
115 120 125
Leu Asp Lys Glu Gly Lys Pro Met Val Asn Glu Thr Asp Pro Ala Lys
130 135 140
Arg Glu Gln Asn Lys Gln Leu Leu Leu Lys Arg Leu Glu Ile His Ile
145 150 155 160
Lys Thr Ile Val Glu Arg Tyr Lys Asp Asp Ile Lys Tyr Trp Asp Val
165 170 175
Val Asn Glu Val Val Gly Asp Asp Gly Lys Leu Arg Asn Ser Pro Trp
180 185 190
Tyr Gln Ile Ala Gly Ile Asp Tyr Ile Lys Val Ala Phe Gln Thr Ala
195 200 205
Arg Thr Tyr Gly Gly Asn Lys Ile Lys Leu Tyr Ile Asn Asp Tyr Asn
210 215 220
Thr Glu Val Glu Pro Lys Arg Ser Ala Leu Tyr Asn Leu Val Lys Gln
225 230 235 240
Leu Lys Glu Glu Gly Val Pro Ile Asp Gly Ile Gly His Gln Ser His
245 250 255
Ile Gln Ile Gly Trp Pro Ser Glu Glu Glu Ile Glu Lys Thr Ile Asn
260 265 270
Met Phe Ala Asp Leu Gly Leu Asp Asn Gln Ile Thr Glu Leu Asp Val
275 280 285
Ser Met Tyr Gly Trp Pro Pro Arg Ala Tyr Pro Ser Tyr Asp Ala Ile
290 295 300
Pro Glu Gln Lys Phe Leu Asp Gln Ala Ala Arg Tyr Asp Arg Leu Phe
305 310 315 320
Lys Leu Tyr Glu Lys Leu Gly Asp Lys Ile Ser Asn Val Thr Phe Trp
325 330 335
Gly Ile Ala Asp Asn His Thr Trp Leu Asp Ser Arg Ala Asp Val Tyr
340 345 350
Tyr Asp Ala Asn Gly Asn Val Val Val Asp Pro Asn Ala Pro Tyr Ala
355 360 365
Lys Val Glu Lys Gly Lys Gly Lys Asp Ala Pro Phe Leu Phe Asp Pro
370 375 380
Glu Tyr His Val Lys Pro Ala Tyr Trp Ala Ile Ile Asp His Lys
385 390 395

<210> 125
<211> 1089
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 125
atgttgacga ccccgacaac tcaagatcat gtccccgtgc tcaaggacgc tttcaaaggc 60
aagctcctca ttggagccgt gctcggttac gatgctctcc aggggaagga cccgctgagt 120
gagaaaattg cgaccactca cttcgatgct ctcactgctg aaaacagcat gaagccggct 180
ctcgtgcaac ccaaagaggg cgagtttgat ttcgctgatg gagatcgtct ccttgaaatc 240
gcgcagcaat gcggcgctac tgcaatcggc catactctgc tctggcacca acaaacgcca 300
cgctggtttt ttgaagggcc agatggtcag cctgctgacc gtgagttggc cctggcacgc 360
atgaggaagc acatttccac tctcgttggt cgctataaag gtcgcattaa acaatgggat 420

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gtggtgaatg aggcgattag cgatgcagag ggcgagtact taagaccaaa gagcccctgg     480
ttcaaagccg ttggagagga tcacatcgcg catgctttcc aggcagcaca tgaagctgat     540
cccgatgcca tccttatcta taacgactac aacatcgagc aggagtacaa gcgcccgaag     600
gcgatacgcc tactgaggtc attacttgag caggacgttc ccattcatgc cgtgggcatt     660
cagggccatt ggcgtatgga cactctgaat gttgccgaaa tcgaagaagc tatcgaagaa     720
tttgctgcgc tgggtctcaa ggtcatgatc accgagcttg atatcagcgt gctaccgaca     780
aagtatcagg gagccgatct cgctactcgg gaagaattga cgcctgaaat caatccctat     840
acggaggaac tacctgagga cgttgcccgg caacatgccg agtgttatcg gcaggtcttc     900
gaaatgttcc tgcgccacaa ggatgccatt agccgtgtca cgctctgggg cattcacgat     960
ggcagatcat ggttcaacaa ctttccggtc agggggcgca cagactatcc tctgctattc    1020
gaccgggaat gtaaccccaa gccagcgttt ttcgccgtct tgaaagctgc gcaagaccag    1080
ccacaatga                                                            1089
```

<210> 126
<211> 362
<212> PRT
<213> Unknown

<220>
<223> obtained from an environmental sample

<400> 126

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Met Leu Thr Thr Pro Thr Thr Gln Asp His Val Pro Val Leu Lys Asp
1               5                   10                  15
Ala Phe Lys Gly Lys Leu Leu Ile Gly Ala Val Leu Gly Tyr Asp Ala
            20                  25                  30
Leu Gln Gly Lys Asp Pro Leu Ser Glu Lys Ile Ala Thr Thr His Phe
        35                  40                  45
Asp Ala Leu Thr Ala Glu Asn Ser Met Lys Pro Ala Leu Val Gln Pro
    50                  55                  60
Lys Glu Gly Glu Phe Asp Phe Ala Asp Gly Asp Arg Leu Leu Glu Ile
65                  70                  75                  80
Ala Gln Gln Cys Gly Ala Thr Ala Ile Gly His Thr Leu Leu Trp His
                85                  90                  95
Gln Gln Thr Pro Arg Trp Phe Phe Glu Gly Pro Asp Gly Gln Pro Ala
            100                 105                 110
Asp Arg Glu Leu Ala Leu Ala Arg Met Arg Lys His Ile Ser Thr Leu
        115                 120                 125
Val Gly Arg Tyr Lys Gly Arg Ile Lys Gln Trp Asp Val Val Asn Glu
    130                 135                 140
Ala Ile Ser Asp Ala Glu Gly Glu Tyr Leu Arg Pro Lys Ser Pro Trp
145                 150                 155                 160
Phe Lys Ala Val Gly Glu Asp His Ile Ala His Ala Phe Gln Ala Ala
                165                 170                 175
His Glu Ala Asp Pro Asp Ala Ile Leu Ile Tyr Asn Asp Tyr Asn Ile
            180                 185                 190
Glu Gln Glu Tyr Lys Arg Pro Lys Ala Ile Arg Leu Leu Arg Ser Leu
        195                 200                 205
Leu Glu Gln Asp Val Pro Ile His Ala Val Gly Ile Gln Gly His Trp
    210                 215                 220
Arg Met Asp Thr Leu Asn Val Ala Glu Ile Glu Glu Ala Ile Glu Glu
225                 230                 235                 240
Phe Ala Ala Leu Gly Leu Lys Val Met Ile Thr Glu Leu Asp Ile Ser
                245                 250                 255
Val Leu Pro Thr Lys Tyr Gln Gly Ala Asp Leu Ala Thr Arg Glu Glu
            260                 265                 270
Leu Thr Pro Glu Ile Asn Pro Tyr Thr Glu Glu Leu Pro Glu Asp Val
        275                 280                 285
Ala Arg Gln His Ala Glu Cys Tyr Arg Gln Val Phe Glu Met Phe Leu
    290                 295                 300
Arg His Lys Asp Ala Ile Ser Arg Val Thr Leu Trp Gly Ile His Asp
305                 310                 315                 320
Gly Arg Ser Trp Phe Asn Asn Phe Pro Val Arg Gly Arg Thr Asp Tyr
                325                 330                 335
Pro Leu Leu Phe Asp Arg Glu Cys Asn Pro Lys Pro Ala Phe Phe Ala
            340                 345                 350
Val Leu Lys Ala Ala Gln Asp Gln Pro Gln
        355                 360
```

<210> 127
<211> 960
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 127
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gtggatctcg ctgagaaatg cggcatatat attggtgcag cggttgaacc cggatattta      60
attatcaggg aatacgctga gattttatcc cgcgaattta acgtggtaac cgcggaaaat     120
gcattaaaat ttgaagctat tcatccgcag cgtggagtat attcatttga aggtgcagat     180
gcaatagttc gatttgcaga aactcatgga atgaaggttc gtggacatac acttgtttgg     240
caccagcagc ttcctgcatg gataacttct ggaagttacg cttgggagga gtggaagaat     300
attctccgtg agcatgtaat gagcgttgtt ggacgatata agggccaaat atatgcatgg     360
gatgtggtta acgaagcaat attagataac ggttcattaa gagataatgt ttggtttaga     420
aatgtaggtc cagaatatat tgagtcagcc tttagatggg ctcatgaagc tgacccaaac     480
gctcttctct tctataatga ttatgaagct gaggacttga atgataagtc gcatgctgtt     540
tataacctgg ttaagagttt acttgagaaa ggtgtaccga tacatggcgt aggattacag     600
atgcatatta acgtagaaaa tccgccgaaa ccggaagatg ttgcagcaaa cattaaacgt     660
ctaaatgatc tgggcttgat tgtccacata acggaaatgg atgtgcgcat tagaacccca     720
ccatcaaatg aagatctcat taaacaagca gaaatttacc gtgatatatt aagagtttgt     780
ctttcatcag aaaaatgcac agcattcatt atgtggggat ttactgaccg ctattcatgg     840
ataccaaatt acttcagcgg ctacggttca gctttaatat tcgatgagca atataagccc     900
aaactagcat attactatat acttcggaca ttcatcgaaa aactaggcat taaaggttaa     960
```

<210> 128
<211> 319
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 128
```
Val Asp Leu Ala Glu Lys Cys Gly Ile Tyr Ile Gly Ala Ala Val Glu
1               5                   10                  15
Pro Gly Tyr Leu Ile Ile Arg Glu Tyr Ala Glu Ile Leu Ser Arg Glu
            20                  25                  30
Phe Asn Val Val Thr Ala Glu Asn Ala Leu Lys Phe Glu Ala Ile His
        35                  40                  45
Pro Gln Arg Gly Val Tyr Ser Phe Glu Gly Ala Asp Ala Ile Val Arg
    50                  55                  60
Phe Ala Glu Thr His Gly Met Lys Val Arg Gly His Thr Leu Val Trp
65                  70                  75                  80
His Gln Gln Leu Pro Ala Trp Ile Thr Ser Gly Ser Tyr Ala Trp Glu
                85                  90                  95
Glu Trp Lys Asn Ile Leu Arg Glu His Val Met Ser Val Val Gly Arg
            100                 105                 110
Tyr Lys Gly Gln Ile Tyr Ala Trp Asp Val Val Asn Glu Ala Ile Leu
        115                 120                 125
Asp Asn Gly Ser Leu Arg Asp Asn Val Trp Phe Arg Asn Val Gly Pro
    130                 135                 140
Glu Tyr Ile Glu Ser Ala Phe Arg Trp Ala His Glu Ala Asp Pro Asn
145                 150                 155                 160
Ala Leu Leu Phe Tyr Asn Asp Tyr Glu Ala Glu Asp Leu Asn Asp Lys
                165                 170                 175
Ser His Ala Val Tyr Asn Leu Val Lys Ser Leu Leu Glu Lys Gly Val
            180                 185                 190
Pro Ile His Gly Val Gly Leu Gln Met His Ile Asn Val Glu Asn Pro
        195                 200                 205
Pro Lys Pro Glu Asp Val Ala Ala Asn Ile Lys Arg Leu Asn Asp Leu
    210                 215                 220
Gly Leu Ile Val His Ile Thr Glu Met Asp Val Arg Ile Arg Thr Pro
225                 230                 235                 240
Pro Ser Asn Glu Asp Leu Ile Lys Gln Ala Glu Ile Tyr Arg Asp Ile
                245                 250                 255
Leu Arg Val Cys Leu Ser Ser Glu Lys Cys Thr Ala Phe Ile Met Trp
            260                 265                 270
```

Gly Phe Thr Asp Arg Tyr Ser Trp Ile Pro Asn Tyr Phe Ser Gly Tyr
        275   280   285
Gly Ser Ala Leu Ile Phe Asp Glu Gln Tyr Lys Pro Lys Leu Ala Tyr
    290   295   300
Tyr Tyr Ile Leu Arg Thr Phe Ile Glu Lys Leu Gly Ile Lys Gly
305   310   315

<210> 129
<211> 3021
<212> DNA
<213> Bacteria

<400> 129
atggtaataa atcgctccag tgcgagtgac ggtgcgtatt cggaaaaagg tttctatctc 60
gacggtggtg tagaatacaa gtacagtgtt tttgtaaaac acaacgggac cggcaccgaa 120
actttcaaac tttctgtgtc ctatttggat tcggaaacag aagaagaaaa taaggaagta 180
attgcaacaa aggatgttgt ggccggagaa tggactgaga tttcggcaaa atacaaagca 240
cccaaaactg cagtgaatat tactttgtca attacaaccg acagcactgt agatttcatt 300
tttgacgatg taaccataac ccgtaaagga atggctgagg caaacacagt atatgcagca 360
aacgctgtgc tgaaagatat gtatgcaaac tatttcagag ttggttcggt acttaactcc 420
ggaacggtaa acaattcatc aataaaggcc ttgattttaa gagagtttaa cagtattacc 480
tgtgaaaatg aaatgaagcc tgatgccaca ctggttcaat caggatcaac caatacaaat 540
atcagggttt ctcttaatcg tgcagcaagt attttaaact tctgtgcaca aaataatata 600
gccgtcagag gtcatacact ggtttggcac agccagacac ctcaatggtt tttcaaagac 660
aatttccagg acaacggaaa ctgggtttcc caatcagtta tggaccagcg tttggaaagc 720
tacataaaaa atatgtttgc tgaaatccaa agacagtatc cgtctttgaa tctttatgcc 780
tatgacgttg taaatgaggc agtaagtgat gatgcaaaca ggaccagata ttatggcggg 840
gcgagggaac ctggatacgg aaatggtaga tctccatggg ttcagatcta cggagacaac 900
aaatttattg agaaagcatt tacatatgca agaaaatatg ctccggcaaa ttgtaagctt 960
tactacaacg attacaacga atattgggat cataagagag actgtattgc ctcaatttgt 1020
gcaaacttgt acaacaaggg cttgcttgac ggtgtgggaa tgcagtccca tattaatgcg 1080
gatatgaatg gattctcagg tatacaaaat tataaagcag ctttgcagaa atatataaat 1140
atcggttgtg atgtccaaat taccgagctt gatattagta cagaaaacgg caaatttagc 1200
ttacagcagc aggctgataa atataaagct gttttccagg cagctgttga tataaacaga 1260
acctccagca aaggaaaggt tacggctgtc tgtgtatggg gacctaatga cgccaatact 1320
tggctcggtt cacaaaatgc acctcttttg tttaacgcaa acaatcaacc gaaaccggca 1380
tacaatgcgg ttgcatccat tattcctcag tccgaatggg gcgacggtaa caatccggcc 1440
ggcggcggag gaggaggcaa accggaagag ccggatgcaa acggatatta ttatcatgac 1500
acttttgaag gaagcgtagg acagtggaca gccagaggac ctgcggaagt tctgcttagc 1560
ggaagaacgg cttacaaagg ttcagaatca ctcttggtaa ggaaccgtac ggcagcatgg 1620
aacggagcac aacgggcgct gaatcccaga acgtttgttc ccggaaacac atattgtttc 1680
agcgtagtgg catcgtttat tgaaggtgcg tcttccacaa cattctgcat gaagctgcaa 1740
tacgtagacg gaagcggcac tcaacggtat gataccatag atatgaaaac tgtgggtcca 1800
aatcagtggg ttcacctgta caatccgcaa tacagaattc cttccgatgc aacagatatg 1860
tatgtttatg tggaaacagc ggatgacacc attaacttct acatagatga ggcaatcgga 1920
gcggttgccg gaactgtaat cgaaggacct gctccacagc ctacacagcc tccggtactg 1980
cttggcgatg taaacggtga tggaaccatt aactcaactg acttgacaat gttaaagaga 2040
agcgtgttga gggcaatcac ccttaccgac gatgcaaagg ctagagcaga cgttgacaag 2100
aatggatcga taaacagcac tgatgtttta cttctttcac gctacctttt aagagtaatc 2160
gacaaatttc ctgtagcaga aaatccttct tcttctttta aatatgagtc ggccgtgcaa 2220
tatcggccgg ctcctgattc ttatttaaac ccttgtccgc aggcgggaag aattgtcaag 2280
gaaacatata caggaataaa cggaactaag agtcttaatg tatatcttcc atacggttat 2340
gatccgaaca aaaaatataa cattttctac cttatgcatg gcggcggtga aaatgagaat 2400
acgattttca gcaacgatgt taaattgcaa aatatccttg accacgcgat tatgaacggt 2460
gaacttgagc ctttgattgt agtaacaccc actttcaacg gcggaaactg cacggcccaa 2520
aacttttatc aggaattcag gcaaaatgtc attcctttg tggaaagcaa gtactctact 2580
tatgcagaat caacaacccc acagggaata gccgcttcaa gaatgcacag aggtttcggc 2640
ggattctcaa tgggaggatt gacaacatgg tatgtaatgg ttaactgcct tgattacgtt 2700
gcatatttta tgcctttaag cggtgactac tggtatggaa acagtccgca ggataaggct 2760
aattcaattg ctgaagcaat taacagatcc ggactttcaa agagggagta tttcgtattt 2820
gcggccaccg gttccgagga tattgcatat gctaatatga atcctcaaat tgaagctatg 2880
aaggctttgc cgcattttga ttatacttcg gatttttcca aaggtaattt ttactttctt 2940
gtagctccgg gcgccactca ctggtgggga tacgtaagac attatattta tgatgcactt 3000
ccatatttct tccatgaatg a 3021

<210> 130
<211> 1006
<212> PRT
<213> Bacteria

<400> 130
Met Val Ile Asn Arg Ser Ser Ala Ser Asp Gly Ala Tyr Ser Glu Lys
1 5 10 15
Gly Phe Tyr Leu Asp Gly Gly Val Glu Tyr Lys Tyr Ser Val Phe Val
20 25 30
Lys His Asn Gly Thr Gly Thr Glu Thr Phe Lys Leu Ser Val Ser Tyr
35 40 45
Leu Asp Ser Glu Thr Glu Glu Glu Asn Lys Glu Val Ile Ala Thr Lys
50 55 60
Asp Val Val Ala Gly Glu Trp Thr Glu Ile Ser Ala Lys Tyr Lys Ala
65 70 75 80
Pro Lys Thr Ala Val Asn Ile Thr Leu Ser Ile Thr Thr Asp Ser Thr
85 90 95
Val Asp Phe Ile Phe Asp Asp Val Thr Ile Thr Arg Lys Gly Met Ala
100 105 110
Glu Ala Asn Thr Val Tyr Ala Ala Asn Ala Val Leu Lys Asp Met Tyr
115 120 125
Ala Asn Tyr Phe Arg Val Gly Ser Val Leu Asn Ser Gly Thr Val Asn
130 135 140
Asn Ser Ser Ile Lys Ala Leu Ile Leu Arg Glu Phe Asn Ser Ile Thr
145 150 155 160
Cys Glu Asn Glu Met Lys Pro Asp Ala Thr Leu Val Gln Ser Gly Ser
165 170 175
Thr Asn Thr Asn Ile Arg Val Ser Leu Asn Arg Ala Ala Ser Ile Leu
180 185 190
Asn Phe Cys Ala Gln Asn Asn Ile Ala Val Arg Gly His Thr Leu Val
195 200 205
Trp His Ser Gln Thr Pro Gln Trp Phe Phe Lys Asp Asn Phe Gln Asp
210 215 220
Asn Gly Asn Trp Val Ser Gln Ser Val Met Asp Gln Arg Leu Glu Ser
225 230 235 240
Tyr Ile Lys Asn Met Phe Ala Glu Ile Gln Arg Gln Tyr Pro Ser Leu
245 250 255
Asn Leu Tyr Ala Tyr Asp Val Val Asn Glu Ala Val Ser Asp Asp Ala
260 265 270
Asn Arg Thr Arg Tyr Tyr Gly Gly Ala Arg Glu Pro Gly Tyr Gly Asn
275 280 285
Gly Arg Ser Pro Trp Val Gln Ile Tyr Gly Asp Asn Lys Phe Ile Glu
290 295 300
Lys Ala Phe Thr Tyr Ala Arg Lys Tyr Ala Pro Ala Asn Cys Lys Leu
305 310 315 320
Tyr Tyr Asn Asp Tyr Asn Glu Tyr Trp Asp His Lys Arg Asp Cys Ile
325 330 335
Ala Ser Ile Cys Ala Asn Leu Tyr Asn Lys Gly Leu Leu Asp Gly Val
340 345 350
Gly Met Gln Ser His Ile Asn Ala Asp Met Asn Gly Phe Ser Gly Ile
355 360 365
Gln Asn Tyr Lys Ala Ala Leu Gln Lys Tyr Ile Asn Ile Gly Cys Asp
370 375 380
Val Gln Ile Thr Glu Leu Asp Ile Ser Thr Glu Asn Gly Lys Phe Ser
385 390 395 400
Leu Gln Gln Gln Ala Asp Lys Tyr Lys Ala Val Phe Gln Ala Ala Val
405 410 415
Asp Ile Asn Arg Thr Ser Ser Lys Gly Lys Val Thr Ala Val Cys Val
420 425 430
Trp Gly Pro Asn Asp Ala Asn Thr Trp Leu Gly Ser Gln Asn Ala Pro
435 440 445
Leu Leu Phe Asn Ala Asn Asn Gln Pro Lys Pro Ala Tyr Asn Ala Val
450 455 460
Ala Ser Ile Ile Pro Gln Ser Glu Trp Gly Asp Gly Asn Asn Pro Ala
465 470 475 480
Gly Gly Gly Gly Gly Gly Lys Pro Glu Glu Pro Asp Ala Asn Gly Tyr
485 490 495
Tyr Tyr His Asp Thr Phe Glu Gly Ser Val Gly Gln Trp Thr Ala Arg
500 505 510
Gly Pro Ala Glu Val Leu Leu Ser Gly Arg Thr Ala Tyr Lys Gly Ser
515 520 525
Glu Ser Leu Leu Val Arg Asn Arg Thr Ala Ala Trp Asn Gly Ala Gln

```
        530                     535                     540
Arg Ala Leu Asn Pro Arg Thr Phe Val Pro Gly Asn Thr Tyr Cys Phe
545                 550                 555                 560
Ser Val Val Ala Ser Phe Ile Glu Gly Ala Ser Ser Thr Thr Phe Cys
                565                 570                 575
Met Lys Leu Gln Tyr Val Asp Gly Ser Gly Thr Gln Arg Tyr Asp Thr
            580                 585                 590
Ile Asp Met Lys Thr Val Gly Pro Asn Gln Trp Val His Leu Tyr Asn
        595                 600                 605
Pro Gln Tyr Arg Ile Pro Ser Asp Ala Thr Asp Met Tyr Val Tyr Val
    610                 615                 620
Glu Thr Ala Asp Asp Thr Ile Asn Phe Tyr Ile Asp Glu Ala Ile Gly
625                 630                 635                 640
Ala Val Ala Gly Thr Val Ile Glu Gly Pro Ala Pro Gln Pro Thr Gln
                645                 650                 655
Pro Pro Val Leu Leu Gly Asp Val Asn Gly Asp Gly Thr Ile Asn Ser
            660                 665                 670
Thr Asp Leu Thr Met Leu Lys Arg Ser Val Leu Arg Ala Ile Thr Leu
        675                 680                 685
Thr Asp Asp Ala Lys Ala Arg Ala Asp Val Asp Lys Asn Gly Ser Ile
    690                 695                 700
Asn Ser Thr Asp Val Leu Leu Leu Ser Arg Tyr Leu Leu Arg Val Ile
705                 710                 715                 720
Asp Lys Phe Pro Val Ala Glu Asn Pro Ser Ser Ser Phe Lys Tyr Glu
                725                 730                 735
Ser Ala Val Gln Tyr Arg Pro Ala Pro Asp Ser Tyr Leu Asn Pro Cys
            740                 745                 750
Pro Gln Ala Gly Arg Ile Val Lys Glu Thr Tyr Thr Gly Ile Asn Gly
        755                 760                 765
Thr Lys Ser Leu Asn Val Tyr Leu Pro Tyr Gly Tyr Asp Pro Asn Lys
    770                 775                 780
Lys Tyr Asn Ile Phe Tyr Leu Met His Gly Gly Gly Glu Asn Glu Asn
785                 790                 795                 800
Thr Ile Phe Ser Asn Asp Val Lys Leu Gln Asn Ile Leu Asp His Ala
                805                 810                 815
Ile Met Asn Gly Glu Leu Glu Pro Leu Ile Val Val Thr Pro Thr Phe
            820                 825                 830
Asn Gly Gly Asn Cys Thr Ala Gln Asn Phe Tyr Gln Glu Phe Arg Gln
        835                 840                 845
Asn Val Ile Pro Phe Val Glu Ser Lys Tyr Ser Thr Tyr Ala Glu Ser
    850                 855                 860
Thr Thr Pro Gln Gly Ile Ala Ala Ser Arg Met His Arg Gly Phe Gly
865                 870                 875                 880
Gly Phe Ser Met Gly Gly Leu Thr Thr Trp Tyr Val Met Val Asn Cys
                885                 890                 895
Leu Asp Tyr Val Ala Tyr Phe Met Pro Leu Ser Gly Asp Tyr Trp Tyr
            900                 905                 910
Gly Asn Ser Pro Gln Asp Lys Ala Asn Ser Ile Ala Glu Ala Ile Asn
        915                 920                 925
Arg Ser Gly Leu Ser Lys Arg Glu Tyr Phe Val Phe Ala Ala Thr Gly
    930                 935                 940
Ser Glu Asp Ile Ala Tyr Ala Asn Met Asn Pro Gln Ile Glu Ala Met
945                 950                 955                 960
Lys Ala Leu Pro His Phe Asp Tyr Thr Ser Asp Phe Ser Lys Gly Asn
                965                 970                 975
Phe Tyr Phe Leu Val Ala Pro Gly Ala Thr His Trp Trp Gly Tyr Val
            980                 985                 990
Arg His Tyr Ile Tyr Asp Ala Leu Pro Tyr Phe Phe His Glu
        995                 1000                1005
```

<210> 131
<211> 1218
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 131

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atgccgatca tccgaaccct atcgagttac atgcgaaatc atcaagcgat ctaccgtcag      60
ctcctcacgc tggccgccgc cgtcacgctg gcgggcgcgg ccaccgcgga ggaagaagcc     120
accctgcgcg ggtttacga aaaggacttc accatcggcg tggccatgaa cgggggccag     180
gcctccggcc gcaatgccgc cgccggcgag atcatcggca agcagttctc ctcgctcacc     240
gcggagaacg acatgaagtg gcagatgatc cacccccagg agggtcaata ccgcttcgaa     300
acgtccgacg cctacgtcgc gttcgcggaa aagcacaaga tggaagtcat cggccacacc     360
ctcgtgtggc acagccagac cccgcagtgg gtcttccagg gtgaaaacgg ccagcccgcc     420
accaaggaag agctgctcaa gcgcatgcgc gaccacatcc acgccgtggc cggccgttac     480
aagggcaaga tcaagggctg ggacgtcgtc aacgaagcgc tctccgacgg cggggacgac     540
attctccgcc agtcccctg gcgccgcatc atcggcgacg acttcatcga ctacgccttc      600
cgctacgcca aggaagccgc cccggatgcc gagctctact acaacgacta caacctcgag     660
atcccccgca agcgcgccaa ttgcatcacg ctggtcaagg gcatgctcga gcgcggcgtg     720
ccgatcgacg gcatcggcac ccagtcgcac ttccagctcg gctttccctc cttggacgac     780
gtggaagcca ccatcaagga attcgccgcc ctgggcatga aggtgatgat caccgagctc     840
gacgtggatg tcctgccccg caacaacccc ggggtcgccg acatcgccaa ccgcgaacag     900
ggagccaacc cctacaccga aggccttccg gacgacgtgc aggaaaagct cgcgaagcgc     960
tacgaggaca tcttccgcat ctacctgaag taccgcgacc acgtcacccg cgtcaccttc    1020
tggggcctgg atgacggcat gacctggctg aacggcttcc cggtccgcgg ccgcaccaac    1080
cacccccctgc tctacgaccg gcagctcaat gccaagcccg ccttccacgc cctcgtcaag  1140
ctgggtcagg aagagcgtcc ggaagccgcc aaggtcgagg tccagaagat cgaagcgaag    1200
aaagaagagg cgaagtaa                                                  1218
```

<210> 132
<211> 405
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(26)

<400> 132

```
Met Pro Ile Ile Arg Thr Leu Ser Ser Tyr Met Arg Asn His Gln Ala
 1               5                  10                  15
Ile Tyr Arg Gln Leu Leu Thr Leu Ala Ala Ala Val Thr Leu Ala Gly
            20                  25                  30
Ala Ala Thr Ala Glu Glu Glu Ala Thr Leu Arg Gly Val Tyr Glu Lys
        35                  40                  45
Asp Phe Thr Ile Gly Val Ala Met Asn Gly Gly Gln Ala Ser Gly Arg
    50                  55                  60
Asn Ala Ala Ala Gly Glu Ile Ile Gly Lys Gln Phe Ser Ser Leu Thr
65                  70                  75                  80
Ala Glu Asn Asp Met Lys Trp Gln Met Ile His Pro Gln Glu Gly Gln
                85                  90                  95
Tyr Arg Phe Glu Thr Ser Asp Ala Tyr Val Ala Phe Ala Glu Lys His
            100                 105                 110
Lys Met Glu Val Ile Gly His Thr Leu Val Trp His Ser Gln Thr Pro
        115                 120                 125
Gln Trp Val Phe Gln Gly Glu Asn Gly Gln Pro Ala Thr Lys Glu Glu
    130                 135                 140
Leu Leu Lys Arg Met Arg Asp His Ile His Ala Val Ala Gly Arg Tyr
145                 150                 155                 160
Lys Gly Lys Ile Lys Gly Trp Asp Val Val Asn Glu Ala Leu Ser Asp
                165                 170                 175
Gly Gly Asp Asp Ile Leu Arg Gln Ser Pro Trp Arg Arg Ile Ile Gly
            180                 185                 190
Asp Asp Phe Ile Asp Tyr Ala Phe Arg Tyr Ala Lys Glu Ala Ala Pro
        195                 200                 205
Asp Ala Glu Leu Tyr Tyr Asn Asp Tyr Asn Leu Glu Ile Pro Arg Lys
    210                 215                 220
Arg Ala Asn Cys Ile Thr Leu Val Lys Gly Met Leu Glu Arg Gly Val
225                 230                 235                 240
Pro Ile Asp Gly Ile Gly Thr Gln Ser His Phe Gln Leu Gly Phe Pro
                245                 250                 255
Ser Leu Asp Asp Val Glu Ala Thr Ile Lys Glu Phe Ala Ala Leu Gly
            260                 265                 270
Met Lys Val Met Ile Thr Glu Leu Asp Val Asp Val Leu Pro Arg Asn
```

```
                275                     280                     285
Asn Pro Gly Val Ala Asp Ile Ala Asn Arg Glu Gln Gly Ala Asn Pro
        290                     295                     300
Tyr Thr Glu Gly Leu Pro Asp Asp Val Gln Glu Lys Leu Ala Lys Arg
305                     310                     315                 320
Tyr Glu Asp Ile Phe Arg Ile Tyr Leu Lys Tyr Arg Asp His Val Thr
                    325                     330                 335
Arg Val Thr Phe Trp Gly Leu Asp Asp Gly Met Thr Trp Leu Asn Gly
            340                     345                 350
Phe Pro Val Arg Gly Arg Thr Asn His Pro Leu Leu Tyr Asp Arg Gln
        355                     360                 365
Leu Asn Ala Lys Pro Ala Phe His Ala Leu Val Lys Leu Gly Gln Glu
    370                     375                 380
Glu Arg Pro Glu Ala Ala Lys Val Glu Val Gln Lys Ile Glu Ala Lys
385                     390                     395                 400
Lys Glu Glu Ala Lys
                405
```

<210> 133
<211> 1011
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 133

```
atgaaaaata atcaatttag gaaaatccct tccctacata aggtatataa gagtcatttt      60
ttaattgggg cagctgtaaa tccacttaca cttcaaacac aacaggaact aatcaaaaag     120
cactttaata gtattacggc agaaaatgaa atgaaatttg aagagttgca acctgagcct     180
ggacatttta catttgatgt aggagataaa atggtcgctt tcgcaaaaga aaatggtatg     240
aaagttagag gtcatacatt aatctggcac aatcaaacac ctgattggat gtttaagaat     300
gaagatggtt ctgtcacaga tcgagataca cttcttgaaa gaatgaaatt acatattaca     360
actgttatgg agcattataa ggggcaaatt tattgttggg atgttgtcaa tgaagcgatt     420
gctgatgaag gatcagagtt attacgtcac tctaaatgga ctgaaattat tggcgacgat     480
tttattgaaa aggcatttga gtatgcacat gaagcagacc cagaagcttt actattctat     540
aatgactata atgagtccca ccctcataag cgagataaaa tttacacact aataaaaaga     600
ttggtagaca aaggcatacc tattcacggg gttggcttgc aagcacattg gaatttaaca     660
gacccttctt atgaggagat tagggctgca attgaaaaat atgcctcatt aggcttggaa     720
atacatctta cagaaatgga tgtttcagtg ttcaattttg aagatcgaag aacagactta     780
acagagccga ctaatgaaat gaagactctt caagtagaac gttatacgga atttttcaaa     840
atacttagag aatatagcca tgtgattagc tctgtcactt tttggggagc tgcagatgat     900
tatacttggt tggatgggtt tccagttaga ggaaggaaaa actggccatt tgtttttgac     960
gaaaaccacc aaccgaaaga atctttctgg ggaattgtcg attttgaata a             1011
```

<210> 134
<211> 336
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 134

```
Met Lys Asn Asn Gln Phe Arg Lys Ile Pro Ser Leu His Lys Val Tyr
 1               5                  10                  15
Lys Ser His Phe Leu Ile Gly Ala Ala Val Asn Pro Leu Thr Leu Gln
            20                  25                  30
Thr Gln Gln Glu Leu Ile Lys Lys His Phe Asn Ser Ile Thr Ala Glu
        35                  40                  45
Asn Glu Met Lys Phe Glu Glu Leu Gln Pro Glu Pro Gly His Phe Thr
    50                  55                  60
Phe Asp Val Gly Asp Lys Met Val Ala Phe Ala Lys Glu Asn Gly Met
65                  70                  75                  80
Lys Val Arg Gly His Thr Leu Ile Trp His Asn Gln Thr Pro Asp Trp
                85                  90                  95
Met Phe Lys Asn Glu Asp Gly Ser Val Thr Asp Arg Asp Thr Leu Leu
            100                 105                 110
Glu Arg Met Lys Leu His Ile Thr Thr Val Met Glu His Tyr Lys Gly
```

```
        115                     120                     125
Gln Ile Tyr Cys Trp Asp Val Val Asn Glu Ala Ile Ala Asp Glu Gly
    130                     135                     140
Ser Glu Leu Leu Arg His Ser Lys Trp Thr Glu Ile Ile Gly Asp Asp
145                     150                     155                 160
Phe Ile Glu Lys Ala Phe Glu Tyr Ala His Glu Ala Asp Pro Glu Ala
                165                     170                     175
Leu Leu Phe Tyr Asn Asp Tyr Asn Glu Ser His Pro His Lys Arg Asp
            180                     185                     190
Lys Ile Tyr Thr Leu Ile Lys Arg Leu Val Asp Lys Gly Ile Pro Ile
        195                     200                     205
His Gly Val Gly Leu Gln Ala His Trp Asn Leu Thr Asp Pro Ser Tyr
    210                     215                     220
Glu Glu Ile Arg Ala Ala Ile Glu Lys Tyr Ala Ser Leu Gly Leu Glu
225                     230                     235                 240
Ile His Leu Thr Glu Met Asp Val Ser Val Phe Asn Phe Glu Asp Arg
                245                     250                     255
Arg Thr Asp Leu Thr Glu Pro Thr Asn Glu Met Lys Thr Leu Gln Val
            260                     265                     270
Glu Arg Tyr Thr Glu Phe Phe Lys Ile Leu Arg Glu Tyr Ser His Val
        275                     280                     285
Ile Ser Ser Val Thr Phe Trp Gly Ala Ala Asp Asp Tyr Thr Trp Leu
    290                     295                     300
Asp Gly Phe Pro Val Arg Gly Arg Lys Asn Trp Pro Phe Val Phe Asp
305                     310                     315                 320
Glu Asn His Gln Pro Lys Glu Ser Phe Trp Gly Ile Val Asp Phe Glu
                325                     330                     335
```

<210> 135
<211> 1170
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 135
```
atgcgacgcc tcatcgccct tgtcctatat ataggaaccg ccgcgagcgg gacctccgtg      60
gagaccgttg cggccgaatc gaaacagccg aaagctagcc taaagaatgc gttcgcagac     120
gattttcgtg tcggcgctgc aattggcacc aatcaggtca tgggcgagga gccaaaatcg     180
ctcgaggttg tcgcccagca gttcaacaca atcacgcctg agaatctcct caaatgggct     240
gaggtccacc cagaagcaga ccgctacaac ttcgaaccgt ccgatcgctt cgtcgaattt     300
ggcgaaaaga acaacatgtt catcgtcggc cacacgctcg tgtggcataa ccaaacgccg     360
gactgggcct ttgagggcaa ggacggcaag ccgctcgatc gcgaaacagc gctcgcccga     420
atcaaggaac acattgaaac cgtggtcggc cgatatcgcg gccgcatcca tgcttgggac     480
gtcgtgaacg aggcaatcga cgacaacggc aaacttcgta gtgggccggt cggagtgccc     540
ggtcagcgcg gcgaaccgtg gcacgccgcc atcggagacg actacatcca gaaggcgttc     600
gaattcgcgc acaccgccga ccccgacgct gaactctatt acaacgacta caacgaatgg     660
cacccgaaaa agatcgaagc catctcgcag ctggtgcggt cgctcaaaga gaagggcgtt     720
cgtatcgatg gcctcggtct ccagggccat tgggggatgg attacccgaa agtcgaagag     780
atcgatcaca tgctaaccga gtatggcaag ctcggcgtga agctcatgat taccgaactc     840
gacatcaaca tgcttccgca gcccgacccg agtcaacgcg gcgccgatat cactcgcaac     900
tacgagctca gaaaggagct cgatccgtat tccgacggac tcccgcccga tatgcaaaag     960
gcactcgcgg cgcgttatgc tgaaatcttc gaagtcttcg ctaagcatcg cgataagctc    1020
gaccgcgtca cattttgggg cgttcacgac ggccattcat ggctcaacaa ctggcctgtt    1080
cccggtcgca ctgcctaccc gcttctcttc gacacgaagc ttcagcccaa gccggcattt    1140
gatgccgtca tcggagtcgc agagcaatga                                    1170
```

<210> 136
<211> 389
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(25)

<400> 136
Met Arg Arg Leu Ile Ala Leu Val Leu Tyr Ile Gly Thr Ala Ala Ser
1 5 10 15
Gly Thr Ser Val Glu Thr Val Ala Ala Glu Ser Lys Gln Pro Lys Ala
20 25 30
Ser Leu Lys Asn Ala Phe Ala Asp Asp Phe Arg Val Gly Ala Ala Ile
35 40 45
Gly Thr Asn Gln Val Met Gly Glu Glu Pro Lys Ser Leu Glu Val Val
50 55 60
Ala Gln Gln Phe Asn Thr Ile Thr Pro Glu Asn Leu Leu Lys Trp Ala
65 70 75 80
Glu Val His Pro Glu Ala Asp Arg Tyr Asn Phe Glu Pro Ser Asp Arg
85 90 95
Phe Val Glu Phe Gly Glu Lys Asn Asn Met Phe Ile Val Gly His Thr
100 105 110
Leu Val Trp His Asn Gln Thr Pro Asp Trp Ala Phe Glu Gly Lys Asp
115 120 125
Gly Lys Pro Leu Asp Arg Glu Thr Ala Leu Ala Arg Ile Lys Glu His
130 135 140
Ile Glu Thr Val Val Gly Arg Tyr Arg Gly Arg Ile His Ala Trp Asp
145 150 155 160
Val Val Asn Glu Ala Ile Asp Asp Asn Gly Lys Leu Arg Ser Gly Pro
165 170 175
Val Gly Val Pro Gly Gln Arg Gly Glu Pro Trp His Ala Ala Ile Gly
180 185 190
Asp Asp Tyr Ile Gln Lys Ala Phe Glu Phe Ala His Thr Ala Asp Pro
195 200 205
Asp Ala Glu Leu Tyr Tyr Asn Asp Tyr Asn Glu Trp His Pro Lys Lys
210 215 220
Ile Glu Ala Ile Ser Gln Leu Val Arg Ser Leu Lys Glu Lys Gly Val
225 230 235 240
Arg Ile Asp Gly Leu Gly Leu Gln Gly His Trp Gly Met Asp Tyr Pro
245 250 255
Lys Val Glu Glu Ile Asp His Met Leu Thr Glu Tyr Gly Lys Leu Gly
260 265 270
Val Lys Leu Met Ile Thr Glu Leu Asp Ile Asn Met Leu Pro Gln Pro
275 280 285
Asp Pro Ser Gln Arg Gly Ala Asp Ile Thr Arg Asn Tyr Glu Leu Arg
290 295 300
Lys Glu Leu Asp Pro Tyr Ser Asp Gly Leu Pro Pro Asp Met Gln Lys
305 310 315 320
Ala Leu Ala Ala Arg Tyr Ala Glu Ile Phe Glu Val Phe Ala Lys His
325 330 335
Arg Asp Lys Leu Asp Arg Val Thr Phe Trp Gly Val His Asp Gly His
340 345 350
Ser Trp Leu Asn Asn Trp Pro Val Pro Gly Arg Thr Ala Tyr Pro Leu
355 360 365
Leu Phe Asp Thr Lys Leu Gln Pro Lys Pro Ala Phe Asp Ala Val Ile
370 375 380
Gly Val Ala Glu Gln
385

<210> 137
<211> 1044
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 137
gtggatcctt cgctgaagga agcagcttcg ggcaagtttc tgatgggggt agcgttgaat 60
gtacgtcagg cagcaggtca ggatacttgc gcctcgaaag tggtaaaacg tcattttaat 120
tccattgtgg ccgagaattg catgaaatgc gaagtgattc atccggagga agaccatttt 180
gattttacgg aagcggaccg gttggttcgt tttggcgagg agaacgatat ggctgttatc 240
gggcattgcc ttatctggca ttcacagctg gcaccttggt tctgtgtgga caaacaagga 300
aaaacagtaa gtgccgacat cttgaaggag cgtataaaaa aacatatcca gactattgtg 360
acgcactata aagggcgtat aaagggctgg gatgtgttga atgaagccat tgaatcggac 420
ggctcctggc gtaaatctcc tttttacgag atattaggcg aagagtacat cccgcttatt 480

tttcagtatg ctcatgaggc agatccggaa gccgaacttt actataatga ttatggcatg 540
gacgggaagg ctaagcgtga caaagtagtc gaattggtaa agatgctgaa agatcgtgga 600
ctgcgcatcg acgcggtagg tatgcaggga cacatgggaa tggattatcc gtcagtgtcc 660
gaatttgaag ccagtatact ggcatttgca gctgccggag taaaggtgat ggtaaccgaa 720
tgggatatga gtgcattgcc cacgacacgg atgggagcca atatttcgga cacggtgtct 780
tataaacaat ccctgaatcc ctatcccgac ggtttgcccg actctgtgtc tgtggcatgg 840
aataaccgga tgaaggaatt tttcggtctt ttcctgaaac attcgaatat cattacccgt 900
gtgacggcgt ggggggtgac ggacggtgac tcatggaaga ataatttccc tgtgcccgga 960
cgtgtggatt atcctttatt gttcgaccgt gattgccggc cgaaaccttt tgtggaagaa 1020
ctgattggaa aacagaacat ttaa 1044

<210> 138
<211> 347
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 138
Val Asp Pro Ser Leu Lys Glu Ala Ala Ser Gly Lys Phe Leu Met Gly
1 5 10 15
Val Ala Leu Asn Val Arg Gln Ala Ala Gly Gln Asp Thr Cys Ala Ser
20 25 30
Lys Val Val Lys Arg His Phe Asn Ser Ile Val Ala Glu Asn Cys Met
35 40 45
Lys Cys Glu Val Ile His Pro Glu Glu Asp His Phe Asp Phe Thr Glu
50 55 60
Ala Asp Arg Leu Val Arg Phe Gly Glu Glu Asn Asp Met Ala Val Ile
65 70 75 80
Gly His Cys Leu Ile Trp His Ser Gln Leu Ala Pro Trp Phe Cys Val
85 90 95
Asp Lys Gln Gly Lys Thr Val Ser Ala Asp Ile Leu Lys Glu Arg Ile
100 105 110
Lys Lys His Ile Gln Thr Ile Val Thr His Tyr Lys Gly Arg Ile Lys
115 120 125
Gly Trp Asp Val Leu Asn Glu Ala Ile Glu Ser Asp Gly Ser Trp Arg
130 135 140
Lys Ser Pro Phe Tyr Glu Ile Leu Gly Glu Glu Tyr Ile Pro Leu Ile
145 150 155 160
Phe Gln Tyr Ala His Glu Ala Asp Pro Glu Ala Glu Leu Tyr Tyr Asn
165 170 175
Asp Tyr Gly Met Asp Gly Lys Ala Lys Arg Asp Lys Val Val Glu Leu
180 185 190
Val Lys Met Leu Lys Asp Arg Gly Leu Arg Ile Asp Ala Val Gly Met
195 200 205
Gln Gly His Met Gly Met Asp Tyr Pro Ser Val Ser Glu Phe Glu Ala
210 215 220
Ser Ile Leu Ala Phe Ala Ala Ala Gly Val Lys Val Met Val Thr Glu
225 230 235 240
Trp Asp Met Ser Ala Leu Pro Thr Thr Arg Met Gly Ala Asn Ile Ser
245 250 255
Asp Thr Val Ser Tyr Lys Gln Ser Leu Asn Pro Tyr Pro Asp Gly Leu
260 265 270
Pro Asp Ser Val Ser Val Ala Trp Asn Asn Arg Met Lys Glu Phe Phe
275 280 285
Gly Leu Phe Leu Lys His Ser Asn Ile Ile Thr Arg Val Thr Ala Trp
290 295 300
Gly Val Thr Asp Gly Asp Ser Trp Lys Asn Asn Phe Pro Val Pro Gly
305 310 315 320
Arg Val Asp Tyr Pro Leu Leu Phe Asp Arg Asp Cys Arg Pro Lys Pro
325 330 335
Phe Val Glu Glu Leu Ile Gly Lys Gln Asn Ile
340 345

<210> 139
<211> 1143
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 139
atgaaaaaaa cgattgcaca tttcacctta tggatagtgt tttttctctt cacttcctgt 60
actgttacgg cgcagaagaa tgctaagaat gcaagagtaa aacccactac cctaaaagag 120
gcttaccaag gtaaattcta tatcggtact gcgatgaact tgagacagat tcacggagat 180
gatccccaat ctgaaaatat tatcaaaaaa cagttcaatt ccatagttgc cgaaaactgc 240
atgaagagta tgtatcttca gccggaggaa ggaaaatttt tcttcgatga tgcggacaag 300
tttgtggatt ttggtcttca gaacaatatg ttcattatcg ggcattgtct gatttggcat 360
tcgcaggcgc caaaatggtt tttcaccgac gaaaatggaa acacggtttc tccagaagtt 420
cttaaacaaa ggatgaaagc ccatatcacc gctgtcgttt cccgctacaa agggaaaatc 480
aaaggttggg atgtggtgaa cgaagccatt atggaagatg gttcttaccg caaaagcaaa 540
ttttacgaga ttttgggaga agaatttatt ccgttggcat ttcagtatgc gcatgaagca 600
gatcctgatg cagaacttta ttacaacgat tataacgaat ggtatcccgg gaaaagagct 660
atggtgacca aaataatccg cgatttcaaa actagaggaa tccgcatcga tgccatcgga 720
atgcaggctc atttcgggat ggattcgccc actgtagaag agtatgaaca aactattcag 780
ggctatataa aagaaggcgt gaaagtcaat attacggaac tcgatttaag tccgcttcct 840
tctccttggg gaacttccgc caacgttgct gatacgcagc agtatcagga aaaaatgaat 900
ccttacacca aaggacttcc tgtcgatgta gaaaaagcat gggaaaaccg ttatctcgat 960
tttttcaaac ttttcctaaa atatcatcag catattgagc gtgtaacttt ttggggagtg 1020
agcgacatcg attcctggaa aaacgatttt ccgataagag gacgtaccga ttatccacta 1080
ccgtttaacc gtcaatatca ggcaaaacct ttggttcaga aattaataga cttaacgaaa 1140
tag 1143

<210> 140
<211> 380
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(24)

<400> 140
Met Lys Lys Thr Ile Ala His Phe Thr Leu Trp Ile Val Phe Phe Leu
1 5 10 15
Phe Thr Ser Cys Thr Val Thr Ala Gln Lys Asn Ala Lys Asn Ala Arg
20 25 30
Val Lys Pro Thr Thr Leu Lys Glu Ala Tyr Gln Gly Lys Phe Tyr Ile
35 40 45
Gly Thr Ala Met Asn Leu Arg Gln Ile His Gly Asp Asp Pro Gln Ser
50 55 60
Glu Asn Ile Ile Lys Lys Gln Phe Asn Ser Ile Val Ala Glu Asn Cys
65 70 75 80
Met Lys Ser Met Tyr Leu Gln Pro Glu Glu Gly Lys Phe Phe Phe Asp
85 90 95
Asp Ala Asp Lys Phe Val Asp Phe Gly Leu Gln Asn Asn Met Phe Ile
100 105 110
Ile Gly His Cys Leu Ile Trp His Ser Gln Ala Pro Lys Trp Phe Phe
115 120 125
Thr Asp Glu Asn Gly Asn Thr Val Ser Pro Glu Val Leu Lys Gln Arg
130 135 140
Met Lys Ala His Ile Thr Ala Val Val Ser Arg Tyr Lys Gly Lys Ile
145 150 155 160
Lys Gly Trp Asp Val Val Asn Glu Ala Ile Met Glu Asp Gly Ser Tyr
165 170 175
Arg Lys Ser Lys Phe Tyr Glu Ile Leu Gly Glu Glu Phe Ile Pro Leu
180 185 190
Ala Phe Gln Tyr Ala His Glu Ala Asp Pro Asp Ala Glu Leu Tyr Tyr
195 200 205
Asn Asp Tyr Asn Glu Trp Tyr Pro Gly Lys Arg Ala Met Val Thr Lys
210 215 220
Ile Ile Arg Asp Phe Lys Thr Arg Gly Ile Arg Ile Asp Ala Ile Gly
225 230 235 240
Met Gln Ala His Phe Gly Met Asp Ser Pro Thr Val Glu Glu Tyr Glu

```
                245                 250                 255
Gln Thr Ile Gln Gly Tyr Ile Lys Glu Gly Val Lys Val Asn Ile Thr
            260                 265                 270
Glu Leu Asp Leu Ser Pro Leu Pro Ser Pro Trp Gly Thr Ser Ala Asn
        275                 280                 285
Val Ala Asp Thr Gln Gln Tyr Gln Glu Lys Met Asn Pro Tyr Thr Lys
    290                 295                 300
Gly Leu Pro Val Asp Val Glu Lys Ala Trp Glu Asn Arg Tyr Leu Asp
305                 310                 315                 320
Phe Phe Lys Leu Phe Leu Lys Tyr His Gln His Ile Glu Arg Val Thr
                325                 330                 335
Phe Trp Gly Val Ser Asp Ile Asp Ser Trp Lys Asn Asp Phe Pro Ile
            340                 345                 350
Arg Gly Arg Thr Asp Tyr Pro Leu Pro Phe Asn Arg Gln Tyr Gln Ala
        355                 360                 365
Lys Pro Leu Val Gln Lys Leu Ile Asp Leu Thr Lys
    370                 375                 380
```

<210> 141
<211> 1134
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 141

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atgaatatct cacgcagaca actactggcg ctcacgggtg ctacggcggc gatcacagca      60
gccaaattac aggcggcaga aaaagccagc gccgcgaccg gcttgcgcga tgcctacaaa     120
aatgattttt tgattggcgc tgcgctgagt gcatcgatca ttcaacagca agatccacag     180
ctagttgcac tgattaataa agactttaat tccatcaccc cagaaaactg tatgaaatgg     240
ggcgagatgc gcaatgatga cggcagctgg aagtggcagg atgcagacgc atttgtcgag     300
tatggaagca aatacaaact acatatggtc ggccacacat tggggtggca cagccagatt     360
cccgatagcg tgtttaaaaa taaagacggt agctatattt ccaaaaccga actcgcgaaa     420
aaacaaaaag aacacatcac cactattgtt ggccgctaca aaggcaaact tgccgcgtgg     480
gatgtggtga atgaagctgt cggcgatgac aacaaaatgc gcgatagtca ctggtataaa     540
atcatgggcg atgattttct cgttaatgca tttaaccttg ctcatgaagt agatccgaag     600
gcgcatctga tgtacaacga ctacaacaac gagcgcccgg aaaaacgcca ggcgactatc     660
gatatgatca agcgtctgca acaacgcggt acaccaatcc atggtttggg catgcaagcg     720
catatcggat tggaaaccaa tatgcaggat tttgaagata gtattctcgc ctattcagca     780
ttgggtttaa aaatccatct caccgaacta gatatagatg tgctgccctc tgtatggaat     840
ttaccggtgg ccgaaatttc tacccgcttt gaatacaagc cggaacgcga tccttataca     900
aaaggtttgc cgaaagagat tgatgaaaaa cttgcaaaag cctatgaatc gctatttaaa     960
atattgctta aacatcgcga caaaatagat agagttacgt tttggggcgt aagcgatgat    1020
gccagctggc tcaatgattt cccaatcaat ggcagaacca actatccgtt attgtttaac    1080
cgtcaacgcc aacctaaagc tgcttatttc cgtttgctgg atttaaaacg ctag          1134
```

<210> 142
<211> 377
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(25)

<400> 142

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Met Asn Ile Ser Arg Arg Gln Leu Leu Ala Leu Thr Gly Ala Thr Ala
1               5                   10                  15
Ala Ile Thr Ala Ala Lys Leu Gln Ala Ala Glu Lys Ala Ser Ala Ala
            20                  25                  30
Thr Gly Leu Arg Asp Ala Tyr Lys Asn Asp Phe Leu Ile Gly Ala Ala
        35                  40                  45
Leu Ser Ala Ser Ile Ile Gln Gln Gln Asp Pro Gln Leu Val Ala Leu
    50                  55                  60
Ile Asn Lys Asp Phe Asn Ser Ile Thr Pro Glu Asn Cys Met Lys Trp
65                  70                  75                  80
```

```
Gly Glu Met Arg Asn Asp Asp Gly Ser Trp Lys Trp Gln Asp Ala Asp
                85                  90                  95
Ala Phe Val Glu Tyr Gly Ser Lys Tyr Lys Leu His Met Val Gly His
            100                 105                 110
Thr Leu Gly Trp His Ser Gln Ile Pro Asp Ser Val Phe Lys Asn Lys
        115                 120                 125
Asp Gly Ser Tyr Ile Ser Lys Thr Glu Leu Ala Lys Lys Gln Lys Glu
    130                 135                 140
His Ile Thr Thr Ile Val Gly Arg Tyr Lys Gly Lys Leu Ala Ala Trp
145                 150                 155                 160
Asp Val Val Asn Glu Ala Val Gly Asp Asp Asn Lys Met Arg Asp Ser
                165                 170                 175
His Trp Tyr Lys Ile Met Gly Asp Asp Phe Leu Val Asn Ala Phe Asn
            180                 185                 190
Leu Ala His Glu Val Asp Pro Lys Ala His Leu Met Tyr Asn Asp Tyr
        195                 200                 205
Asn Asn Glu Arg Pro Glu Lys Arg Gln Ala Thr Ile Asp Met Ile Lys
    210                 215                 220
Arg Leu Gln Gln Arg Gly Thr Pro Ile His Gly Leu Gly Met Gln Ala
225                 230                 235                 240
His Ile Gly Leu Glu Thr Asn Met Gln Asp Phe Glu Asp Ser Ile Leu
                245                 250                 255
Ala Tyr Ser Ala Leu Gly Leu Lys Ile His Leu Thr Glu Leu Asp Ile
            260                 265                 270
Asp Val Leu Pro Ser Val Trp Asn Leu Pro Val Ala Glu Ile Ser Thr
        275                 280                 285
Arg Phe Glu Tyr Lys Pro Glu Arg Asp Pro Tyr Thr Lys Gly Leu Pro
    290                 295                 300
Lys Glu Ile Asp Glu Lys Leu Ala Lys Ala Tyr Glu Ser Leu Phe Lys
305                 310                 315                 320
Ile Leu Leu Lys His Arg Asp Lys Ile Asp Arg Val Thr Phe Trp Gly
                325                 330                 335
Val Ser Asp Asp Ala Ser Trp Leu Asn Asp Phe Pro Ile Asn Gly Arg
            340                 345                 350
Thr Asn Tyr Pro Leu Leu Phe Asn Arg Gln Arg Gln Pro Lys Ala Ala
        355                 360                 365
Tyr Phe Arg Leu Leu Asp Leu Lys Arg
    370                 375
```

<210> 143
<211> 3285
<212> DNA
<213> Bacteria

<400> 143

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atgagtttaa aaataaataa aatcatatca tttatcatag ttttttcgat ggtttttggg     60
acgttaatgt atgtgccaca tctaaaagca tttgcggata ataccggtat taatttggtt    120
tctaatggtg attttgaatc aggcacaatt gatggctggt ttaaacaagg taatccgaca    180
ttaacagtaa caactgagca ggcaattggg caatacagta tgaaagttac aggtagaaca    240
cagacatatg aaggacccgc atatagcttt ttggggaaaa tgcagaaagg tgaatcatat    300
aacgtatcac ttaaagttag acttgtttct ggacaaaatt catctaatcc tttgatcact    360
gtaactatgt ttagagaaga tgacaatggc aatcattatg acacaatagt ttggcaaaaa    420
caagtttctg aagattcatg gactactgta agtgggactt atacattgga ttatactgga    480
acattaaaaa cattatatat gtatgtagaa tcacccgatc caacgcttga atattatatt    540
gatgatgttg tagtcacacc gcaaaatcca acgcaaatag gaaatgtagt tgccaatgga    600
acttttgaaa atgaaaatac ttctggatgg gttggaacag gttcatctgt tgttaaagca    660
gtatatggtg atgctcacag cggagattat agcttattga cgacaggaag gacagctaac    720
tggaatggtc ctagttatga tttgactggc aaaatagttc ccggacaaca atacaatgtg    780
gatttttggg taaaatttat tgatggcaat gatacagagc aaatcaaggc tactgttaaa    840
gcgacttctg acaaagacaa ttatatacaa gttaatgatt ttgcagatgt aagtaaaggt    900
gaatggacag aaataaaagg cagttttact ttacctgttg cagattacag cggcattagc    960
atctatgtgg aatctcaaaa tcctacttta gagttttaca ttgatgattt ttctgtaata   1020
ggtgaaattg caaataatca gattactatt caaaatgaca ttccagattt gtactctgta   1080
tttaaagatt attttcctat aggcgttgcg gttgatccaa gtagattaaa tgatactgat   1140
ccgcatgctc aattgacggc taaacatttt aatatgcttg ttgcagaaaa cgccatgaaa   1200
cctgaaagtt tacaacccac agaaggaaat tttacttttg ataatgctga taagattgtt   1260
gattatgcaa tatcacataa tatgaagatg agggggcata ctttactttg gcataatcaa   1320
gttccagatt ggtttttcca agatccgtct gacccatcca agcctgcttc gagagattta   1380
ctattacaaa gattaaaaac tcatattaca actgtgttag accattttaa aacaaagtat   1440
```

ggttctcaga atccaataat tggatgggat gtcgtaaatg aagttcttga tgataatggc 1500
agtttgagaa attcgaagtg gttgcaaatt attggacccg actatataga aaaagccttt 1560
gaatatgcac atgaagcgga tccatcgatg aagttgttta ttaatgatta caatatcgaa 1620
aataatggcg ttaaaactca agctatgtat gacttggtaa aaagattaaa gagtgaaggc 1680
gttcctatag atggaatagg gatgcaaatg cacataaata taaattccaa tatagataat 1740
ataaaagcat caatagaaaa actggcatcg ttaggcgttg aaatacaagt aactgaatta 1800
gatatgaaca tgaacggtaa tatatctaac gaagcattgc tcaagcaagc tagattgtat 1860
aaacaattat ttgacttatt taaagcagag aaacaatata taactgctgt agtttttgg 1920
ggagtttcag acgatgtaac ttggcttagc aagccaaatg ctccgctact ttttgataca 1980
aagttgcaag caaagccagc atactgggca atagtagatc cgaataaagc tacaccagac 2040
attcaatctg caaaggcttt ggaaggatca ccgacaatgg gtacaaatgt tgataactct 2100
tggaaacttg taaagccgtt atatgcaaat acttttgtag aagggtcggt cggagcaact 2160
gctgctgtta agtctatgtg ggatactaaa aacttgtatt tgttagtaca agtttcagac 2220
aataccccat ctagtaatga tggtattgag atttttgtag ataagaatga tgacaaatcc 2280
acttcttatg aaactgatga tgaacattat acaattaaga gggatggtac agggagttca 2340
gatattacca aatatgtgac ttctaatgct gacggatatg tagcacagct agctattcca 2400
attgaagata ttaatcctgc acttaatgat aaaattggat ttgacattag aataaatgat 2460
gataaaggta ttggtaatat agatgcaata acagtttgga acgattatac aaacagtcaa 2520
gatactaata catcgtattt tggcgattta gtattatcaa aacctgcaca aattgcaaca 2580
gctatatatg gcactcctgt tattgatggt aaagtagatg atatttggaa taatgttgaa 2640
gctatttcaa caaatacatg ggttttgggt tcaaatggtg ctactgcgac agcaaaaatg 2700
atgtgggacg ataagtacct ttatgttttg gcggatgtta cagattcaaa tctgaacaaa 2760
tctagtgtta atccatatga acaagattct gtagaagttt ttgtagatca aaataatgac 2820
aagacgacat attataaaaa tgatgatgga cagtttagag ttaactatga caatgaacaa 2880
agctttgggg gaagcactaa ttcaaatgga tttaaatcgg caactagtct tacacaaagt 2940
ggatatattg tagaagaagc tattccttgg acgagtatca ctccatcaaa tggcactatc 3000
ataggatttg acttgcaagt taatgatgca gatgaaaatg gtaagaggac aggtattgta 3060
acatggtgtg atccgagcgg aaattcatgg caagatactt ctgggtttgg gaatttattg 3120
cttacaggta aaccatccgg tgttggtaca aaaagaatgg cgtttaacga cataaaagac 3180
agttgggcaa aagatgcaat agaagtatta gcatcaaggc acatagtaga aggtatgaca 3240
gacactcagt atgaaccaaa caagacagta acgagagcgg aataa 3285

<210> 144
<211> 1094
<212> PRT
<213> Bacteria

<220>
<221> SIGNAL
<222> (1)...(32)

<400> 144
Met Ser Leu Lys Ile Asn Lys Ile Ile Ser Phe Ile Ile Val Phe Ser
1 5 10 15
Met Val Phe Gly Thr Leu Met Tyr Val Pro His Leu Lys Ala Phe Ala
20 25 30
Asp Asn Thr Gly Ile Asn Leu Val Ser Asn Gly Asp Phe Glu Ser Gly
35 40 45
Thr Ile Asp Gly Trp Phe Lys Gln Gly Asn Pro Thr Leu Thr Val Thr
50 55 60
Thr Glu Gln Ala Ile Gly Gln Tyr Ser Met Lys Val Thr Gly Arg Thr
65 70 75 80
Gln Thr Tyr Glu Gly Pro Ala Tyr Ser Phe Leu Gly Lys Met Gln Lys
85 90 95
Gly Glu Ser Tyr Asn Val Ser Leu Lys Val Arg Leu Val Ser Gly Gln
100 105 110
Asn Ser Ser Asn Pro Leu Ile Thr Val Thr Met Phe Arg Glu Asp Asp
115 120 125
Asn Gly Asn His Tyr Asp Thr Ile Val Trp Gln Lys Gln Val Ser Glu
130 135 140
Asp Ser Trp Thr Thr Val Ser Gly Thr Tyr Thr Leu Asp Tyr Thr Gly
145 150 155 160
Thr Leu Lys Thr Leu Tyr Met Tyr Val Glu Ser Pro Asp Pro Thr Leu
165 170 175
Glu Tyr Tyr Ile Asp Asp Val Val Val Thr Pro Gln Asn Pro Thr Gln
180 185 190
Ile Gly Asn Val Val Ala Asn Gly Thr Phe Glu Asn Glu Asn Thr Ser
195 200 205
Gly Trp Val Gly Thr Gly Ser Ser Val Val Lys Ala Val Tyr Gly Asp

210 215 220
Ala His Ser Gly Asp Tyr Ser Leu Leu Thr Thr Gly Arg Thr Ala Asn
225 230 235 240
Trp Asn Gly Pro Ser Tyr Asp Leu Thr Gly Lys Ile Val Pro Gly Gln
245 250 255
Gln Tyr Asn Val Asp Phe Trp Val Lys Phe Ile Asp Gly Asn Asp Thr
260 265 270
Glu Gln Ile Lys Ala Thr Val Lys Ala Thr Ser Asp Lys Asp Asn Tyr
275 280 285
Ile Gln Val Asn Asp Phe Ala Asp Val Ser Lys Gly Glu Trp Thr Glu
290 295 300
Ile Lys Gly Ser Phe Thr Leu Pro Val Ala Asp Tyr Ser Gly Ile Ser
305 310 315 320
Ile Tyr Val Glu Ser Gln Asn Pro Thr Leu Glu Phe Tyr Ile Asp Asp
325 330 335
Phe Ser Val Ile Gly Glu Ile Ala Asn Asn Gln Ile Thr Ile Gln Asn
340 345 350
Asp Ile Pro Asp Leu Tyr Ser Val Phe Lys Asp Tyr Phe Pro Ile Gly
355 360 365
Val Ala Val Asp Pro Ser Arg Leu Asn Asp Thr Asp Pro His Ala Gln
370 375 380
Leu Thr Ala Lys His Phe Asn Met Leu Val Ala Glu Asn Ala Met Lys
385 390 395 400
Pro Glu Ser Leu Gln Pro Thr Glu Gly Asn Phe Thr Phe Asp Asn Ala
405 410 415
Asp Lys Ile Val Asp Tyr Ala Ile Ser His Asn Met Lys Met Arg Gly
420 425 430
His Thr Leu Leu Trp His Asn Gln Val Pro Asp Trp Phe Phe Gln Asp
435 440 445
Pro Ser Asp Pro Ser Lys Pro Ala Ser Arg Asp Leu Leu Leu Gln Arg
450 455 460
Leu Lys Thr His Ile Thr Thr Val Leu Asp His Phe Lys Thr Lys Tyr
465 470 475 480
Gly Ser Gln Asn Pro Ile Ile Gly Trp Asp Val Val Asn Glu Val Leu
485 490 495
Asp Asp Asn Gly Ser Leu Arg Asn Ser Lys Trp Leu Gln Ile Ile Gly
500 505 510
Pro Asp Tyr Ile Glu Lys Ala Phe Glu Tyr Ala His Glu Ala Asp Pro
515 520 525
Ser Met Lys Leu Phe Ile Asn Asp Tyr Asn Ile Glu Asn Asn Gly Val
530 535 540
Lys Thr Gln Ala Met Tyr Asp Leu Val Lys Arg Leu Lys Ser Glu Gly
545 550 555 560
Val Pro Ile Asp Gly Ile Gly Met Gln Met His Ile Asn Ile Asn Ser
565 570 575
Asn Ile Asp Asn Ile Lys Ala Ser Ile Glu Lys Leu Ala Ser Leu Gly
580 585 590
Val Glu Ile Gln Val Thr Glu Leu Asp Met Asn Met Asn Gly Asn Ile
595 600 605
Ser Asn Glu Ala Leu Leu Lys Gln Ala Arg Leu Tyr Lys Gln Leu Phe
610 615 620
Asp Leu Phe Lys Ala Glu Lys Gln Tyr Ile Thr Ala Val Val Phe Trp
625 630 635 640
Gly Val Ser Asp Asp Val Thr Trp Leu Ser Lys Pro Asn Ala Pro Leu
645 650 655
Leu Phe Asp Thr Lys Leu Gln Ala Lys Pro Ala Tyr Trp Ala Ile Val
660 665 670
Asp Pro Asn Lys Ala Thr Pro Asp Ile Gln Ser Ala Lys Ala Leu Glu
675 680 685
Gly Ser Pro Thr Met Gly Thr Asn Val Asp Asn Ser Trp Lys Leu Val
690 695 700
Lys Pro Leu Tyr Ala Asn Thr Phe Val Glu Gly Ser Val Gly Ala Thr
705 710 715 720
Ala Ala Val Lys Ser Met Trp Asp Thr Lys Asn Leu Tyr Leu Leu Val
725 730 735
Gln Val Ser Asp Asn Thr Pro Ser Ser Asn Asp Gly Ile Glu Ile Phe
740 745 750
Val Asp Lys Asn Asp Asp Lys Ser Thr Ser Tyr Glu Thr Asp Asp Glu
755 760 765

His Tyr Thr Ile Lys Arg Asp Gly Thr Gly Ser Ser Asp Ile Thr Lys
770 775 780
Tyr Val Thr Ser Asn Ala Asp Gly Tyr Val Ala Gln Leu Ala Ile Pro
785 790 795 800
Ile Glu Asp Ile Asn Pro Ala Leu Asn Asp Lys Ile Gly Phe Asp Ile
805 810 815
Arg Ile Asn Asp Asp Lys Gly Ile Gly Asn Ile Asp Ala Ile Thr Val
820 825 830
Trp Asn Asp Tyr Thr Asn Ser Gln Asp Thr Asn Thr Ser Tyr Phe Gly
835 840 845
Asp Leu Val Leu Ser Lys Pro Ala Gln Ile Ala Thr Ala Ile Tyr Gly
850 855 860
Thr Pro Val Ile Asp Gly Lys Val Asp Asp Ile Trp Asn Asn Val Glu
865 870 875 880
Ala Ile Ser Thr Asn Thr Trp Val Leu Gly Ser Asn Gly Ala Thr Ala
885 890 895
Thr Ala Lys Met Met Trp Asp Asp Lys Tyr Leu Tyr Val Leu Ala Asp
900 905 910
Val Thr Asp Ser Asn Leu Asn Lys Ser Ser Val Asn Pro Tyr Glu Gln
915 920 925
Asp Ser Val Glu Val Phe Val Asp Gln Asn Asn Asp Lys Thr Thr Tyr
930 935 940
Tyr Lys Asn Asp Asp Gly Gln Phe Arg Val Asn Tyr Asp Asn Glu Gln
945 950 955 960
Ser Phe Gly Gly Ser Thr Asn Ser Asn Gly Phe Lys Ser Ala Thr Ser
965 970 975
Leu Thr Gln Ser Gly Tyr Ile Val Glu Glu Ala Ile Pro Trp Thr Ser
980 985 990
Ile Thr Pro Ser Asn Gly Thr Ile Ile Gly Phe Asp Leu Gln Val Asn
995 1000 1005
Asp Ala Asp Glu Asn Gly Lys Arg Thr Gly Ile Val Thr Trp Cys Asp
1010 1015 1020
Pro Ser Gly Asn Ser Trp Gln Asp Thr Ser Gly Phe Gly Asn Leu Leu
1025 1030 1035 1040
Leu Thr Gly Lys Pro Ser Gly Val Gly Thr Lys Arg Met Ala Phe Asn
1045 1050 1055
Asp Ile Lys Asp Ser Trp Ala Lys Asp Ala Ile Glu Val Leu Ala Ser
1060 1065 1070
Arg His Ile Val Glu Gly Met Thr Asp Thr Gln Tyr Glu Pro Asn Lys
1075 1080 1085
Thr Val Thr Arg Ala Glu
1090

<210> 145
<211> 1629
<212> DNA
<213> Eukaryote

<400> 145
atgaagattg tggatacaac ttccgcagag ataaagattg aaatggaacc tgaaaaagag 60
atacctgctc tgaaagaagt actaaaagac tacttcaaag tcggagttgc actgccgtcc 120
aaggtcttcc tcaacccgaa ggacatagaa ctcatcacga aacacttcaa cagcatcacc 180
gcagaaaacg agatgaaacc ggatagtctg ctcgcgggca tcgaaaacgg taagctgaag 240
ttcaggtttg aaacagcaga caaatacatt cagttcgtcg aggaaaacgg catggttata 300
agaggtcaca cactggtgtg gcacaaccag acacccgact ggttcttcaa agacgaaaac 360
ggaaacctcc tctccaaaga agcgatgacg gaaagactca aagagtacat ccacaccgtt 420
gtcggacact tcaaaggaaa agtctacgca tgggacgtgg tgaacgaagc ggtcgatccg 480
aaccagccgg atggactgag aagatccacc tggtaccaga tcatggggcc tgactacata 540
gaactcgcct tcaagttcgc aagagaagca gatccagatg caaaactctt ctacaacgac 600
tacaacacat tcgagcccag aaagagagat atcatctaca acctcgtgaa ggatctcaag 660
gagaagggac tcatcgatgg gataggcatg cagtgtcaca tcagtcttgc aacagacatc 720
aaacagatcg aagaggccat caaaaagttc agcaccatac ccggtataga aattcacatc 780
acagaactcg atatgagtgt ctacagagat tccagttcca actacccaga ggcaccgagg 840
acggcactca tcgaacaggc tcacaaaatg atgcagctct ttgagatttt caagaagtac 900
agcaacgtga tcacgaacgt cacattctgg ggtctcaagg acgattactc ctggagagca 960
acaagaagaa acgactggcc gctcatcttc gacaaagatc accaggcgaa actcgcttac 1020
tgggcgatag tggcacctga ggtccttcca ccacttccaa aagaaagcag gatctccgaa 1080
ggcgaggctg tggtagtggg gatgatggat gactcgtacc tgatgtcgaa gccgatagag 1140
atccttgacg aagaagggaa cgtgaaggca acgatcaggg cggtgtggaa agacagcacg 1200

atctacatct acggagaggt acaggacaag acgaaaaaac cagcagaaga cggagtggcc 1260
atattcatca acccgaacaa cgaaagaaca ccctatctgc agcctgatga cacctacgct 1320
gtgctgtgga caaactggaa gacggaggtc aacagagaag acgtacaggt gaagaaattc 1380
gttgggcctg gctttagaag atacagcttc gagatgtcga tcacgatacc gggtgtggag 1440
ttcaagaaag acagctacat aggattcgac gctgcggtga tagacgacgg gaagtggtac 1500
agctggagcg acacgacgaa cagccagaag acgaacacga tgaactacgg aacgctgaaa 1560
ctcgaaggaa taatggtagc gacagcaaaa tacggaacac cggtcatcga tggagagata 1620
gacgagtaa 1629

<210> 146
<211> 542
<212> PRT
<213> Eukaryote

<400> 146
Met Lys Ile Val Asp Thr Thr Ser Ala Glu Ile Lys Ile Glu Met Glu
1 5 10 15
Pro Glu Lys Glu Ile Pro Ala Leu Lys Glu Val Leu Lys Asp Tyr Phe
20 25 30
Lys Val Gly Val Ala Leu Pro Ser Lys Val Phe Leu Asn Pro Lys Asp
35 40 45
Ile Glu Leu Ile Thr Lys His Phe Asn Ser Ile Thr Ala Glu Asn Glu
50 55 60
Met Lys Pro Asp Ser Leu Leu Ala Gly Ile Glu Asn Gly Lys Leu Lys
65 70 75 80
Phe Arg Phe Glu Thr Ala Asp Lys Tyr Ile Gln Phe Val Glu Glu Asn
85 90 95
Gly Met Val Ile Arg Gly His Thr Leu Val Trp His Asn Gln Thr Pro
100 105 110
Asp Trp Phe Phe Lys Asp Glu Asn Gly Asn Leu Leu Ser Lys Glu Ala
115 120 125
Met Thr Glu Arg Leu Lys Glu Tyr Ile His Thr Val Val Gly His Phe
130 135 140
Lys Gly Lys Val Tyr Ala Trp Asp Val Val Asn Glu Ala Val Asp Pro
145 150 155 160
Asn Gln Pro Asp Gly Leu Arg Arg Ser Thr Trp Tyr Gln Ile Met Gly
165 170 175
Pro Asp Tyr Ile Glu Leu Ala Phe Lys Phe Ala Arg Glu Ala Asp Pro
180 185 190
Asp Ala Lys Leu Phe Tyr Asn Asp Tyr Asn Thr Phe Glu Pro Arg Lys
195 200 205
Arg Asp Ile Ile Tyr Asn Leu Val Lys Asp Leu Lys Glu Lys Gly Leu
210 215 220
Ile Asp Gly Ile Gly Met Gln Cys His Ile Ser Leu Ala Thr Asp Ile
225 230 235 240
Lys Gln Ile Glu Glu Ala Ile Lys Lys Phe Ser Thr Ile Pro Gly Ile
245 250 255
Glu Ile His Ile Thr Glu Leu Asp Met Ser Val Tyr Arg Asp Ser Ser
260 265 270
Ser Asn Tyr Pro Glu Ala Pro Arg Thr Ala Leu Ile Glu Gln Ala His
275 280 285
Lys Met Met Gln Leu Phe Glu Ile Phe Lys Lys Tyr Ser Asn Val Ile
290 295 300
Thr Asn Val Thr Phe Trp Gly Leu Lys Asp Asp Tyr Ser Trp Arg Ala
305 310 315 320
Thr Arg Arg Asn Asp Trp Pro Leu Ile Phe Asp Lys Asp His Gln Ala
325 330 335
Lys Leu Ala Tyr Trp Ala Ile Val Ala Pro Glu Val Leu Pro Pro Leu
340 345 350
Pro Lys Glu Ser Arg Ile Ser Glu Gly Glu Ala Val Val Val Gly Met
355 360 365
Met Asp Asp Ser Tyr Leu Met Ser Lys Pro Ile Glu Ile Leu Asp Glu
370 375 380
Glu Gly Asn Val Lys Ala Thr Ile Arg Ala Val Trp Lys Asp Ser Thr
385 390 395 400
Ile Tyr Ile Tyr Gly Glu Val Gln Asp Lys Thr Lys Lys Pro Ala Glu
405 410 415
Asp Gly Val Ala Ile Phe Ile Asn Pro Asn Asn Glu Arg Thr Pro Tyr
420 425 430

Leu Gln Pro Asp Asp Thr Tyr Ala Val Leu Trp Thr Asn Trp Lys Thr
        435   440   445
Glu Val Asn Arg Glu Asp Val Gln Val Lys Lys Phe Val Gly Pro Gly
    450   455   460
Phe Arg Arg Tyr Ser Phe Glu Met Ser Ile Thr Ile Pro Gly Val Glu
465   470   475   480
Phe Lys Lys Asp Ser Tyr Ile Gly Phe Asp Ala Ala Val Ile Asp Asp
                485   490   495
Gly Lys Trp Tyr Ser Trp Ser Asp Thr Thr Asn Ser Gln Lys Thr Asn
            500   505   510
Thr Met Asn Tyr Gly Thr Leu Lys Leu Glu Gly Ile Met Val Ala Thr
        515   520   525
Ala Lys Tyr Gly Thr Pro Val Ile Asp Gly Glu Ile Asp Glu
    530   535   540

<210> 147
<211> 1146
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 147
atgactttct ctcgacggca atttttgctg caaacctccg ccggcctggc acttttgagc 60
actgccaaaa tgcgcgcttt cgcccgcgca gtcgatgaag tgggccttaa agaccatttt 120
aaagaccatt ttcatattgg gactgccatc agcggtcgac tgatgacgga aatgccggcc 180
ttttaccgcg acctggttac ccgtgaattc agtgccatta ccatggaaaa cgacatgaaa 240
tgggagcgtc tgcatcccaa agaaggccaa tgggattggg agattgccga caaattcgtc 300
aattttggcg aagaaaacga catgtacatt gtcgggcatg ttctggtctg gcactcacag 360
accccggatt gggtgttcca ggattccaga ggcaagccca tttctcgcga cgctttgctg 420
aaacgcatgc gccaccagat tgaacagatg gcgggccgct ataagggccg ggtacacgcg 480
tgggatgtgg tcaatgaggc ggtggacgag gaccaaggct ggcgcaaaag cccgtggttt 540
aacattattg ggcccgagtt tatggagcac gccttcaatt acgcccacga agtggacccc 600
gacgctcacc tgttgtacaa cgactacaat atgcacggtc gggaaaaacg cgaattcgtc 660
ctggatttca tcaaaagata caagaaaaaa ggcattccga tccagggcat aggcatgcaa 720
ggccatgtgg gcctgagctt tcccgatatc agcgagtttg agaaaagcct gcaagcctac 780
gccaaacagg gcatgcggat gcacattacc gagctggata tggacgtgtt accagtggcc 840
tgggatcaca ttggcgccga gatttccacc gagtttgact acgctgatga actggacccc 900
tggcccaaag ggctgccgga agaagtcgaa caggaattta ccgatcgcta caccgctttc 960
tttaaactgt ttttgaaata ccgcgatgat attgaaaggg tcaccttctg ggaaccgga 1020
gatgcggaat cgtggaaaaa taatttccca gtaagggggc gcaccaacta cccgctgctg 1080
tttgatcgcc gataccgcag aaaaccggcc tatgattcga ttgtcgaact gaccaaaaac 1140
ctttaa 1146

<210> 148
<211> 381
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<400> 148
Met Thr Phe Ser Arg Arg Gln Phe Leu Leu Gln Thr Ser Ala Gly Leu
1   5   10   15
Ala Leu Leu Ser Thr Ala Lys Met Arg Ala Phe Ala Arg Ala Val Asp
            20   25   30
Glu Val Gly Leu Lys Asp His Phe Lys Asp His Phe His Ile Gly Thr
        35   40   45
Ala Ile Ser Gly Arg Leu Met Thr Glu Met Pro Ala Phe Tyr Arg Asp
    50   55   60
Leu Val Thr Arg Glu Phe Ser Ala Ile Thr Met Glu Asn Asp Met Lys
65   70   75   80
Trp Glu Arg Leu His Pro Lys Glu Gly Gln Trp Asp Trp Glu Ile Ala
                85   90   95

```
Asp Lys Phe Val Asn Phe Gly Glu Glu Asn Asp Met Tyr Ile Val Gly
            100                 105                 110
His Val Leu Val Trp His Ser Gln Thr Pro Asp Trp Val Phe Gln Asp
        115                 120                 125
Ser Arg Gly Lys Pro Ile Ser Arg Asp Ala Leu Leu Lys Arg Met Arg
    130                 135                 140
His Gln Ile Glu Gln Met Ala Gly Arg Tyr Lys Gly Arg Val His Ala
145                 150                 155                 160
Trp Asp Val Val Asn Glu Ala Val Asp Glu Asp Gln Gly Trp Arg Lys
                165                 170                 175
Ser Pro Trp Phe Asn Ile Ile Gly Pro Glu Phe Met Glu His Ala Phe
            180                 185                 190
Asn Tyr Ala His Glu Val Asp Pro Asp Ala His Leu Leu Tyr Asn Asp
        195                 200                 205
Tyr Asn Met His Gly Arg Glu Lys Arg Glu Phe Val Leu Asp Phe Ile
    210                 215                 220
Lys Arg Tyr Lys Lys Lys Gly Ile Pro Ile Gln Gly Ile Gly Met Gln
225                 230                 235                 240
Gly His Val Gly Leu Ser Phe Pro Asp Ile Ser Glu Phe Glu Lys Ser
                245                 250                 255
Leu Gln Ala Tyr Ala Lys Gln Gly Met Arg Met His Ile Thr Glu Leu
            260                 265                 270
Asp Met Asp Val Leu Pro Val Ala Trp Asp His Ile Gly Ala Glu Ile
        275                 280                 285
Ser Thr Glu Phe Asp Tyr Ala Asp Glu Leu Asp Pro Trp Pro Lys Gly
    290                 295                 300
Leu Pro Glu Glu Val Glu Gln Glu Phe Thr Asp Arg Tyr Thr Ala Phe
305                 310                 315                 320
Phe Lys Leu Phe Leu Lys Tyr Arg Asp Asp Ile Glu Arg Val Thr Phe
                325                 330                 335
Trp Gly Thr Gly Asp Ala Glu Ser Trp Lys Asn Asn Phe Pro Val Arg
            340                 345                 350
Gly Arg Thr Asn Tyr Pro Leu Leu Phe Asp Arg Arg Tyr Arg Arg Lys
        355                 360                 365
Pro Ala Tyr Asp Ser Ile Val Glu Leu Thr Lys Asn Leu
    370                 375                 380
```

<210> 149
<211> 1044
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 149

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atgaagaagc tttttgtcgc ggtcgttttg ttgcccttag caactttttt cgcgtcggac      60
ggattggagg gagaaccttt gagatcgtta gccgagaaac ttggcatcta catcggttac     120
gcttcgatca accatttctg gactcttccg gattcaaaca agtacacaga agtggcaaag     180
agggagttca acatactcac gccagagaac caaatgaagt gggacagcct tcacccagag     240
cctgacaggt acaacttcac ttacgcagag cgtcatgtcg agttcgcttt ggaaaacaac     300
atgctcgttc acggccacac actcgtttgg cacaaccaac ttccgttctg gttgaacaga     360
cagtggacca aagaagaact cctgaaagtc cttgaggacc acatcaaaac agtcgtcggt     420
cacttcaaag gaagggtgaa gatttgggac gtggtgaacg aagcggtcag cgacatgggc     480
agttacagag agaccatttg gtacaagacc atcggacccg agtacatcga aaaggcattc     540
gtgtgggcaa gacaagccga tccggaagcg atcctcatat acaacgacta caatatagaa     600
acgatcaatc ccaaatcgaa tttcacctac cagctcatca aggagctgaa agaaaaaggt     660
gtgccgatag acggcatcgg ttttcaaatg cacatagaca tcaacggaat aaactatgac     720
agtttcagaa acaacctgaa gaggttcgct gatctcggtc tgaagctcta catcacggaa     780
atggatgtga gaatacccaa gaacgcaact gaaaaagact tggacagaca ggcagaaatc     840
tacgcgaaga tcttcgaaat ctgcttagag aatcctgcgg tccaagccat acagttctgg     900
ggtttcacgg acaagtattc ctgggtgcct ggctttttca gcgggtacga tcatgcgctg     960
atctttgaca gggactacag ccccaagccc gcgtattttg cgataaagag ggtgctcgaa    1020
gccaaggtga gcaagggacg ctga                                           1044
```

<210> 150
<211> 347
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(18)

<400> 150
Met Lys Lys Leu Phe Val Ala Val Val Leu Leu Pro Leu Ala Thr Phe
1 5 10 15
Phe Ala Ser Asp Gly Leu Glu Gly Glu Pro Leu Arg Ser Leu Ala Glu
20 25 30
Lys Leu Gly Ile Tyr Ile Gly Tyr Ala Ser Ile Asn His Phe Trp Thr
35 40 45
Leu Pro Asp Ser Asn Lys Tyr Thr Glu Val Ala Lys Arg Glu Phe Asn
50 55 60
Ile Leu Thr Pro Glu Asn Gln Met Lys Trp Asp Ser Leu His Pro Glu
65 70 75 80
Pro Asp Arg Tyr Asn Phe Thr Tyr Ala Glu Arg His Val Glu Phe Ala
85 90 95
Leu Glu Asn Asn Met Leu Val His Gly His Thr Leu Val Trp His Asn
100 105 110
Gln Leu Pro Phe Trp Leu Asn Arg Gln Trp Thr Lys Glu Glu Leu Leu
115 120 125
Lys Val Leu Glu Asp His Ile Lys Thr Val Val Gly His Phe Lys Gly
130 135 140
Arg Val Lys Ile Trp Asp Val Val Asn Glu Ala Val Ser Asp Met Gly
145 150 155 160
Ser Tyr Arg Glu Thr Ile Trp Tyr Lys Thr Ile Gly Pro Glu Tyr Ile
165 170 175
Glu Lys Ala Phe Val Trp Ala Arg Gln Ala Asp Pro Glu Ala Ile Leu
180 185 190
Ile Tyr Asn Asp Tyr Asn Ile Glu Thr Ile Asn Pro Lys Ser Asn Phe
195 200 205
Thr Tyr Gln Leu Ile Lys Glu Leu Lys Glu Lys Gly Val Pro Ile Asp
210 215 220
Gly Ile Gly Phe Gln Met His Ile Asp Ile Asn Gly Ile Asn Tyr Asp
225 230 235 240
Ser Phe Arg Asn Asn Leu Lys Arg Phe Ala Asp Leu Gly Leu Lys Leu
245 250 255
Tyr Ile Thr Glu Met Asp Val Arg Ile Pro Lys Asn Ala Thr Glu Lys
260 265 270
Asp Leu Asp Arg Gln Ala Glu Ile Tyr Ala Lys Ile Phe Glu Ile Cys
275 280 285
Leu Glu Asn Pro Ala Val Gln Ala Ile Gln Phe Trp Gly Phe Thr Asp
290 295 300
Lys Tyr Ser Trp Val Pro Gly Phe Phe Ser Gly Tyr Asp His Ala Leu
305 310 315 320
Ile Phe Asp Arg Asp Tyr Ser Pro Lys Pro Ala Tyr Phe Ala Ile Lys
325 330 335
Arg Val Leu Glu Ala Lys Val Ser Lys Gly Arg
340 345

<210> 151
<211> 1131
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 151
atgcgatcta tgccacttta tgtgttgtta tgcagcgccc ttctgaccgg cagcctatat 60
gcacaagacc aaaatgcttc tttaaaacag gcctttagca aaaactttag tattggcaca 120
gccttaagtg ctacacaaat tcagggcaaa gagccgggca cactggaatt ggtaacacag 180
caatttaacg cggtgacggc agaaaacgtg atgaagtggg aaatcattga acctgtggaa 240
ggccagttca actttgctgc cgccgacgcc atgattgaat tcgccgaagc caatcatatc 300
aaggtgatag gccatgtgct gttatggcac gaacaaacac cagcctgggt atttctggac 360
gccaaaggcc aggccgcctc aaaggaactg gtgttatcac ggctaaaaaa ccatatcaat 420

gccgtaatgg gccgctacaa aggccgtatt catggctggg atgcagtcaa cgaagcctta 480
aatgaagacg gcactctgcg ccaatccaac tggtataaag ctttaggcga cgactatata 540
gccacagtct ttgaactggc gcatcaggcc gacccgaaag ccgaactcta ttacaacgac 600
ttcaatttat ttaaaccgga aaaacgcgct ggtgtactca aactggtggc agctttaaaa 660
gcgaaaaatg tgcctatcca cggcataggc gagcaaggcc attacagcct ggattaccct 720
gagctgcagc aagtagaaga ctctattgtg gcttttaaaa acactggcct gaaagtggtg 780
attaccgaac tggatatctc agttttaccc ttccctgagc cagaaaagat tggtgctgat 840
atctcactca atatgcagtt aaaacaagaa cttaatccct acgccgatgg cttacccaaa 900
gaagtcagcg atcaactgac agaaaaatac ctgcaattat ttcagctatt tttacgccac 960
agcgacgcca tcgaacgcgt gaccttatgg ggcgtaaacg acaaccaaac ctggcgcaac 1020
aactggccaa tgaaaggcag aacagactac cccttactct tcgaccggaa aaaccagcca 1080
aaagaagtgg ttcctgcatt gattaaactg gcggaaaaag ctggtaaata a 1131

<210> 152
<211> 376
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(21)

<400> 152
Met Arg Ser Met Pro Leu Tyr Val Leu Leu Cys Ser Ala Leu Leu Thr
1 5 10 15
Gly Ser Leu Tyr Ala Gln Asp Gln Asn Ala Ser Leu Lys Gln Ala Phe
20 25 30
Ser Lys Asn Phe Ser Ile Gly Thr Ala Leu Ser Ala Thr Gln Ile Gln
35 40 45
Gly Lys Glu Pro Gly Thr Leu Glu Leu Val Thr Gln Gln Phe Asn Ala
50 55 60
Val Thr Ala Glu Asn Val Met Lys Trp Glu Ile Ile Glu Pro Val Glu
65 70 75 80
Gly Gln Phe Asn Phe Ala Ala Ala Asp Ala Met Ile Glu Phe Ala Glu
85 90 95
Ala Asn His Ile Lys Val Ile Gly His Val Leu Leu Trp His Glu Gln
100 105 110
Thr Pro Ala Trp Val Phe Leu Asp Ala Lys Gly Gln Ala Ala Ser Lys
115 120 125
Glu Leu Val Leu Ser Arg Leu Lys Asn His Ile Asn Ala Val Met Gly
130 135 140
Arg Tyr Lys Gly Arg Ile His Gly Trp Asp Ala Val Asn Glu Ala Leu
145 150 155 160
Asn Glu Asp Gly Thr Leu Arg Gln Ser Asn Trp Tyr Lys Ala Leu Gly
165 170 175
Asp Asp Tyr Ile Ala Thr Val Phe Glu Leu Ala His Gln Ala Asp Pro
180 185 190
Lys Ala Glu Leu Tyr Tyr Asn Asp Phe Asn Leu Phe Lys Pro Glu Lys
195 200 205
Arg Ala Gly Val Leu Lys Leu Val Ala Ala Leu Lys Ala Lys Asn Val
210 215 220
Pro Ile His Gly Ile Gly Glu Gln Gly His Tyr Ser Leu Asp Tyr Pro
225 230 235 240
Glu Leu Gln Gln Val Glu Asp Ser Ile Val Ala Phe Lys Asn Thr Gly
245 250 255
Leu Lys Val Val Ile Thr Glu Leu Asp Ile Ser Val Leu Pro Phe Pro
260 265 270
Glu Pro Glu Lys Ile Gly Ala Asp Ile Ser Leu Asn Met Gln Leu Lys
275 280 285
Gln Glu Leu Asn Pro Tyr Ala Asp Gly Leu Pro Lys Glu Val Ser Asp
290 295 300
Gln Leu Thr Glu Lys Tyr Leu Gln Leu Phe Gln Leu Phe Leu Arg His
305 310 315 320
Ser Asp Ala Ile Glu Arg Val Thr Leu Trp Gly Val Asn Asp Asn Gln
325 330 335
Thr Trp Arg Asn Asn Trp Pro Met Lys Gly Arg Thr Asp Tyr Pro Leu
340 345 350

Leu Phe Asp Arg Lys Asn Gln Pro Lys Glu Val Val Pro Ala Leu Ile
        355   360   365
Lys Leu Ala Glu Lys Ala Gly Lys
    370   375

<210> 153
<211> 1020
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 153
atgggtgcta tgggcctggc ggcgctgtat tcgctgccag ccaatgcaca gacctgcatt 60
acgcagagtc agacgggcac caacaacggc cactattttt cgttctggaa ggacaatccg 120
ggaacggtca atttctgtat gtatgccaac ggccgttaca cgtctaactg gaacggcatc 180
aacaattggg tcggcggcaa aggctggcaa accggctcgc gcagaaacgt cacctactct 240
ggctcgttca actctcccgg caatggctat ctggctgctc tactggctgg accaccaatc 300
ctgttggtcg agtactacat catcgagagc tggggaaatt ggcgcccgcc gggttcggat 360
ggaacattgt taggcaccgt cactagcgac ggcggtactt acgatatcta tcgctcgcgc 420
cgcaccaacg cgccttgtat cactggcaac tcctgtaact tcgatcagta ctggagcgta 480
cggcaatcca agcgcgtggg cggcacgatt accacgggca atcacttcga cgcttgggcg 540
gcacgcggct tgaacctcgg cacgcacaac taccaagtga tggcgaccga gggatatcag 600
agcaacggca gctccgacat caccattagc gacaacccgg gaccgacgcc aggacccact 660
ccgaacccga atcccacgcc gggcaccaag aatttcacgg tgcgcgcgcg cggaaccgcg 720
gggggtgagt ccatcacgct gcgtgtgaac aatcagaacg tgcagacctg gacgctgtcg 780
accagctacc agaacttcac ggcgtccacg acgttgagtg gtggcatcac ggtcgcgttc 840
accaatgatg gtggtagtcg agacgttcag gtggattaca tccaggtgaa cggcgcaact 900
cgacaatccg agagccagac gtacaacacc ggcctctatg ccaacggcag ttgcggcggc 960
ggctcgaaca gcgagtggat gcattgcaat ggagcgatcg gctacggcaa cacgccgtag 1020

<210> 154
<211> 339
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(16)

<400> 154
Met Gly Ala Met Gly Leu Ala Ala Leu Tyr Ser Leu Pro Ala Asn Ala
1   5   10   15
Gln Thr Cys Ile Thr Gln Ser Gln Thr Gly Thr Asn Asn Gly His Tyr
            20   25   30
Phe Ser Phe Trp Lys Asp Asn Pro Gly Thr Val Asn Phe Cys Met Tyr
        35   40   45
Ala Asn Gly Arg Tyr Thr Ser Asn Trp Asn Gly Ile Asn Asn Trp Val
    50   55   60
Gly Gly Lys Gly Trp Gln Thr Gly Ser Arg Arg Asn Val Thr Tyr Ser
65   70   75   80
Gly Ser Phe Asn Ser Pro Gly Asn Gly Tyr Leu Ala Ala Leu Leu Ala
                85   90   95
Gly Pro Pro Ile Leu Leu Val Glu Tyr Tyr Ile Ile Glu Ser Trp Gly
            100   105   110
Asn Trp Arg Pro Pro Gly Ser Asp Gly Thr Leu Leu Gly Thr Val Thr
        115   120   125
Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Arg Ser Arg Arg Thr Asn Ala
    130   135   140
Pro Cys Ile Thr Gly Asn Ser Cys Asn Phe Asp Gln Tyr Trp Ser Val
145   150   155   160
Arg Gln Ser Lys Arg Val Gly Gly Thr Ile Thr Thr Gly Asn His Phe
                165   170   175
Asp Ala Trp Ala Ala Arg Gly Leu Asn Leu Gly Thr His Asn Tyr Gln
            180   185   190
Val Met Ala Thr Glu Gly Tyr Gln Ser Asn Gly Ser Ser Asp Ile Thr

```
        195                 200                 205
Ile Ser Asp Asn Pro Gly Pro Thr Pro Gly Pro Thr Pro Asn Pro Asn
    210                 215                 220
Pro Thr Pro Gly Thr Lys Asn Phe Thr Val Arg Ala Arg Gly Thr Ala
225                 230                 235                 240
Gly Gly Glu Ser Ile Thr Leu Arg Val Asn Asn Gln Asn Val Gln Thr
                245                 250                 255
Trp Thr Leu Ser Thr Ser Tyr Gln Asn Phe Thr Ala Ser Thr Thr Leu
            260                 265                 270
Ser Gly Gly Ile Thr Val Ala Phe Thr Asn Asp Gly Gly Ser Arg Asp
        275                 280                 285
Val Gln Val Asp Tyr Ile Gln Val Asn Gly Ala Thr Arg Gln Ser Glu
    290                 295                 300
Ser Gln Thr Tyr Asn Thr Gly Leu Tyr Ala Asn Gly Ser Cys Gly Gly
305                 310                 315                 320
Gly Ser Asn Ser Glu Trp Met His Cys Asn Gly Ala Ile Gly Tyr Gly
                325                 330                 335
Asn Thr Pro
```

<210> 155
<211> 1836
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 155

```
atgaaaggat taattgcggc agcgcttgct ggcttggcat tcggggcctc cctatcctgg      60
ggacagtgca caacgtttac caccagtacc attcagaatt gtaatggcat tgattacgag     120
ctctggagtc agaataacaa gggcaccgta agcatgaaga ttacgggagg gagcacgaat     180
ccgaatggag gaactttcga tgctacctgg aatggcaccg agaatatcct ggctagagct     240
ggtaagaaat ggggctcgtc cagcactacc acccccacgt ccgcaggcaa tattactctt     300
gaattcgcgg cgacatggtc ctcaagcgat aacgtaaaaa tgcttggagt ctatggctgg     360
gcgtactatc caactggaag tatcccgact aaacaggaaa atggagcaag tacctcattc     420
acaaatcaaa ttgagtacta catcatccag gatcgtggta gctataatgc tgcatcgggt     480
ggaacgaact ccaaaaaata cggcgaaggg acgatcgatg gaattctgta tgaattctat     540
atcgcagaca gaatcaacca gcctgatctg tcaggaaaga gtggaaactt caagcaatac     600
ttcagcgtcc cgaaaagtac gagcagccat aggcaaagtg ggacgattac cgtttccaaa     660
catttccagg cctgggaaaa tgccggaatg aaaatgatgt cctgtcgctt gtatgaagtc     720
gcaatgaaag tcgagtccta taccggttct gcgaccggtg ttggctctgc gaaggttaca     780
aagaatatac tcaccattgg tggaatcttg agcagtagca gtactgcaag cagtagcagc     840
acagtaagta gcagtagcag caatgcatat acgcttgtca cgaatgtttc tcccgctgga     900
gccggaacag tgaccaggag ccccaatact gcgacctatg ccccgaatgc ttcagtacag     960
cttactgcaa cgccgagtac cggttggaaa tttgtcggtt gggctgggga tcttacgtca    1020
actacgagta ctgctaccgt caccatgacc aaagatatta ccgcaactgc aaaatttgaa    1080
ctggtatcgg gagatggcac gaccaacttg atcaaggatg gaaacttccc cagtagcagc    1140
gtcatctcca caggtgatgg cacctcctgg aagctcgggc aaggtacaaa ctggggtaat    1200
tccgcagcaa cgacgagtgt cagcaatgga atcgcgactg tcaatgtgac caccattgga    1260
tctcaaacct atcaacccca gctaattcag tataacgtgg ctctttacaa ggatatgagc    1320
tacaagctca ccttcaaggc aaaagctgct gctgcaagga aaattgaagt cgcattccaa    1380
cagtcggtgg acccatgggc tggatatgct tccaaggaat tcgatcttac aacgacagag    1440
cagacatatg agttcgtatt taaaatgact agcgctactg acacggcttc acagttcgcg    1500
ttcaatctcg gccaggcaac aggcgccgtc aatattagtg atgtaaagct agtatatacg    1560
acagctggta caacacccgt attccgtgga tataatgagg cggcaacaca ggagaggcct    1620
gtattcatat ccttggatgg taggacgttg aacattgttc cagtgtatgg agccaaactg    1680
caggtcaagt tagtggacat caatggtaag atgagagcct ccttcaatgt ggtcggaatt    1740
gcttccatcc cgctgtccaa tatccccgct gggcggtatt atattgacgt aagtggtgac    1800
ggcgttaagc aggcatcccc gatagttctg gaataa                              1836
```

<210> 156
<211> 611
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(21)

<400> 156
```
Met Lys Gly Leu Ile Ala Ala Ala Leu Ala Gly Leu Ala Phe Gly Ala
 1               5                  10                  15
Ser Leu Ser Trp Gly Gln Cys Thr Thr Phe Thr Thr Ser Thr Ile Gln
            20                  25                  30
Asn Cys Asn Gly Ile Asp Tyr Glu Leu Trp Ser Gln Asn Asn Lys Gly
        35                  40                  45
Thr Val Ser Met Lys Ile Thr Gly Gly Ser Thr Asn Pro Asn Gly Gly
    50                  55                  60
Thr Phe Asp Ala Thr Trp Asn Gly Thr Glu Asn Ile Leu Ala Arg Ala
65                  70                  75                  80
Gly Lys Lys Trp Gly Ser Ser Ser Thr Thr Thr Pro Thr Ser Ala Gly
                85                  90                  95
Asn Ile Thr Leu Glu Phe Ala Ala Thr Trp Ser Ser Ser Asp Asn Val
            100                 105                 110
Lys Met Leu Gly Val Tyr Gly Trp Ala Tyr Tyr Pro Thr Gly Ser Ile
        115                 120                 125
Pro Thr Lys Gln Glu Asn Gly Ala Ser Thr Ser Phe Thr Asn Gln Ile
    130                 135                 140
Glu Tyr Tyr Ile Ile Gln Asp Arg Gly Ser Tyr Asn Ala Ala Ser Gly
145                 150                 155                 160
Gly Thr Asn Ser Lys Lys Tyr Gly Glu Gly Thr Ile Asp Gly Ile Leu
                165                 170                 175
Tyr Glu Phe Tyr Ile Ala Asp Arg Ile Asn Gln Pro Asp Leu Ser Gly
            180                 185                 190
Lys Ser Gly Asn Phe Lys Gln Tyr Phe Ser Val Pro Lys Ser Thr Ser
        195                 200                 205
Ser His Arg Gln Ser Gly Thr Ile Thr Val Ser Lys His Phe Gln Ala
    210                 215                 220
Trp Glu Asn Ala Gly Met Lys Met Met Ser Cys Arg Leu Tyr Glu Val
225                 230                 235                 240
Ala Met Lys Val Glu Ser Tyr Thr Gly Ser Ala Thr Gly Val Gly Ser
                245                 250                 255
Ala Lys Val Thr Lys Asn Ile Leu Thr Ile Gly Gly Ile Leu Ser Ser
            260                 265                 270
Ser Ser Thr Ala Ser Ser Ser Ser Thr Val Ser Ser Ser Ser Ser Asn
        275                 280                 285
Ala Tyr Thr Leu Val Thr Asn Val Ser Pro Ala Gly Ala Gly Thr Val
    290                 295                 300
Thr Arg Ser Pro Asn Thr Ala Thr Tyr Ala Pro Asn Ala Ser Val Gln
305                 310                 315                 320
Leu Thr Ala Thr Pro Ser Thr Gly Trp Lys Phe Val Gly Trp Ala Gly
                325                 330                 335
Asp Leu Thr Ser Thr Thr Ser Thr Ala Thr Val Thr Met Thr Lys Asp
            340                 345                 350
Ile Thr Ala Thr Ala Lys Phe Glu Leu Val Ser Gly Asp Gly Thr Thr
        355                 360                 365
Asn Leu Ile Lys Asp Gly Asn Phe Pro Ser Ser Ser Val Ile Ser Thr
    370                 375                 380
Gly Asp Gly Thr Ser Trp Lys Leu Gly Gln Gly Thr Asn Trp Gly Asn
385                 390                 395                 400
Ser Ala Ala Thr Thr Ser Val Ser Asn Gly Ile Ala Thr Val Asn Val
                405                 410                 415
Thr Thr Ile Gly Ser Gln Thr Tyr Gln Pro Gln Leu Ile Gln Tyr Asn
            420                 425                 430
Val Ala Leu Tyr Lys Asp Met Ser Tyr Lys Leu Thr Phe Lys Ala Lys
        435                 440                 445
Ala Ala Ala Ala Arg Lys Ile Glu Val Ala Phe Gln Gln Ser Val Asp
    450                 455                 460
Pro Trp Ala Gly Tyr Ala Ser Lys Glu Phe Asp Leu Thr Thr Thr Glu
465                 470                 475                 480
Gln Thr Tyr Glu Phe Val Phe Lys Met Thr Ser Ala Thr Asp Thr Ala
                485                 490                 495
Ser Gln Phe Ala Phe Asn Leu Gly Gln Ala Thr Gly Ala Val Asn Ile
            500                 505                 510
Ser Asp Val Lys Leu Val Tyr Thr Thr Ala Gly Thr Thr Pro Val Phe
```

```
            515                     520                     525
Arg Gly Tyr Asn Glu Ala Ala Thr Gln Glu Arg Pro Val Phe Ile Ser
        530                     535                     540
Leu Asp Gly Arg Thr Leu Asn Ile Val Pro Val Tyr Gly Ala Lys Leu
545                     550                     555                     560
Gln Val Lys Leu Val Asp Ile Asn Gly Lys Met Arg Ala Ser Phe Asn
                565                     570                     575
Val Val Gly Ile Ala Ser Ile Pro Leu Ser Asn Ile Pro Ala Gly Arg
            580                     585                     590
Tyr Tyr Ile Asp Val Ser Gly Asp Gly Val Lys Gln Ala Ser Pro Ile
        595                     600                     605
Val Leu Glu
    610
```

<210> 157
<211> 645
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 157

```
atgtttaagt taagtaagaa aattttgatg gtgttattaa caatttcaat gagttttatt      60
agcttatttg cagtaaccgc gtatgcagct tcgacagact actggcaaaa ttggactgat     120
ggtggtggga cagtaaatgc taccaatgga tctgatggca attacagtgt ttcatggtca     180
aattgcggga attttgttgt tggtaaaggc tggactaccg gatcagcaac tagggtaata     240
aactataatg ccggagcctt ttcgccgtcc ggcaatggat atttagctct ttatgggtgg     300
acgagaaatt cactcataga atattacgtc gttgatagct gggggactta tagacctact     360
ggaacttata aaggcactgt gactagtgat ggagggacat atgacatata cacgactaca     420
cgaaccaacg caccttccat tgacggcaat aatacaaatt tcacccagtt ctggagtgtt     480
aggcagtcaa agagaccgat tggtaccaac aataccatca cttttagcaa ccacgttaac     540
gcctggaaga gtaaaggaat gaatctgggg agtagttggg cttatcaggt attagcgaca     600
gagggatatc aaagtagtgg gtactctaac gtaacggtct ggtaa                     645
```

<210> 158
<211> 214
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(29)

<400> 158

```
Met Phe Lys Leu Ser Lys Lys Ile Leu Met Val Leu Leu Thr Ile Ser
 1               5                  10                  15
Met Ser Phe Ile Ser Leu Phe Ala Val Thr Ala Tyr Ala Ala Ser Thr
            20                  25                  30
Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr Val Asn Ala Thr
        35                  40                  45
Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser Asn Cys Gly Asn
    50                  55                  60
Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala Thr Arg Val Ile
65                  70                  75                  80
Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn Gly Tyr Leu Ala
                85                  90                  95
Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr Tyr Val Val Asp
            100                 105                 110
Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys Gly Thr Val Thr
        115                 120                 125
Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr Arg Thr Asn Ala
    130                 135                 140
Pro Ser Ile Asp Gly Asn Asn Thr Asn Phe Thr Gln Phe Trp Ser Val
145                 150                 155                 160
Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr Ile Thr Phe Ser
                165                 170                 175
```

Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn Leu Gly Ser Ser
            180   185   190
Trp Ala Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln Ser Ser Gly Tyr
        195   200   205
Ser Asn Val Thr Val Trp
    210

<210> 159
<211> 1041
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 159
atgatcagtc tcaaacgagt ggcggcgctc ctgtgcgtcg caggtctggg catgtctgcg 60
gcaaacgcgc agacctgcct cacgtcgagt caaaccggca ctaacaatgg cttctattat 120
tccttctgga aggacagtcc gggcacggtg aatttttgcc tgcagtccgg cggccgttac 180
acatcgaact ggagcggcat caacaactgg gtgggcggca agggatggca gaccggttca 240
cgccggaaca tcacgtactc gggcagcttc aattcaccgg gcaacggcta cctggcgctt 300
tacggatgga ccaccaatcc actcgtcgag tactacgtcg tcgatagctg gggagctgg 360
cgtccgccgg gttcggacgg aacgttcctg ggacggtca acagcgatgg cggaacgtat 420
gacatctatc gcgcgcagcg ggtcaacgcg ccgtccatca tcggcaacgc cacgttctat 480
caatactgga gcgttcggca gtcgaagcgg gtaggtggga cgatcaccac cggaaaccac 540
ttcgacgcgt gggccagcgt gggcctgaac ctgggcactc acaactacca gatcatggcg 600
accgagggct accaaagcag cggcagctcc gacatcacgg tgagtgaagg cggtagcagc 660
agtggtggcg gaagcagcac gagcagcagc agcggcggtg gtggcaccaa gagcttcacg 720
gttcgtgcgc gcggtaccgc gggcggtgag tccatcacgc tgcgcgtgaa caaccagaac 780
gtgcagacct ggacgctggg caccagcatg acgaactaca cggcgtcgac ttcactgagc 840
ggcggcatca ccgtggtgta cacgaacgac agcggtaacc gcgacgtgca ggtggactac 900
atcgtcgtga acggccagac gcgccagtcc gaagcccaga gctacaacac cggcctttat 960
gcgaacgggc gttgcggcgg tggctccaac agcgaatgga tgcattgcaa cggcgccatc 1020
ggctacggca atacaccgta a 1041

<210> 160
<211> 346
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(23)

<400> 160
Met Ile Ser Leu Lys Arg Val Ala Ala Leu Leu Cys Val Ala Gly Leu
 1   5   10   15
Gly Met Ser Ala Ala Asn Ala Gln Thr Cys Leu Thr Ser Ser Gln Thr
            20   25   30
Gly Thr Asn Asn Gly Phe Tyr Tyr Ser Phe Trp Lys Asp Ser Pro Gly
        35   40   45
Thr Val Asn Phe Cys Leu Gln Ser Gly Gly Arg Tyr Thr Ser Asn Trp
    50   55   60
Ser Gly Ile Asn Asn Trp Val Gly Gly Lys Gly Trp Gln Thr Gly Ser
65   70   75   80
Arg Arg Asn Ile Thr Tyr Ser Gly Ser Phe Asn Ser Pro Gly Asn Gly
                85   90   95
Tyr Leu Ala Leu Tyr Gly Trp Thr Thr Asn Pro Leu Val Glu Tyr Tyr
            100   105   110
Val Val Asp Ser Trp Gly Ser Trp Arg Pro Pro Gly Ser Asp Gly Thr
        115   120   125
Phe Leu Gly Thr Val Asn Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Arg
    130   135   140
Ala Gln Arg Val Asn Ala Pro Ser Ile Ile Gly Asn Ala Thr Phe Tyr
145   150   155   160
Gln Tyr Trp Ser Val Arg Gln Ser Lys Arg Val Gly Gly Thr Ile Thr
                165   170   175

Thr Gly Asn His Phe Asp Ala Trp Ala Ser Val Gly Leu Asn Leu Gly
180 185 190
Thr His Asn Tyr Gln Ile Met Ala Thr Glu Gly Tyr Gln Ser Ser Gly
195 200 205
Ser Ser Asp Ile Thr Val Ser Glu Gly Gly Ser Ser Ser Gly Gly Gly
210 215 220
Ser Ser Thr Ser Ser Ser Ser Gly Gly Gly Gly Thr Lys Ser Phe Thr
225 230 235 240
Val Arg Ala Arg Gly Thr Ala Gly Gly Glu Ser Ile Thr Leu Arg Val
245 250 255
Asn Asn Gln Asn Val Gln Thr Trp Thr Leu Gly Thr Ser Met Thr Asn
260 265 270
Tyr Thr Ala Ser Thr Ser Leu Ser Gly Gly Ile Thr Val Val Tyr Thr
275 280 285
Asn Asp Ser Gly Asn Arg Asp Val Gln Val Asp Tyr Ile Val Val Asn
290 295 300
Gly Gln Thr Arg Gln Ser Glu Ala Gln Ser Tyr Asn Thr Gly Leu Tyr
305 310 315 320
Ala Asn Gly Arg Cys Gly Gly Gly Ser Asn Ser Glu Trp Met His Cys
325 330 335
Asn Gly Ala Ile Gly Tyr Gly Asn Thr Pro
340 345

<210> 161
<211> 1047
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 161
atgttcaaag gtcttttgaa atcggtcctc accggcaagc gagccggtgc ggtgttcatc 60
tgtctggccg gactgtggat gacacaggcg caggcgcaga cgtgcatcgg ttcaccacaa 120
acgggcaaca acggcggctt cttcttttcg ttctggaaag acaatccggg gtcggtgaat 180
ttctgcatgt actccggcgg tcgctatacc tccagctgga gcggcatcaa caactgggta 240
ggtgggaagg gctggcaaac cggttcatcc cgcacggtga cgtattcggg cacgttcaac 300
tcgccgggaa acggctacct gactctgtac ggatggacca ccaatccgct ggtcgagtac 360
tacatcgtgg acagctgggg cagctaccgt ccgcctggag gccagggctt catgggcacg 420
gtcaccagcg acggcggaac gtatgacatc taccgggttc gccgcaccaa tgcgccgtgc 480
atcacaggca acaactgcaa cttcgaccag tactggagcg tgcgtcagtc gaggcgggtg 540
ggcggcacca tcaccaccgc caaccatttc aacgcgtggc gtacgctcgg catgaatctc 600
gggcagcaca actaccaggt gatggcgacc gaaggattcc agagcagtgg cagctcggac 660
atcaccgtga gcgaaggatc tggcggtggc ggcggaggtg gcggcggtgg caccaagagc 720
ttcacggtgc gcgcgcgcgg caccgcgggc ggcgagtcca tcacgctgcg cgtcaacaac 780
caggtcgtgc agagctggac cttgagcacc agcatgcaga actacacggc ctcgaccacg 840
atgagcggcg gcatcacggt gaacttcacc aacgacggca ccaaccgcga cgtgcaggtg 900
gactacatca tcgtgaatgg ccagacgcgt cagtccgaag cgcagacgta caacaccggg 960
ctgtacgcca acggccgttg cggtggcggg tcgaacagcg agtggatgca ttgcaatggc 1020
gcgatcgggt acggcgacac gccctga 1047

<210> 162
<211> 348
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(32)

<400> 162
Met Phe Lys Gly Leu Leu Lys Ser Val Leu Thr Gly Lys Arg Ala Gly
1 5 10 15
Ala Val Phe Ile Cys Leu Ala Gly Leu Trp Met Thr Gln Ala Gln Ala
20 25 30
Gln Thr Cys Ile Gly Ser Pro Gln Thr Gly Asn Asn Gly Gly Phe Phe
35 40 45

Phe Ser Phe Trp Lys Asp Asn Pro Gly Ser Val Asn Phe Cys Met Tyr
50 55 60
Ser Gly Gly Arg Tyr Thr Ser Ser Trp Ser Gly Ile Asn Asn Trp Val
65 70 75 80
Gly Gly Lys Gly Trp Gln Thr Gly Ser Ser Arg Thr Val Thr Tyr Ser
85 90 95
Gly Thr Phe Asn Ser Pro Gly Asn Gly Tyr Leu Thr Leu Tyr Gly Trp
100 105 110
Thr Thr Asn Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp Gly Ser
115 120 125
Tyr Arg Pro Pro Gly Gly Gln Gly Phe Met Gly Thr Val Thr Ser Asp
130 135 140
Gly Gly Thr Tyr Asp Ile Tyr Arg Val Arg Arg Thr Asn Ala Pro Cys
145 150 155 160
Ile Thr Gly Asn Asn Cys Asn Phe Asp Gln Tyr Trp Ser Val Arg Gln
165 170 175
Ser Arg Arg Val Gly Gly Thr Ile Thr Thr Ala Asn His Phe Asn Ala
180 185 190
Trp Arg Thr Leu Gly Met Asn Leu Gly Gln His Asn Tyr Gln Val Met
195 200 205
Ala Thr Glu Gly Phe Gln Ser Ser Gly Ser Ser Asp Ile Thr Val Ser
210 215 220
Glu Gly Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Thr Lys Ser
225 230 235 240
Phe Thr Val Arg Ala Arg Gly Thr Ala Gly Gly Glu Ser Ile Thr Leu
245 250 255
Arg Val Asn Asn Gln Val Val Gln Ser Trp Thr Leu Ser Thr Ser Met
260 265 270
Gln Asn Tyr Thr Ala Ser Thr Thr Met Ser Gly Gly Ile Thr Val Asn
275 280 285
Phe Thr Asn Asp Gly Thr Asn Arg Asp Val Gln Val Asp Tyr Ile Ile
290 295 300
Val Asn Gly Gln Thr Arg Gln Ser Glu Ala Gln Thr Tyr Asn Thr Gly
305 310 315 320
Leu Tyr Ala Asn Gly Arg Cys Gly Gly Gly Ser Asn Ser Glu Trp Met
325 330 335
His Cys Asn Gly Ala Ile Gly Tyr Gly Asp Thr Pro
340 345

<210> 163
<211> 1068
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 163
atgaaagcaa agagaatgaa gttgtttgcc gcatttttac tctgttttac gcttgcactt 60
cctggggcag tgcatgcgca gacgatcacc agcaattcgg tcggtacgca tgacggttat 120
gactatgaat actggaagga cagcgggaat ggaactatgg ttctcggtag tggcggtacg 180
ttcagtgccg agtggagcaa tatcaataat attctgttcc gtaaaggcaa gaagttcaat 240
gagacgcaga cccatcagca aattggaaac atttccataa cctatggtgc cacctaccaa 300
ccgaatggca attcgtattt aacggtctat ggctggacgg ttgaccccct cgtcgaatat 360
tacattgtcg atagctgggg cagctggcgt ccgcctggag catcgccaaa ggggactgtt 420
aacgttgacg gaggaacgta tgacatttat gagacaactc gtgtcaacca gccttccatt 480
aaaggcacgg caaccttcaa gcagtattgg agtgtccgga cgtcaaaacg gacgagcgga 540
accatatctg taagcgagca ctttaaggcc tgggagaaat tggggatgac catgggcaag 600
atgtatgaag tcgcgcttac ggttgaaggc tatcaaagca gtggaagcgc taatgtgtat 660
agccatacac tgacgatcgg cgggggaaca acacctccac caaccacagg cacaaagatc 720
gaagccgaga gtatgaccaa aagcggacaa tacactggga atatcagctc gccgttcaac 780
ggagtcgctt tgtatgccaa caatgattcc gtgaaattca cgcataattt cacgaccggc 840
acccataact tctcactccg gggggcatca aacaactcca atatggcccg ggttgacctg 900
aaaatcggcg ggcagacgaa ggggaccttc tatttcggcg gaagcagccc tgcggtctat 960
actctgaata atgtcagcca tggaaccgga aatcaagagg ttgaactcgt tgtaaccgcc 1020
gataacggaa catgggatgc tttcattgat tatctcgaga tccattaa 1068

<210> 164
<211> 355

<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(26)

<400> 164
Met Lys Ala Lys Arg Met Lys Leu Phe Ala Ala Phe Leu Leu Cys Phe
1 5 10 15
Thr Leu Ala Leu Pro Gly Ala Val His Ala Gln Thr Ile Thr Ser Asn
20 25 30
Ser Val Gly Thr His Asp Gly Tyr Asp Tyr Glu Tyr Trp Lys Asp Ser
35 40 45
Gly Asn Gly Thr Met Val Leu Gly Ser Gly Gly Thr Phe Ser Ala Glu
50 55 60
Trp Ser Asn Ile Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys Phe Asn
65 70 75 80
Glu Thr Gln Thr His Gln Gln Ile Gly Asn Ile Ser Ile Thr Tyr Gly
85 90 95
Ala Thr Tyr Gln Pro Asn Gly Asn Ser Tyr Leu Thr Val Tyr Gly Trp
100 105 110
Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp Gly Ser
115 120 125
Trp Arg Pro Pro Gly Ala Ser Pro Lys Gly Thr Val Asn Val Asp Gly
130 135 140
Gly Thr Tyr Asp Ile Tyr Glu Thr Thr Arg Val Asn Gln Pro Ser Ile
145 150 155 160
Lys Gly Thr Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Thr Ser Lys
165 170 175
Arg Thr Ser Gly Thr Ile Ser Val Ser Glu His Phe Lys Ala Trp Glu
180 185 190
Lys Leu Gly Met Thr Met Gly Lys Met Tyr Glu Val Ala Leu Thr Val
195 200 205
Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser His Thr Leu
210 215 220
Thr Ile Gly Gly Gly Thr Thr Pro Pro Pro Thr Thr Gly Thr Lys Ile
225 230 235 240
Glu Ala Glu Ser Met Thr Lys Ser Gly Gln Tyr Thr Gly Asn Ile Ser
245 250 255
Ser Pro Phe Asn Gly Val Ala Leu Tyr Ala Asn Asn Asp Ser Val Lys
260 265 270
Phe Thr His Asn Phe Thr Thr Gly Thr His Asn Phe Ser Leu Arg Gly
275 280 285
Ala Ser Asn Asn Ser Asn Met Ala Arg Val Asp Leu Lys Ile Gly Gly
290 295 300
Gln Thr Lys Gly Thr Phe Tyr Phe Gly Gly Ser Ser Pro Ala Val Tyr
305 310 315 320
Thr Leu Asn Asn Val Ser His Gly Thr Gly Asn Gln Glu Val Glu Leu
325 330 335
Val Val Thr Ala Asp Asn Gly Thr Trp Asp Ala Phe Ile Asp Tyr Leu
340 345 350
Glu Ile His
355

<210> 165
<211> 1047
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 165
gtggggcgca ggagcgccgc cacggcattc atcggcctgg cagcgctgtg tgcctcggcc 60
gccaacgcgc agacctgtct gagctcgagt cagaccggca ccaacaacgg cttctactat 120
tcgttctgga ccgacggcgg tggctccgtg cagttctgcc tgcaatccgc cgggcgctac 180

```
acctccagct ggagcaatgt cggaaactgg gtcggtggca agggctggca gaccggcgcg      240
cgccgcaaca tcaactattc cggcagcttc aatccctcgg gtaacgcgta cctggccgtc      300
tatggctgga ccacgaatcc cctggtggag tactacatcg tcgacaactg ggtacctat       360
cgtccaccgg gtgggcaggg attcatgggc acggttgtca gcgatggcgg cacctacgac      420
gtctaccgca cgcaacgggt caacgcgccc tccattcagg gcaacgcgac cttctaccag      480
tactggagcg ttcgccagtc gaagcgcacc ggtggaacca tctccaccgg caaccatttc      540
gacggctggg cgacgttcgg catgaacctg ggaaccttca attaccagat cgtggcgacc      600
gagggctacc agagcagcgg caattccgac atcacggtga gcgatggcgg cagcagctcc      660
tcgtcctcca gcagcagcag ttcgtcgtcc tccagcagcg gcggtggcgg caccaagagc      720
ttcacggtgc gcgcgcgcgg cacggccgga ggcgagtcga tcagcctgcg ggtcaacaac      780
accaacgtgc agacctggtc gctgaccacc agctaccaga atctcacggc ctcgaccacg      840
ctgaccggcg gcatcaccgt caactacacc aacgacagca gcggtcacga cgtacaggtg      900
gactacatca tcgtgaacgg ccagacccgc cagtccgagg cgcagagcta caacaccgga      960
ctctatgcca acgggcgctg cggtggtggt ggctacagcg agtggatgca ttgcaacggc     1020
gccatcggct acggcaatac gccgtaa                                         1047
```

<210> 166
<211> 348
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(23)

<400> 166
```
Val Gly Arg Arg Ser Ala Ala Thr Ala Phe Ile Gly Leu Ala Ala Leu
1               5                   10                  15
Cys Ala Ser Ala Ala Asn Ala Gln Thr Cys Leu Ser Ser Ser Gln Thr
            20                  25                  30
Gly Thr Asn Asn Gly Phe Tyr Tyr Ser Phe Trp Thr Asp Gly Gly Gly
        35                  40                  45
Ser Val Gln Phe Cys Leu Gln Ser Ala Gly Arg Tyr Thr Ser Ser Trp
    50                  55                  60
Ser Asn Val Gly Asn Trp Val Gly Gly Lys Gly Trp Gln Thr Gly Ala
65                  70                  75                  80
Arg Arg Asn Ile Asn Tyr Ser Gly Ser Phe Asn Pro Ser Gly Asn Ala
                85                  90                  95
Tyr Leu Ala Val Tyr Gly Trp Thr Thr Asn Pro Leu Val Glu Tyr Tyr
            100                 105                 110
Ile Val Asp Asn Trp Gly Thr Tyr Arg Pro Pro Gly Gly Gln Gly Phe
        115                 120                 125
Met Gly Thr Val Val Ser Asp Gly Gly Thr Tyr Asp Val Tyr Arg Thr
    130                 135                 140
Gln Arg Val Asn Ala Pro Ser Ile Gln Gly Asn Ala Thr Phe Tyr Gln
145                 150                 155                 160
Tyr Trp Ser Val Arg Gln Ser Lys Arg Thr Gly Gly Thr Ile Ser Thr
                165                 170                 175
Gly Asn His Phe Asp Gly Trp Ala Thr Phe Gly Met Asn Leu Gly Thr
            180                 185                 190
Phe Asn Tyr Gln Ile Val Ala Thr Glu Gly Tyr Gln Ser Ser Gly Asn
        195                 200                 205
Ser Asp Ile Thr Val Ser Asp Gly Gly Ser Ser Ser Ser Ser Ser Ser
    210                 215                 220
Ser Ser Ser Ser Ser Ser Ser Ser Ser Gly Gly Gly Gly Thr Lys Ser
225                 230                 235                 240
Phe Thr Val Arg Ala Arg Gly Thr Ala Gly Gly Glu Ser Ile Ser Leu
                245                 250                 255
Arg Val Asn Asn Thr Asn Val Gln Thr Trp Ser Leu Thr Thr Ser Tyr
            260                 265                 270
Gln Asn Leu Thr Ala Ser Thr Thr Leu Thr Gly Gly Ile Thr Val Asn
        275                 280                 285
Tyr Thr Asn Asp Ser Ser Gly His Asp Val Gln Val Asp Tyr Ile Ile
    290                 295                 300
Val Asn Gly Gln Thr Arg Gln Ser Glu Ala Gln Ser Tyr Asn Thr Gly
305                 310                 315                 320
Leu Tyr Ala Asn Gly Arg Cys Gly Gly Gly Gly Tyr Ser Glu Trp Met
```

```
                    325                     330                     335
His Cys Asn Gly Ala Ile Gly Tyr Gly Asn Thr Pro
                340                     345

<210> 167
<211> 669
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 167
gtgaagctga aaagactgtt caagatcgga ctgctgccgg ccgtattgtt gtttagtgca      60
acgcagcagt taaccgcgca aaccatctgc agcaaccaga ccggcaccaa caacggctac     120
ttctactcgt tctggaagga caccgggtcg gcgtgcatga cactgggttc cggcggcaac     180
tacagcgtca actggaacct gggttccggg aacatggtct gcggcaaagg ctggagtacc     240
ggatcttcaa gccgcagaat cggctacaac gccggcgtct gggcgccgaa cggcaatgcc     300
tacctgactc tgtatgggtg gaccaggaac ccgctcatcg agtactacgt ggtcgacagt     360
tggggaagct ggaggccgcc aggcggaacc tccgcgggca ccgtcaatag cgatggcggg     420
acctacaacc tctatcggac gcagcgggtc aacgcgcctt ccatcgacgg cacccggacg     480
ttctatcagt actggagtgt ccggacctcg aagaggccca ccgggagcaa ccagaccatc     540
accttcgcga accacgtgaa tgcgtggagg agcaaagggt ggaatctggg gagtcacgtc     600
taccagataa tggcaacaga gggatatcaa agcagcggga attccaacct gacggtgtgg     660
gcgcagtag                                                             669

<210> 168
<211> 222
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(36)

<400> 168
Val Lys Leu Lys Arg Leu Phe Lys Ile Gly Leu Leu Pro Ala Val Leu
 1               5                  10                  15
Leu Phe Ser Ala Thr Gln Gln Leu Thr Ala Gln Thr Ile Cys Ser Asn
            20                  25                  30
Gln Thr Gly Thr Asn Asn Gly Tyr Phe Tyr Ser Phe Trp Lys Asp Thr
        35                  40                  45
Gly Ser Ala Cys Met Thr Leu Gly Ser Gly Gly Asn Tyr Ser Val Asn
    50                  55                  60
Trp Asn Leu Gly Ser Gly Asn Met Val Cys Gly Lys Gly Trp Ser Thr
65                  70                  75                  80
Gly Ser Ser Ser Arg Arg Ile Gly Tyr Asn Ala Gly Val Trp Ala Pro
                85                  90                  95
Asn Gly Asn Ala Tyr Leu Thr Leu Tyr Gly Trp Thr Arg Asn Pro Leu
            100                 105                 110
Ile Glu Tyr Tyr Val Val Asp Ser Trp Gly Ser Trp Arg Pro Pro Gly
        115                 120                 125
Gly Thr Ser Ala Gly Thr Val Asn Ser Asp Gly Gly Thr Tyr Asn Leu
    130                 135                 140
Tyr Arg Thr Gln Arg Val Asn Ala Pro Ser Ile Asp Gly Thr Arg Thr
145                 150                 155                 160
Phe Tyr Gln Tyr Trp Ser Val Arg Thr Ser Lys Arg Pro Thr Gly Ser
                165                 170                 175
Asn Gln Thr Ile Thr Phe Ala Asn His Val Asn Ala Trp Arg Ser Lys
            180                 185                 190
Gly Trp Asn Leu Gly Ser His Val Tyr Gln Ile Met Ala Thr Glu Gly
        195                 200                 205
Tyr Gln Ser Ser Gly Asn Ser Asn Leu Thr Val Trp Ala Gln
    210                 215                 220

<210> 169
<211> 1041
```

<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 169
atgattgtta gtttcaagag cgtgaaggca ctcgcgtgcc tcgccgtgct cggcattacc 60
gccgcgcagg cgcaaacctg catcacttcc agccagaccg gtaccaacaa cggcaactac 120
ttttccttct ggaaggacag cccgggtacc gtcaacttct gcatgtatgc caatgggcgc 180
tacacctcca actggagcgg catcaacaac tgggtgggcg gcaagggctg gcagacgggc 240
tccaaccgca cggtgaccta ctccggttcg ttcaattcgc ccggcaatgg ctatctcacc 300
ttgtacggat ggaccacgaa tccattgatc gagtactaca tcgtcgacag ctggggcacc 360
tatcgaccgc cgggcggcca gggcttcatg ggcaccgtca acagcgatgg cggcacctat 420
gacatctacc gcacgcagcg cgtgaaccag ccttccatca tcggcaccgc cacgttctac 480
cagtactgga gcgtgcggca gtcgaagcgc gtcggcggca cgatcaccac ggccaaccac 540
ttcaacgcct gggccacgct gggcatgaac ctgggccagc acaactacca ggtcatggcc 600
accgagggtt accagagcag tggcagctcc gacatcaccg tgaccgaggg cggcggctcc 660
tcgtcgtcca gtggcggcgg cagcaccagc agtggcggtg gcggcagcaa gagcttcacc 720
gtgcgtgcgc gcggcacggt cggcggcgaa aacatccagc tgcaggtcaa caaccagacg 780
gtggcgagct ggaacctgac caccagcatg cagaactaca acgcctcgac cagcctgagt 840
ggcggcatca ccgtcgtgta caccaatgac agcggcagcc gcgacgtgca ggtggactac 900
atcgtcgtca acggccagac ccgccagtcc gaagcccaga gctacaacac cgggctctat 960
gccaacggac gttgtggtgg cggctcgaac agcgagtgga tgcattgcaa cggcgcgatt 1020
ggctacggca acacgcccta g 1041

<210> 170
<211> 346
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(24)

<400> 170
Met Ile Val Ser Phe Lys Ser Val Lys Ala Leu Ala Cys Leu Ala Val
1 5 10 15
Leu Gly Ile Thr Ala Ala Gln Ala Gln Thr Cys Ile Thr Ser Ser Gln
20 25 30
Thr Gly Thr Asn Asn Gly Asn Tyr Phe Ser Phe Trp Lys Asp Ser Pro
35 40 45
Gly Thr Val Asn Phe Cys Met Tyr Ala Asn Gly Arg Tyr Thr Ser Asn
50 55 60
Trp Ser Gly Ile Asn Asn Trp Val Gly Gly Lys Gly Trp Gln Thr Gly
65 70 75 80
Ser Asn Arg Thr Val Thr Tyr Ser Gly Ser Phe Asn Ser Pro Gly Asn
85 90 95
Gly Tyr Leu Thr Leu Tyr Gly Trp Thr Thr Asn Pro Leu Ile Glu Tyr
100 105 110
Tyr Ile Val Asp Ser Trp Gly Thr Tyr Arg Pro Pro Gly Gly Gln Gly
115 120 125
Phe Met Gly Thr Val Asn Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Arg
130 135 140
Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly Thr Ala Thr Phe Tyr
145 150 155 160
Gln Tyr Trp Ser Val Arg Gln Ser Lys Arg Val Gly Gly Thr Ile Thr
165 170 175
Thr Ala Asn His Phe Asn Ala Trp Ala Thr Leu Gly Met Asn Leu Gly
180 185 190
Gln His Asn Tyr Gln Val Met Ala Thr Glu Gly Tyr Gln Ser Ser Gly
195 200 205
Ser Ser Asp Ile Thr Val Thr Glu Gly Gly Gly Ser Ser Ser Ser Ser
210 215 220
Gly Gly Gly Ser Thr Ser Ser Gly Gly Gly Gly Ser Lys Ser Phe Thr
225 230 235 240
Val Arg Ala Arg Gly Thr Val Gly Gly Glu Asn Ile Gln Leu Gln Val

```
                245                 250                 255
Asn Asn Gln Thr Val Ala Ser Trp Asn Leu Thr Thr Ser Met Gln Asn
            260                 265                 270
Tyr Asn Ala Ser Thr Ser Leu Ser Gly Gly Ile Thr Val Val Tyr Thr
        275                 280                 285
Asn Asp Ser Gly Ser Arg Asp Val Gln Val Asp Tyr Ile Val Val Asn
    290                 295                 300
Gly Gln Thr Arg Gln Ser Glu Ala Gln Ser Tyr Asn Thr Gly Leu Tyr
305                 310                 315                 320
Ala Asn Gly Arg Cys Gly Gly Gly Ser Asn Ser Glu Trp Met His Cys
                325                 330                 335
Asn Gly Ala Ile Gly Tyr Gly Asn Thr Pro
            340                 345
```

<210> 171
<211> 678
<212> DNA
<213> Unknown

<220>
<223> obtained from an environmental sample

<400> 171

```
atggagttga aaaaaatatc cagaaaagga ctgccactag tattcttgtc cttgttgttg      60
ttcagtgtaa cgcagcagtc aaacgcccaa accatctgca gcaatcaaac tggcacaaac     120
aacggtttct tctattcgtt ttggaaggac accggatcag catgcatgac tttgggctct     180
ggcggcaatt acgacgtaag ttggaatctg ggttctggga atatggttgt cggcaaaggc     240
tggagtaccg gatcatcaac caggagagta ggctacaatg ccggcatctg gcagccgaac     300
ggcaatgcat atttggctct ctatgggtgg acgagaaacc cacttataga atattacgtc     360
gttgatagct ggggcacttt caggccgcct ggaggaacgt caataggctc cgtcaccact     420
gatggtggta cataccaaat atatcggacc cagcgagtca acgcgccttc cattgacggc     480
gccagaactt ttatcagta ctggagtgtc cggacctcga agagaccgac cgggagcaac      540
caaaccatca cctttgcgaa tcacgttaac gcgtggagga atctaggttt gaatctgggg     600
agtcatgttt accagataat ggccacagag ggatttcata gcagtgggag atctaaccta     660
acggtgtggt cacagtaa                                                   678
```

<210> 172
<211> 225
<212> PRT
<213> Unknown

<220>
<223> obtained from an environmental sample

<221> SIGNAL
<222> (1)...(29)

<400> 172

```
Met Glu Leu Lys Lys Ile Ser Arg Lys Gly Leu Pro Leu Val Phe Leu
 1               5                  10                  15
Ser Leu Leu Leu Phe Ser Val Thr Gln Gln Ser Asn Ala Gln Thr Ile
            20                  25                  30
Cys Ser Asn Gln Thr Gly Thr Asn Asn Gly Phe Phe Tyr Ser Phe Trp
        35                  40                  45
Lys Asp Thr Gly Ser Ala Cys Met Thr Leu Gly Ser Gly Gly Asn Tyr
    50                  55                  60
Asp Val Ser Trp Asn Leu Gly Ser Gly Asn Met Val Val Gly Lys Gly
65                  70                  75                  80
Trp Ser Thr Gly Ser Ser Thr Arg Arg Val Gly Tyr Asn Ala Gly Ile
                85                  90                  95
Trp Gln Pro Asn Gly Asn Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg
            100                 105                 110
Asn Pro Leu Ile Glu Tyr Tyr Val Val Asp Ser Trp Gly Thr Phe Arg
        115                 120                 125
Pro Pro Gly Gly Thr Ser Ile Gly Ser Val Thr Thr Asp Gly Gly Thr
    130                 135                 140
Tyr Gln Ile Tyr Arg Thr Gln Arg Val Asn Ala Pro Ser Ile Asp Gly
145                 150                 155                 160
Ala Arg Thr Phe Tyr Gln Tyr Trp Ser Val Arg Thr Ser Lys Arg Pro
```

```
                    165                     170                     175
Thr Gly Ser Asn Gln Thr Ile Thr Phe Ala Asn His Val Asn Ala Trp
            180                     185                     190
Arg Asn Leu Gly Leu Asn Leu Gly Ser His Val Tyr Gln Ile Met Ala
        195                     200                     205
Thr Glu Gly Phe His Ser Ser Gly Arg Ser Asn Leu Thr Val Trp Ser
    210                     215                     220
Gln
225
```

<210> 173
<211> 1503
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 173

```
ttgaaaaaac tcgcagctgc cttatcactt gcaattacct ttgccgtacc gacaatagta      60
caagcacaag gtcccacatg gactaccagc acaatacaga aatacaacaa ctacgactat     120
gaactctgga atgaaaacaa tcagggtacc gtttccatga agctcacagg agataacggt     180
accgctgcca atgcggtagg cggaacgttt gagtctactt ggagtggtac aaagaatgtg     240
cttttccgtt ccggcagaaa gtttaccggt acttcagggc aaagcgttga tggtggcggt     300
gctggcaaaa ccgctagtgc ttacggcaat ataagcatta acttcgccgc tacgtggtct     360
tccggtgacg atgtgaagat gcttggcgta tatggttggg cgttttacgc actgccaagt     420
gtaccagaca aacaggaaaa cggcacttct actaattttt ccaatcaaat agaatactac     480
atcattcaag accgcggcag ctataactcg gctacaggtg gcaccaactc aaagaaatac     540
ggtgaggcta ccattgacgg cattgcttat gagttccgtg tatgtgatag aatagggcaa     600
cctatgttaa ctggcaacgg gaattttaag cagtatttca gtgttcctaa aagcactata     660
aaccaccgca ccagcggtac aatctctgtt tccaaacact ttgaagaatg ggaaaaagtc     720
ggcatgaaaa tggacggtcc cttatacgaa gtagcgatga aagttgaatc ctattctggc     780
aatgggaata gtaacggcaa tgctaaaatt acaaagaata ttttgaccat tggcggaaca     840
accacaactc aaagcagttc aagcggaggt tcaacggttc cagatgaatg tggcgaatat     900
aaaaagagtt tctgtggtgg cttgggatat ggaagcgtat attccaattt aaccgcaata     960
ccctcaacgg gcgactgctt atacatcgga gattttgaag taatccagcc agctttgaat    1020
tcaaccgttg ccataaacgg tgtggaaaat acctgcggaa gcgagtggtc agattgccct    1080
tacaatgata aacccgattc aaaaaaagat ggcggctatt atgtttatgt gaaaacaggc    1140
tcaattaaca attatgagaa taacggttgg caaaacattg tagctaaagc aaaaccggct    1200
tgcacaccac cttctagcag ttccggtgct gcaccaggtt cttcttcttc agacgaagaa    1260
gacccagagc caattttgaa aaatcgcatt cctataactc atttttccct tcaaacgctt    1320
agcgataaag ccttgcgcat agaagtaaat gctccaacta ttgtggacat ttttgacctg    1380
agagggaata aggttaaaag tttgaatgtt tacggttcgc aaagggttaa attatccctg    1440
ccgagcgggg tgtattttgc caaagtgcgc gggatgaaaa gcgttagatt tgtgttgagg    1500
taa                                                                   1503
```

<210> 174
<211> 500
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<400> 174

```
Leu Lys Lys Leu Ala Ala Ala Leu Ser Leu Ala Ile Thr Phe Ala Val
 1               5                  10                  15
Pro Thr Ile Val Gln Ala Gln Gly Pro Thr Trp Thr Thr Ser Thr Ile
            20                  25                  30
Gln Lys Tyr Asn Asn Tyr Asp Tyr Glu Leu Trp Asn Glu Asn Asn Gln
        35                  40                  45
Gly Thr Val Ser Met Lys Leu Thr Gly Asp Asn Gly Thr Ala Ala Asn
    50                  55                  60
Ala Val Gly Gly Thr Phe Glu Ser Thr Trp Ser Gly Thr Lys Asn Val
65                  70                  75                  80
Leu Phe Arg Ser Gly Arg Lys Phe Thr Gly Thr Ser Gly Gln Ser Val
```

85 90 95
Asp Gly Gly Gly Ala Gly Lys Thr Ala Ser Ala Tyr Gly Asn Ile Ser
100 105 110
Ile Asn Phe Ala Ala Thr Trp Ser Ser Gly Asp Asp Val Lys Met Leu
115 120 125
Gly Val Tyr Gly Trp Ala Phe Tyr Ala Leu Pro Ser Val Pro Asp Lys
130 135 140
Gln Glu Asn Gly Thr Ser Thr Asn Phe Ser Asn Gln Ile Glu Tyr Tyr
145 150 155 160
Ile Ile Gln Asp Arg Gly Ser Tyr Asn Ser Ala Thr Gly Gly Thr Asn
165 170 175
Ser Lys Lys Tyr Gly Glu Ala Thr Ile Asp Gly Ile Ala Tyr Glu Phe
180 185 190
Arg Val Cys Asp Arg Ile Gly Gln Pro Met Leu Thr Gly Asn Gly Asn
195 200 205
Phe Lys Gln Tyr Phe Ser Val Pro Lys Ser Thr Ile Asn His Arg Thr
210 215 220
Ser Gly Thr Ile Ser Val Ser Lys His Phe Glu Glu Trp Glu Lys Val
225 230 235 240
Gly Met Lys Met Asp Gly Pro Leu Tyr Glu Val Ala Met Lys Val Glu
245 250 255
Ser Tyr Ser Gly Asn Gly Asn Ser Asn Gly Asn Ala Lys Ile Thr Lys
260 265 270
Asn Ile Leu Thr Ile Gly Gly Thr Thr Thr Thr Gln Ser Ser Ser Ser
275 280 285
Gly Gly Ser Thr Val Pro Asp Glu Cys Gly Glu Tyr Lys Lys Ser Phe
290 295 300
Cys Gly Gly Leu Gly Tyr Gly Ser Val Tyr Ser Asn Leu Thr Ala Ile
305 310 315 320
Pro Ser Thr Gly Asp Cys Leu Tyr Ile Gly Asp Phe Glu Val Ile Gln
325 330 335
Pro Ala Leu Asn Ser Thr Val Ala Ile Asn Gly Val Glu Asn Thr Cys
340 345 350
Gly Ser Glu Trp Ser Asp Cys Pro Tyr Asn Asp Lys Pro Asp Ser Lys
355 360 365
Lys Asp Gly Gly Tyr Tyr Val Tyr Val Lys Thr Gly Ser Ile Asn Asn
370 375 380
Tyr Glu Asn Asn Gly Trp Gln Asn Ile Val Ala Lys Ala Lys Pro Ala
385 390 395 400
Cys Thr Pro Pro Ser Ser Ser Ser Gly Ala Ala Pro Gly Ser Ser Ser
405 410 415
Ser Asp Glu Glu Asp Pro Glu Pro Ile Leu Lys Asn Arg Ile Pro Ile
420 425 430
Thr His Phe Ser Leu Gln Thr Leu Ser Asp Lys Ala Leu Arg Ile Glu
435 440 445
Val Asn Ala Pro Thr Ile Val Asp Ile Phe Asp Leu Arg Gly Asn Lys
450 455 460
Val Lys Ser Leu Asn Val Tyr Gly Ser Gln Arg Val Lys Leu Ser Leu
465 470 475 480
Pro Ser Gly Val Tyr Phe Ala Lys Val Arg Gly Met Lys Ser Val Arg
485 490 495
Phe Val Leu Arg
500

<210> 175
<211> 1053
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 175
atgaagtcca ttcgcagccg cagcctcgcc accgccgtcc tggctggcgc cctcggcgtc 60
gcagccgcag gcgcgcaggc gcagacgctc aacaacaatt ccaccggcac gcacgacggc 120
tactactaca cgttctggaa ggactcgggc agcgcctcga tgaccctcca tccgggcgga 180
cgctacagct cccagtggac cagcaacacc aacaactggg tcggcgggaa aggctggaat 240
cccggtggcc cgcgcgtggt caactactcg ggctactacg ggtcaacaa cagccagaac 300
tcctacctgg cgctgtacgg ctggacccgc aatccgctgg tcgagtacta cgtgatcgag 360

```
agctacggct cctacaaccc ggccagttgc gccggcgggg tggactacgg cagcttccag      420
agcgatggcg ccacctacaa cgtacgtcgc tgcctgcgcc agaacgcgcc gtcgatcgaa      480
ggcaacaaca gcaccttcta ccagtacttc agcgtgcgca atcccaagaa gggattcggc      540
aacatctccg gcacgatcac cgtcgccaac cacttcaact actgggccag ccgcggcctc      600
aacctcggca accacgacta catggtgttc gccaccgagg gctaccagag ccagggcagc      660
agcgacatca ccgtgagttc gggtaccggc ggcggcggtg gcggcggcaa cacgggcagc      720
aagaccatcg tggtgcgcgc gcgcggcacc gccggcggag agaacatctc gctcaaggtc      780
aacaacgcca ccatcgccag ctggacgctc accaccagca tggccaacta cacggccacc      840
acctcggcat cgggcggctc gctggtggag ttcaccaacg acggcggcaa ccgcgacgtg      900
caggtggact acctcagcgt caatggcgcc gtccgccagg ccgaggacca gacctacaac      960
accggcgtgt accagaacgg ccagtgcggc ggcggcaacg gccgcagcga atggctgcac     1020
tgcaacggtg ccatcggctt cggaaatctc tga                                  1053
```

<210> 176
<211> 350
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(27)

<400> 176

```
Met Lys Ser Ile Arg Ser Arg Ser Leu Ala Thr Ala Val Leu Ala Gly
 1               5                  10                  15
Ala Leu Gly Val Ala Ala Ala Gly Ala Gln Ala Gln Thr Leu Asn Asn
            20                  25                  30
Asn Ser Thr Gly Thr His Asp Gly Tyr Tyr Tyr Thr Phe Trp Lys Asp
        35                  40                  45
Ser Gly Ser Ala Ser Met Thr Leu His Pro Gly Gly Arg Tyr Ser Ser
    50                  55                  60
Gln Trp Thr Ser Asn Thr Asn Asn Trp Val Gly Gly Lys Gly Trp Asn
65                  70                  75                  80
Pro Gly Gly Pro Arg Val Val Asn Tyr Ser Gly Tyr Tyr Gly Val Asn
                85                  90                  95
Asn Ser Gln Asn Ser Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Pro
            100                 105                 110
Leu Val Glu Tyr Tyr Val Ile Glu Ser Tyr Gly Ser Tyr Asn Pro Ala
        115                 120                 125
Ser Cys Ala Gly Gly Val Asp Tyr Gly Ser Phe Gln Ser Asp Gly Ala
    130                 135                 140
Thr Tyr Asn Val Arg Arg Cys Leu Arg Gln Asn Ala Pro Ser Ile Glu
145                 150                 155                 160
Gly Asn Asn Ser Thr Phe Tyr Gln Tyr Phe Ser Val Arg Asn Pro Lys
                165                 170                 175
Lys Gly Phe Gly Asn Ile Ser Gly Thr Ile Thr Val Ala Asn His Phe
            180                 185                 190
Asn Tyr Trp Ala Ser Arg Gly Leu Asn Leu Gly Asn His Asp Tyr Met
        195                 200                 205
Val Phe Ala Thr Glu Gly Tyr Gln Ser Gln Gly Ser Ser Asp Ile Thr
    210                 215                 220
Val Ser Ser Gly Thr Gly Gly Gly Gly Gly Gly Gly Asn Thr Gly Ser
225                 230                 235                 240
Lys Thr Ile Val Val Arg Ala Arg Gly Thr Ala Gly Gly Glu Asn Ile
                245                 250                 255
Ser Leu Lys Val Asn Asn Ala Thr Ile Ala Ser Trp Thr Leu Thr Thr
            260                 265                 270
Ser Met Ala Asn Tyr Thr Ala Thr Thr Ser Ala Ser Gly Gly Ser Leu
        275                 280                 285
Val Glu Phe Thr Asn Asp Gly Gly Asn Arg Asp Val Gln Val Asp Tyr
    290                 295                 300
Leu Ser Val Asn Gly Ala Val Arg Gln Ala Glu Asp Gln Thr Tyr Asn
305                 310                 315                 320
Thr Gly Val Tyr Gln Asn Gly Gln Cys Gly Gly Gly Asn Gly Arg Ser
                325                 330                 335
Glu Trp Leu His Cys Asn Gly Ala Ile Gly Phe Gly Asn Leu
            340                 345                 350
```

<210> 177
<211> 1299
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 177
atgaaattgt tgaaaacgca caggcgtgcg attgctgccg cagcactagc ggtggcgact 60
gttccaatcg ctcatgcgca aacgcttagc tcaaatgcca ctggaaccca gaatggttac 120
tactattcgt tttggaagga ttccggtaac gccaccatga cactcggtgc cggtggaaac 180
tattcttcat cctggaacag cagcactaac aactgggttg gcggtaaagg ctggatgccg 240
ggtactcggc gcacagtcac ctattcgggc agttatagcg cgagtggaac cagctacctc 300
gcactttacg gctggactcg aaacccgctg atcgaatatt acattgtcga aaactgggtc 360
aattacaatc ctgcgtccgg cgcaacgaat tatgggactg tcaatattga cggcagcacc 420
taccagctgg gccgcagcca acgggttaat cagccatcta ttgaaggcac ggccacgttc 480
taccaatact ggagtgtgcg ccaaaacaag cgcaccagcg gaacgattaa tattggagcg 540
catttcgatg catgggctgc tgtgggcttg aacctgggga ctcacgatta tcagattatg 600
gcgaccgagg gctaccagag cagcggccag tccaatatca cggtgagcga aggcagtagc 660
ggcagcacga cttcgagcac atccagctcc agctcaagta cgagttccag tagttcttcc 720
agcagttctt ccggcggcgg cacaggaagt tgtgccggag tgaatgtgta ccccaattgg 780
accgcacgcg actggtctgg cggcgcatac aatcacgcca atgccggtga ccaaatggtc 840
tatcaaaaca atttgtaccg ggcaaactgg tacaccaact ccacgcctgg aagcgatgcc 900
tcctggacca gtctcgggtc ctgtagcggc ggcggtagca ccagttcaac aacgagctcc 960
tccagttcct cttccacctc ggcgtcgagc agctccaact catccagcag cagttcaagc 1020
agctccagca gcggtggctg tcgggaaatg tgtaactggt acggacaggg tatgtatcct 1080
ctgtgtcaga acaccagcgg ttggggatgg gaaaataacc agaactgtat cggtcgccaa 1140
acctgtcaaa gtcagaacgg cggctccggg ggtgtggtga acagctgtgg taccagcagc 1200
tcttcgtcca gtagcacctc ctcatcgagc agttcaagtt cgtcgagtgg caccacgtca 1260
tcgtcctccg gaattcctgc agcccggggg atccactag 1299

<210> 178
<211> 432
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(26)

<400> 178
Met Lys Leu Leu Lys Thr His Arg Arg Ala Ile Ala Ala Ala Ala Leu
1 5 10 15
Ala Val Ala Thr Val Pro Ile Ala His Ala Gln Thr Leu Ser Ser Asn
20 25 30
Ala Thr Gly Thr Gln Asn Gly Tyr Tyr Tyr Ser Phe Trp Lys Asp Ser
35 40 45
Gly Asn Ala Thr Met Thr Leu Gly Ala Gly Gly Asn Tyr Ser Ser Ser
50 55 60
Trp Asn Ser Ser Thr Asn Asn Trp Val Gly Gly Lys Gly Trp Met Pro
65 70 75 80
Gly Thr Arg Arg Thr Val Thr Tyr Ser Gly Ser Tyr Ser Ala Ser Gly
85 90 95
Thr Ser Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Pro Leu Ile Glu
100 105 110
Tyr Tyr Ile Val Glu Asn Trp Val Asn Tyr Asn Pro Ala Ser Gly Ala
115 120 125
Thr Asn Tyr Gly Thr Val Asn Ile Asp Gly Ser Thr Tyr Gln Leu Gly
130 135 140
Arg Ser Gln Arg Val Asn Gln Pro Ser Ile Glu Gly Thr Ala Thr Phe
145 150 155 160
Tyr Gln Tyr Trp Ser Val Arg Gln Asn Lys Arg Thr Ser Gly Thr Ile
165 170 175
Asn Ile Gly Ala His Phe Asp Ala Trp Ala Ala Val Gly Leu Asn Leu
180 185 190

Gly Thr His Asp Tyr Gln Ile Met Ala Thr Glu Gly Tyr Gln Ser Ser
195 200 205
Gly Gln Ser Asn Ile Thr Val Ser Glu Gly Ser Ser Gly Ser Thr Thr
210 215 220
Ser Ser Thr Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Ser Ser Ser
225 230 235 240
Ser Ser Ser Ser Gly Gly Gly Thr Gly Ser Cys Ala Gly Val Asn Val
245 250 255
Tyr Pro Asn Trp Thr Ala Arg Asp Trp Ser Gly Gly Ala Tyr Asn His
260 265 270
Ala Asn Ala Gly Asp Gln Met Val Tyr Gln Asn Asn Leu Tyr Arg Ala
275 280 285
Asn Trp Tyr Thr Asn Ser Thr Pro Gly Ser Asp Ala Ser Trp Thr Ser
290 295 300
Leu Gly Ser Cys Ser Gly Gly Gly Ser Thr Ser Ser Thr Thr Ser Ser
305 310 315 320
Ser Ser Ser Ser Ser Thr Ser Ala Ser Ser Ser Ser Asn Ser Ser Ser
325 330 335
Ser Ser Ser Ser Ser Ser Ser Ser Gly Gly Cys Arg Glu Met Cys Asn
340 345 350
Trp Tyr Gly Gln Gly Met Tyr Pro Leu Cys Gln Asn Thr Ser Gly Trp
355 360 365
Gly Trp Glu Asn Asn Gln Asn Cys Ile Gly Arg Gln Thr Cys Gln Ser
370 375 380
Gln Asn Gly Gly Ser Gly Gly Val Val Asn Ser Cys Gly Thr Ser Ser
385 390 395 400
Ser Ser Ser Ser Ser Thr Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
405 410 415
Gly Thr Thr Ser Ser Ser Ser Gly Ile Pro Ala Ala Arg Gly Ile His
420 425 430

<210> 179
<211> 852
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 179
atgaagaatt ggccgggaac gggtattata ttattattgg cgggcggcct tttggcggct 60
tgtttgacgg gcaaacggca agaggggcaa aaagtggatc cggatactca aaacgagaaa 120
ttgacaggcg ggaccgtgtt tacagctaac agcaggggga acaggcccct ggaaggttcg 180
ccttatggtt acgaaatgtg gacgcagggc gggaataata acaagcttgt ttggttcggg 240
ccggatcagg ggggaggggc ggctttcagg gcagaatgga acgagccgga tgattttttg 300
ggacgactgg gtttctggtg gggaaacggc gggcaattta aagaatataa aaatatgtac 360
gcggatttca attacacaag gtcggggcgc ggcaccggcg gcagttattc ttatataggc 420
atttacggct gggcgagaaa cccgaacgcc gcgaacgagg aagacaggtt aatagaatac 480
tatattgtgg acgactggtt cgggaatcaa tggcagtccg acgacacccc cattaccaca 540
agaacaacag gaggctccgt attgggtacc attatagcgg acggcgcgtt ttacaacgtc 600
gtcaggaatg tgagaaccca aaagccttcg atagacggca tcaaaacatt cgcccaatac 660
ttcagcatac gccaaacacc gcgccaaagc gggacaatct ccatcaccga acatttcaaa 720
caatgggaaa gcatgggcct gaagctcgga aatatgtacg aggcaaaatt cctggtagaa 780
gccggcggcg gcaccggctg gctggagttt acgtatctta aactgacgca ggaagaaaaa 840
aaaagaaatt ag 852

<210> 180
<211> 283
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(19)

<400> 180
Met Lys Asn Trp Pro Gly Thr Gly Ile Ile Leu Leu Leu Ala Gly Gly

```
1               5                   10                  15
Leu Leu Ala Ala Cys Leu Thr Gly Lys Arg Gln Glu Gly Gln Lys Val
            20                  25                  30
Asp Pro Asp Thr Gln Asn Glu Lys Leu Thr Gly Gly Thr Val Phe Thr
        35                  40                  45
Ala Asn Ser Arg Gly Asn Arg Pro Leu Glu Gly Ser Pro Tyr Gly Tyr
    50                  55                  60
Glu Met Trp Thr Gln Gly Gly Asn Asn Asn Lys Leu Val Trp Phe Gly
65                  70                  75                      80
Pro Asp Gln Gly Gly Gly Ala Ala Phe Arg Ala Glu Trp Asn Glu Pro
                85                  90                  95
Asp Asp Phe Leu Gly Arg Leu Gly Phe Trp Trp Gly Asn Gly Gly Gln
            100                 105                 110
Phe Lys Glu Tyr Lys Asn Met Tyr Ala Asp Phe Asn Tyr Thr Arg Ser
        115                 120                 125
Gly Arg Gly Thr Gly Gly Ser Tyr Ser Tyr Ile Gly Ile Tyr Gly Trp
    130                 135                 140
Ala Arg Asn Pro Asn Ala Ala Asn Glu Glu Asp Arg Leu Ile Glu Tyr
145                 150                 155                     160
Tyr Ile Val Asp Asp Trp Phe Gly Asn Gln Trp Gln Ser Asp Asp Thr
                165                 170                 175
Pro Ile Thr Thr Arg Thr Thr Gly Gly Ser Val Leu Gly Thr Ile Ile
            180                 185                 190
Ala Asp Gly Ala Phe Tyr Asn Val Val Arg Asn Val Arg Thr Gln Lys
        195                 200                 205
Pro Ser Ile Asp Gly Ile Lys Thr Phe Ala Gln Tyr Phe Ser Ile Arg
    210                 215                 220
Gln Thr Pro Arg Gln Ser Gly Thr Ile Ser Ile Thr Glu His Phe Lys
225                 230                 235                     240
Gln Trp Glu Ser Met Gly Leu Lys Leu Gly Asn Met Tyr Glu Ala Lys
                245                 250                 255
Phe Leu Val Glu Ala Gly Gly Gly Thr Gly Trp Leu Glu Phe Thr Tyr
            260                 265                 270
Leu Lys Leu Thr Gln Glu Glu Lys Lys Arg Asn
        275                 280
```

<210> 181
<211> 1077
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 181

```
atgaacttca gtctcaggaa ggctgcagcg gcgctggctt gcgtcgcggg cctgtatgca      60
tcatcggcgg gcgctcagac ctgcctgacc aacaaccaga ccggcaacaa cggcgggtac     120
tactactcgt tctggaagga cagcggcaac gtcaccttct gcctgcagtc cggcgggcga     180
tacacgtccc agtggagcaa cgtcaacaac tgggtgggcg gcaagggctg gaacccgggt     240
gggcgacgca ccgtcaccta ttccggcacc tacaacccca atggcaattc gtacctgacc     300
ctgtacggct ggaccacgaa tccactggtc gagtactaca tcgtcgacag ctggggttcc     360
tggcgcccac cgggctcggg atacatgggc acggtcacca gcgatggcgg cacctacgac     420
atctatcgca cgcagcgtgt gaaccagcct tccatcatcg gcaccgcgac gttctaccaa     480
tactggagcg tgcggcaatc gaagcgcgtg ggtggcacca tcacctcggg caatcacttc     540
gatgcctggg cctcgctggg catgaacctc ggcacgcaca actacatggt gatggccacc     600
gagggctacc agagcagcgg cagctcggac atcacggtgg gcagcggcag ttcgtcgtcg     660
agcagcagct cgtccagcag tagcagctcg tcgtccagta gcagcagcag ttcttcgtcc     720
agcagcagcg gtggcggcgg caccaagagc ttcaccgtgc gcgcacgcgg cacggcgggt     780
ggcgagtcca tcaccttgcg ggtgaacaac cagaacgtgc agacctggac gctgggcacc     840
agcatgcaga actacacggc gtccacctcg ctgagcggcg gcatcacggt ggccttcacc     900
aacgacggcg gcaaccgcga cgtccaggtg gattacatca tcgtgaatgg ccagacgcgc     960
cagtccgagg cgcagaccta caacaccggc ctgtatgcca atggccgctg cggtggtggc    1020
tctaacagcg agtggatgca ctgcaacggc gccatcggct acggcaacac gccctag       1077
```

<210> 182
<211> 358
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(25)

<400> 182
Met Asn Phe Ser Leu Arg Lys Ala Ala Ala Ala Leu Ala Cys Val Ala
1   5   10   15
Gly Leu Tyr Ala Ser Ser Ala Gly Ala Gln Thr Cys Leu Thr Asn Asn
            20   25   30
Gln Thr Gly Asn Asn Gly Gly Tyr Tyr Tyr Ser Phe Trp Lys Asp Ser
        35   40   45
Gly Asn Val Thr Phe Cys Leu Gln Ser Gly Gly Arg Tyr Thr Ser Gln
    50   55   60
Trp Ser Asn Val Asn Asn Trp Val Gly Gly Lys Gly Trp Asn Pro Gly
65   70   75   80
Gly Arg Arg Thr Val Thr Tyr Ser Gly Thr Tyr Asn Pro Asn Gly Asn
                85   90   95
Ser Tyr Leu Thr Leu Tyr Gly Trp Thr Thr Asn Pro Leu Val Glu Tyr
            100   105   110
Tyr Ile Val Asp Ser Trp Gly Ser Trp Arg Pro Pro Gly Ser Gly Tyr
        115   120   125
Met Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Arg Thr
    130   135   140
Gln Arg Val Asn Gln Pro Ser Ile Ile Gly Thr Ala Thr Phe Tyr Gln
145   150   155   160
Tyr Trp Ser Val Arg Gln Ser Lys Arg Val Gly Gly Thr Ile Thr Ser
                165   170   175
Gly Asn His Phe Asp Ala Trp Ala Ser Leu Gly Met Asn Leu Gly Thr
            180   185   190
His Asn Tyr Met Val Met Ala Thr Glu Gly Tyr Gln Ser Ser Gly Ser
        195   200   205
Ser Asp Ile Thr Val Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Ser
    210   215   220
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
225   230   235   240
Ser Ser Ser Gly Gly Gly Gly Thr Lys Ser Phe Thr Val Arg Ala Arg
                245   250   255
Gly Thr Ala Gly Gly Glu Ser Ile Thr Leu Arg Val Asn Asn Gln Asn
            260   265   270
Val Gln Thr Trp Thr Leu Gly Thr Ser Met Gln Asn Tyr Thr Ala Ser
        275   280   285
Thr Ser Leu Ser Gly Gly Ile Thr Val Ala Phe Thr Asn Asp Gly Gly
    290   295   300
Asn Arg Asp Val Gln Val Asp Tyr Ile Ile Val Asn Gly Gln Thr Arg
305   310   315   320
Gln Ser Glu Ala Gln Thr Tyr Asn Thr Gly Leu Tyr Ala Asn Gly Arg
                325   330   335
Cys Gly Gly Gly Ser Asn Ser Glu Trp Met His Cys Asn Gly Ala Ile
            340   345   350
Gly Tyr Gly Asn Thr Pro
        355

<210> 183
<211> 1083
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 183
atgatcgaag gtctcaggag acctgccttc agtggcagga gcatcgtcaa ggcattgctc 60
tgcgtcgcgg ccctgtatgc atcggcggcg caggcgcaga cctgtctcag ttcgagccag 120
accggcacca acaacggctt ctactattcg ttctggaagg acagcccggg cagcgtgcag 180
ttctgcatgt attccggcgg ccgctacaca tccaactgga gcggcatcaa caactgggtc 240
ggcggcaagg ggtggcagac cggcgcctcg cgcgtggtca gctactcggg cacgttcaat 300
tcaccgggca acggctacct ggcgctgtac ggctggacca ccaatccact ggtcgagtac 360

```
tacatcgtcg acaactgggg cacctatcgc ccgccgggcg gcacgggatt ccagggcacg     420
gtgaccagtg acggcggtac ctacgacatc taccggaccg agcgcaccaa cgcgccctgc     480
atcaccggca acaactgcaa cttctcgcag ttctggagcg tgcggcagtc gaagcgcacc     540
ggcggcacca tcaccaccgg caatcacttc agcgcctggg cgtcgcacgg catgaacatg     600
ggccagcaca actaccagat catggccacc gagggttacc agagcaacgg cagctcggac     660
atcacggtct cggaaggcag cagttcgtcg agcagcagca gttcgtcctc ttcgtcgagc     720
agcagctcgt cgagcggcgg cggcggcagc aagagcttca cggtgcgcgc ccgcggcacc     780
gcgggtggcg agcagatccg gctgcgcgtg aacaatacga ccgtgcagac ctggacgctg     840
aacaccacga tgacgaacta caccgcttcg accacgctga gcggcggcat cacggtggag     900
tacttcaacg acagcaccaa tcacgacgtg caggtggact acatcatcgt gaacggcgcg     960
acgcgccagt ccgaagcgca gagctacaac accggcctgt atgccaacgg ccgttgcggt    1020
ggcggttcca acagcgaatg gatgcattgc aatggcgcca tcggctacgg caacactcca    1080
taa                                                                  1083
```

<210> 184
<211> 360
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(32)

<400> 184

```
Met Ile Glu Gly Leu Arg Arg Pro Ala Phe Ser Gly Arg Ser Ile Val
 1               5                  10                  15
Lys Ala Leu Leu Cys Val Ala Ala Leu Tyr Ala Ser Ala Ala Gln Ala
            20                  25                  30
Gln Thr Cys Leu Ser Ser Ser Gln Thr Gly Thr Asn Asn Gly Phe Tyr
        35                  40                  45
Tyr Ser Phe Trp Lys Asp Ser Pro Gly Ser Val Gln Phe Cys Met Tyr
    50                  55                  60
Ser Gly Gly Arg Tyr Thr Ser Asn Trp Ser Gly Ile Asn Asn Trp Val
65                  70                  75                  80
Gly Gly Lys Gly Trp Gln Thr Gly Ala Ser Arg Val Val Ser Tyr Ser
                85                  90                  95
Gly Thr Phe Asn Ser Pro Gly Asn Gly Tyr Leu Ala Leu Tyr Gly Trp
            100                 105                 110
Thr Thr Asn Pro Leu Val Glu Tyr Tyr Ile Val Asp Asn Trp Gly Thr
        115                 120                 125
Tyr Arg Pro Pro Gly Gly Thr Gly Phe Gln Gly Thr Val Thr Ser Asp
    130                 135                 140
Gly Gly Thr Tyr Asp Ile Tyr Arg Thr Glu Arg Thr Asn Ala Pro Cys
145                 150                 155                 160
Ile Thr Gly Asn Asn Cys Asn Phe Ser Gln Phe Trp Ser Val Arg Gln
                165                 170                 175
Ser Lys Arg Thr Gly Gly Thr Ile Thr Thr Gly Asn His Phe Ser Ala
            180                 185                 190
Trp Ala Ser His Gly Met Asn Met Gly Gln His Asn Tyr Gln Ile Met
        195                 200                 205
Ala Thr Glu Gly Tyr Gln Ser Asn Gly Ser Ser Asp Ile Thr Val Ser
    210                 215                 220
Glu Gly Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
225                 230                 235                 240
Ser Ser Ser Ser Ser Gly Gly Gly Gly Ser Lys Ser Phe Thr Val Arg
                245                 250                 255
Ala Arg Gly Thr Ala Gly Gly Glu Gln Ile Arg Leu Arg Val Asn Asn
            260                 265                 270
Thr Thr Val Gln Thr Trp Thr Leu Asn Thr Thr Met Thr Asn Tyr Thr
        275                 280                 285
Ala Ser Thr Thr Leu Ser Gly Gly Ile Thr Val Glu Tyr Phe Asn Asp
    290                 295                 300
Ser Thr Asn His Asp Val Gln Val Asp Tyr Ile Ile Val Asn Gly Ala
305                 310                 315                 320
Thr Arg Gln Ser Glu Ala Gln Ser Tyr Asn Thr Gly Leu Tyr Ala Asn
                325                 330                 335
Gly Arg Cys Gly Gly Gly Ser Asn Ser Glu Trp Met His Cys Asn Gly
```

340 345 350
Ala Ile Gly Tyr Gly Asn Thr Pro
355 360

<210> 185
<211> 684
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 185
atgaatttga aaagattgag gctgttgttt gtgatgtgta ttggatttgt gctgacactg 60
acggctgtgc cagctcatgc ggaaacgatt tatgataata ggatagggac acacagcgga 120
tacgattttg aattatggaa ggattacgga aatacctcga tgacactcaa taacggcggg 180
gcatttagtg caagctggaa caatattgga aatgccttat ttcgaaaagg aaagaagttt 240
gattccacta aaactcatca tcaacttggc aacatctcca tcaactacaa cgcagccttt 300
aacccgggcg ggaattccta tttatgtgtc tatggctgga cacaatctcc attagctgaa 360
tactacattg ttgagtcatg gggcacatat cgtccaacag gaacgtataa aggatcattt 420
tatgccgatg gaggcacata tgacatatat gaaacgctcc gtgtcaatca gccttctatc 480
attggagacg ctaccttcaa acaatattgg agtgtacgtc aaacaaaacg cacaagcgga 540
actgtttccg tcagtgagca ttttaaaaaa tgggaaagct taggcatgcc aatgggaaaa 600
atgtatgaaa cagcattaac tgtagaaggc taccgaagca acggaagtgc gaatgtcatg 660
acgaatcagc tgatgattcg ataa 684

<210> 186
<211> 227
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(27)

<400> 186
Met Asn Leu Lys Arg Leu Arg Leu Leu Phe Val Met Cys Ile Gly Phe
1 5 10 15
Val Leu Thr Leu Thr Ala Val Pro Ala His Ala Glu Thr Ile Tyr Asp
20 25 30
Asn Arg Ile Gly Thr His Ser Gly Tyr Asp Phe Glu Leu Trp Lys Asp
35 40 45
Tyr Gly Asn Thr Ser Met Thr Leu Asn Asn Gly Gly Ala Phe Ser Ala
50 55 60
Ser Trp Asn Asn Ile Gly Asn Ala Leu Phe Arg Lys Gly Lys Lys Phe
65 70 75 80
Asp Ser Thr Lys Thr His His Gln Leu Gly Asn Ile Ser Ile Asn Tyr
85 90 95
Asn Ala Ala Phe Asn Pro Gly Gly Asn Ser Tyr Leu Cys Val Tyr Gly
100 105 110
Trp Thr Gln Ser Pro Leu Ala Glu Tyr Tyr Ile Val Glu Ser Trp Gly
115 120 125
Thr Tyr Arg Pro Thr Gly Thr Tyr Lys Gly Ser Phe Tyr Ala Asp Gly
130 135 140
Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro Ser Ile
145 150 155 160
Ile Gly Asp Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Gln Thr Lys
165 170 175
Arg Thr Ser Gly Thr Val Ser Val Ser Glu His Phe Lys Lys Trp Glu
180 185 190
Ser Leu Gly Met Pro Met Gly Lys Met Tyr Glu Thr Ala Leu Thr Val
195 200 205
Glu Gly Tyr Arg Ser Asn Gly Ser Ala Asn Val Met Thr Asn Gln Leu
210 215 220
Met Ile Arg
225

<210> 187
<211> 642
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 187
```
atgtttaagt ttaaaaagaa tttcttagtt ggattatcgg cagctttaat gagtattagc      60
ttgttttcgg caaccgcctc tgcagctagc acagactact ggcaaaattg gactgatggg     120
ggcggtatag taaacgctgt caatgggtct ggcgggaatt acagtgttaa ttggtctaat     180
accggaaatt ttgttgttgg taaaggttgg actacaggtt cgccatttag gacgataaac     240
tataatgccg gagtttgggc gccgaatggc aatggatatt taactttata tggttggacg     300
agatcacctc tcatagaata ttatgtagtg gattcatggg gtacttatag acctactgga     360
acgtataaag gtactgtaaa aagtgatggg ggtacatatg acatatatac aactacacgt     420
tataacgcac cttccattga tggcgatcgc actactttta cgcagtactg gagtgttcgc     480
cagtcgaaga gaccaaccgg aagcaacgct acaatcactt tcagcaatca tgtgaacgca     540
tggaagagcc atggaatgaa tctgggcagt aattgggctt accaagtcat ggcgacagaa     600
ggatatcaaa gtagtggaag ttctaacgta acagtgtggt aa                        642
```

<210> 188
<211> 213
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<400> 188
```
Met Phe Lys Phe Lys Lys Asn Phe Leu Val Gly Leu Ser Ala Ala Leu
 1               5                  10                  15
Met Ser Ile Ser Leu Phe Ser Ala Thr Ala Ser Ala Ala Ser Thr Asp
            20                  25                  30
Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Ile Val Asn Ala Val Asn
        35                  40                  45
Gly Ser Gly Gly Asn Tyr Ser Val Asn Trp Ser Asn Thr Gly Asn Phe
    50                  55                  60
Val Val Gly Lys Gly Trp Thr Thr Gly Ser Pro Phe Arg Thr Ile Asn
65                  70                  75                  80
Tyr Asn Ala Gly Val Trp Ala Pro Asn Gly Asn Gly Tyr Leu Thr Leu
                85                  90                  95
Tyr Gly Trp Thr Arg Ser Pro Leu Ile Glu Tyr Tyr Val Val Asp Ser
            100                 105                 110
Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys Gly Thr Val Lys Ser
        115                 120                 125
Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr Arg Tyr Asn Ala Pro
    130                 135                 140
Ser Ile Asp Gly Asp Arg Thr Thr Phe Thr Gln Tyr Trp Ser Val Arg
145                 150                 155                 160
Gln Ser Lys Arg Pro Thr Gly Ser Asn Ala Thr Ile Thr Phe Ser Asn
                165                 170                 175
His Val Asn Ala Trp Lys Ser His Gly Met Asn Leu Gly Ser Asn Trp
            180                 185                 190
Ala Tyr Gln Val Met Ala Thr Glu Gly Tyr Gln Ser Ser Gly Ser Ser
        195                 200                 205
Asn Val Thr Val Trp
    210
```

<210> 189
<211> 570
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 189
atggccctta tggcttcgac agactactgg caaaattgga ctgatggtgg tgggacagta 60
aatgctacca atggatctga tggcaattac agcgtttcat ggtcaaattg cgggaatttt 120
gttgttggta aaggctggac taccggatca gcaactaggg taataaacta taatgccgga 180
gccttttcgc cgtccggtaa tggatatttg gctctttatg ggtggacgag aaattcactc 240
atagaatatt acgtcgttga tagctggggg acttatagac ctactggaac ttataaaggc 300
actgtgacta gtgatggagg gacttatgac atatacacga ctacacgaac caacgcacct 360
tccattgacg gcaataatac aactttcacc cagttctgga gtgttaggca gtcgaagaga 420
ccgattggta ccaacaatac catcaccttt agcaaccatg ttaacgcctg gaagagtaaa 480
ggaatgaatt tggggagtag ttggtcttat caggtattag caacagaggg ctatcaaagt 540
agtgggtact ctaacgtaac ggtctggtaa 570

<210> 190
<211> 189
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 190
Met Ala Leu Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly
1 5 10 15
Gly Gly Thr Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val
20 25 30
Ser Trp Ser Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr
35 40 45
Gly Ser Ala Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro
50 55 60
Ser Gly Asn Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu
65 70 75 80
Ile Glu Tyr Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly
85 90 95
Thr Tyr Lys Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr
100 105 110
Thr Thr Thr Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr
115 120 125
Phe Thr Gln Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr
130 135 140
Asn Asn Thr Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys
145 150 155 160
Gly Met Asn Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu
165 170 175
Gly Tyr Gln Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 191
<211> 1053
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 191
atgaagtcca ttcgcagccg cagcctcgcc accgccgtcc tggctggcgc cctcggcgtc 60
gcagccgccg gcgcgcaggc gcagacgctc aacaacaatt ccaccggcac gcacgacggc 120
ttctactaca cgttctggaa ggactcgggc agcgcctcga tgaccctcca tccgggcgga 180
cgctacagct cccagtggac cagcaacacc aacaactggg tcggcgggaa aggctggaat 240
cccggtggcc cgcgcgtggt caactactcg ggctactacg ggggtcaacaa cagccagaac 300
tcctacctgg cgctgtacgg ctggacccgc aatccgctgg tcgagtacta cgtgatcgag 360
agctacggct cctacaaccc ggccagttgc gccggcgggg tggactacgg cagcttccag 420
agcgatggcg ccacctacaa cgtacgccgc tgcctgcgcc agaacgcgcc gtcgatcgaa 480
ggcaacaaca gcaccttcta ccagtacttc agcgtgcgca atcccaagaa gggattcggc 540
aacatctccg gcacgatcac cgtcgccaac cacttcaact actgggccag ccgcggcctc 600
aacctcggca accacgacta catggtgttc gccaccgagg gctaccagag ccagggcagc 660
agcgacatca ccgtgagttc gggtaccggc ggcggcggtg gcggcggcaa cacgggcagc 720
aagaccatcg tggtgcgcgc gcgcggcacc gccggcggag agaacatctc gctcaaggtc 780

aacaacgcca ccatcgccag ctggacgctc accaccagca tggccaacta cacggccacc 840
acctcggcat cgggcggctc gctggtggag ttcaccaacg acggcggcaa ccgcgacgtg 900
caggtggact acctcagcgt caatggcgcc gtccgccagg ccgaggacca gacctacaac 960
accggcgtgt accagaacgg ccagtgcggc ggcggcaacg gccgcagcga atggctgcac 1020
tgcaacggtg ccatcggctt cggaaatctc tga 1053

<210> 192
<211> 350
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(27)

<400> 192
Met Lys Ser Ile Arg Ser Arg Ser Leu Ala Thr Ala Val Leu Ala Gly
1 5 10 15
Ala Leu Gly Val Ala Ala Ala Gly Ala Gln Ala Gln Thr Leu Asn Asn
20 25 30
Asn Ser Thr Gly Thr His Asp Gly Phe Tyr Tyr Thr Phe Trp Lys Asp
35 40 45
Ser Gly Ser Ala Ser Met Thr Leu His Pro Gly Gly Arg Tyr Ser Ser
50 55 60
Gln Trp Thr Ser Asn Thr Asn Asn Trp Val Gly Gly Lys Gly Trp Asn
65 70 75 80
Pro Gly Gly Pro Arg Val Val Asn Tyr Ser Gly Tyr Tyr Gly Val Asn
85 90 95
Asn Ser Gln Asn Ser Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Pro
100 105 110
Leu Val Glu Tyr Tyr Val Ile Glu Ser Tyr Gly Ser Tyr Asn Pro Ala
115 120 125
Ser Cys Ala Gly Gly Val Asp Tyr Gly Ser Phe Gln Ser Asp Gly Ala
130 135 140
Thr Tyr Asn Val Arg Arg Cys Leu Arg Gln Asn Ala Pro Ser Ile Glu
145 150 155 160
Gly Asn Asn Ser Thr Phe Tyr Gln Tyr Phe Ser Val Arg Asn Pro Lys
165 170 175
Lys Gly Phe Gly Asn Ile Ser Gly Thr Ile Thr Val Ala Asn His Phe
180 185 190
Asn Tyr Trp Ala Ser Arg Gly Leu Asn Leu Gly Asn His Asp Tyr Met
195 200 205
Val Phe Ala Thr Glu Gly Tyr Gln Ser Gln Gly Ser Ser Asp Ile Thr
210 215 220
Val Ser Ser Gly Thr Gly Gly Gly Gly Gly Gly Gly Asn Thr Gly Ser
225 230 235 240
Lys Thr Ile Val Val Arg Ala Arg Gly Thr Ala Gly Gly Glu Asn Ile
245 250 255
Ser Leu Lys Val Asn Asn Ala Thr Ile Ala Ser Trp Thr Leu Thr Thr
260 265 270
Ser Met Ala Asn Tyr Thr Ala Thr Thr Ser Ala Ser Gly Gly Ser Leu
275 280 285
Val Glu Phe Thr Asn Asp Gly Gly Asn Arg Asp Val Gln Val Asp Tyr
290 295 300
Leu Ser Val Asn Gly Ala Val Arg Gln Ala Glu Asp Gln Thr Tyr Asn
305 310 315 320
Thr Gly Val Tyr Gln Asn Gly Gln Cys Gly Gly Gly Asn Gly Arg Ser
325 330 335
Glu Trp Leu His Cys Asn Gly Ala Ile Gly Phe Gly Asn Leu
340 345 350

<210> 193
<211> 840
<212> DNA
<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 193
atgacgaagt atcggttagg aataggtatt ttcattttgt tggtttgttg cttttcggcg 60
gcatgtattg tgcctaaaca acaagaggaa caaaaagtgg ctcctacaga attgaccggc 120
gcgataacat tcacagccaa cagcaacgga aacaagcccc tgaacggctc gccctacggt 180
tacgaaatat ggacacaggg cgggaccaat aacaaactga tctggttcgg gccggatcag 240
ggcggcggcg cggctttcag agccgaatgg aacaacccta acgatttttt aggccgcgtg 300
ggtttttact ggggtaatgg cggaaaatat accgagtaca aaaatatgta tgcggatttt 360
agctacacta gatctggacg caacaccgcc ggtaattatt catatatagg gatttatggc 420
tgggctagaa atccaaatgc cgcaaaagaa gaagacaaat tgatagagta ttatattgtg 480
gaagattggt ttggcaatca atggcaagag gatagctcac ccattaccac taatacaaca 540
agtggaaccg tattgggaag ttttactata gatggcgcgg tttataatgt cgttagaaat 600
gtcagagtcc aacaaccttc gatagacgga accaaaacat tcacccaata cttcagcata 660
cgacaaacgc cccgacagag cgggacaatt tccattaccg ggcatttcag gcaatgggag 720
agcatgggtt tacagcttgg caatatgtac gaggcaaagt ttcttgttga agccggcggc 780
ggcacaggat ggctggaatt ttcatacctt aaattaacga tggaagacag cttaaggtaa 840

<210> 194
<211> 279
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(21)

<400> 194
Met Thr Lys Tyr Arg Leu Gly Ile Gly Ile Phe Ile Leu Leu Val Cys
1   5   10   15
Cys Phe Ser Ala Ala Cys Ile Val Pro Lys Gln Gln Glu Glu Gln Lys
            20   25   30
Val Ala Pro Thr Glu Leu Thr Gly Ala Ile Thr Phe Thr Ala Asn Ser
        35   40   45
Asn Gly Asn Lys Pro Leu Asn Gly Ser Pro Tyr Gly Tyr Glu Ile Trp
    50   55   60
Thr Gln Gly Gly Thr Asn Asn Lys Leu Ile Trp Phe Gly Pro Asp Gln
65   70   75   80
Gly Gly Gly Ala Ala Phe Arg Ala Glu Trp Asn Asn Pro Asn Asp Phe
                85   90   95
Leu Gly Arg Val Gly Phe Tyr Trp Gly Asn Gly Gly Lys Tyr Thr Glu
            100   105   110
Tyr Lys Asn Met Tyr Ala Asp Phe Ser Tyr Thr Arg Ser Gly Arg Asn
        115   120   125
Thr Ala Gly Asn Tyr Ser Tyr Ile Gly Ile Tyr Gly Trp Ala Arg Asn
    130   135   140
Pro Asn Ala Ala Lys Glu Glu Asp Lys Leu Ile Glu Tyr Tyr Ile Val
145   150   155   160
Glu Asp Trp Phe Gly Asn Gln Trp Gln Glu Asp Ser Ser Pro Ile Thr
                165   170   175
Thr Asn Thr Thr Ser Gly Thr Val Leu Gly Ser Phe Thr Ile Asp Gly
            180   185   190
Ala Val Tyr Asn Val Val Arg Asn Val Arg Val Gln Gln Pro Ser Ile
        195   200   205
Asp Gly Thr Lys Thr Phe Thr Gln Tyr Phe Ser Ile Arg Gln Thr Pro
    210   215   220
Arg Gln Ser Gly Thr Ile Ser Ile Thr Gly His Phe Arg Gln Trp Glu
225   230   235   240
Ser Met Gly Leu Gln Leu Gly Asn Met Tyr Glu Ala Lys Phe Leu Val
                245   250   255
Glu Ala Gly Gly Gly Thr Gly Trp Leu Glu Phe Ser Tyr Leu Lys Leu
            260   265   270
Thr Met Glu Asp Ser Leu Arg
        275

<210> 195
<211> 1044

<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 195
```
atgttcaatc tgaagagagt ggcggcgctc ctgtgcgtcg cagggctggg ggtgtctgcg      60
gcaaatgcgc agacctgtct caattcgagt gggaccggca ccaacaacgg cttctattat     120
tccttctgga aagacagtcc gggttcagtg aatttctgca tgtactccgg cggtcgctac     180
acgtcgagct ggagcggcat caacaactgg gtcggcggca agggctggca aaccggatcg     240
cgccggacca tcaactactc cggcagcttc aactcgccgg gcaatggcta cctcgcgctc     300
tacggatgga ccaccaatcc actcgtcgag tactacatcg tcgacaactg gggcacgtat     360
cgtccgcccg gcggccaggg ctacatgggc acggtcacga gcgacggcgc cacgtacgac     420
gtctatcgaa cgcaacgagt cgatgcgccg tcgatcattg gtgatcacca gaccttctat     480
caatactgga gcgtgcgtca gtcgaagagg accggcggaa ccatcaccac cggcaaccac     540
ttcgatggct gggcgagcta cggcatgaac ctgggaactc acaactacca gatcctggcg     600
accgagggtt atcaaagcag cggcagctcg gacctcaccg tgagcgaagg cagcagcagt     660
agcagcagcg gtggcgggag cagttcgagc agcagcggcg gcggtggcac caagagcttc     720
acggtccgcg cgcgcggcac ggccggtgga gagtcgatca cgttgcgcgt gaataaccag     780
aacgtgcaga cctggacgct cggcacgagc atgacgaact acacggcgtc gacgtcgctg     840
agcggcggca tcaccgtggc gttcacgaac gacggtggca accgcgatgt tcaggtggac     900
tacatcatcg tgaacggcca gacacgccag tcggaagcgc agagctacaa caccgggctc     960
tacgcgaatg gacgttgcgg cggtggctcg aacagcgagt ggatgcactg caacggcgcg    1020
attggctacg gaaacacgcc gtaa                                           1044
```

<210> 196
<211> 347
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(23)

<400> 196
```
Met Phe Asn Leu Lys Arg Val Ala Ala Leu Leu Cys Val Ala Gly Leu
 1               5                  10                  15
Gly Val Ser Ala Ala Asn Ala Gln Thr Cys Leu Asn Ser Ser Gly Thr
            20                  25                  30
Gly Thr Asn Asn Gly Phe Tyr Tyr Ser Phe Trp Lys Asp Ser Pro Gly
        35                  40                  45
Ser Val Asn Phe Cys Met Tyr Ser Gly Gly Arg Tyr Thr Ser Ser Trp
    50                  55                  60
Ser Gly Ile Asn Asn Trp Val Gly Gly Lys Gly Trp Gln Thr Gly Ser
65                  70                  75                  80
Arg Arg Thr Ile Asn Tyr Ser Gly Ser Phe Asn Ser Pro Gly Asn Gly
                85                  90                  95
Tyr Leu Ala Leu Tyr Gly Trp Thr Thr Asn Pro Leu Val Glu Tyr Tyr
            100                 105                 110
Ile Val Asp Asn Trp Gly Thr Tyr Arg Pro Pro Gly Gly Gln Gly Tyr
        115                 120                 125
Met Gly Thr Val Thr Ser Asp Gly Ala Thr Tyr Asp Val Tyr Arg Thr
    130                 135                 140
Gln Arg Val Asp Ala Pro Ser Ile Ile Gly Asp His Gln Thr Phe Tyr
145                 150                 155                 160
Gln Tyr Trp Ser Val Arg Gln Ser Lys Arg Thr Gly Gly Thr Ile Thr
                165                 170                 175
Thr Gly Asn His Phe Asp Gly Trp Ala Ser Tyr Gly Met Asn Leu Gly
            180                 185                 190
Thr His Asn Tyr Gln Ile Leu Ala Thr Glu Gly Tyr Gln Ser Ser Gly
        195                 200                 205
Ser Ser Asp Leu Thr Val Ser Glu Gly Ser Ser Ser Ser Ser Ser Gly
    210                 215                 220
Gly Gly Ser Ser Ser Ser Ser Ser Gly Gly Gly Gly Thr Lys Ser Phe
225                 230                 235                 240
Thr Val Arg Ala Arg Gly Thr Ala Gly Gly Glu Ser Ile Thr Leu Arg
```

```
                245                     250                     255
Val Asn Asn Gln Asn Val Gln Thr Trp Thr Leu Gly Thr Ser Met Thr
            260                     265                     270
Asn Tyr Thr Ala Ser Thr Ser Leu Ser Gly Gly Ile Thr Val Ala Phe
        275                     280                     285
Thr Asn Asp Gly Gly Asn Arg Asp Val Gln Val Asp Tyr Ile Ile Val
    290                     295                     300
Asn Gly Gln Thr Arg Gln Ser Glu Ala Gln Ser Tyr Asn Thr Gly Leu
305                     310                     315                     320
Tyr Ala Asn Gly Arg Cys Gly Gly Gly Ser Asn Ser Glu Trp Met His
                325                     330                     335
Cys Asn Gly Ala Ile Gly Tyr Gly Asn Thr Pro
            340                     345
```

<210> 197
<211> 636
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 197

```
atgtttaagt tcagtaagaa aatgatgacg gttattcttg cagctaccat gagttttggt      60
ttatttgcaa caacctcaag tgcagcaacc gactattggc aaaattggac cgatggcggc     120
ggaacggtta atgctgtaaa cggctccggc ggtaattaca gcgtgacatg gcaaaatacc     180
ggaaattttg tcgtcggcaa aggctggaat accggatcgc ctaaccgaac cattaactac     240
aatgccggcg tctgggcgcc ttccggcaat gggtatttga ctctctacgg atggacgaga     300
aacgcactca ttgaatatta cgtcgtggat agctggggta cttatcggcc tacaggaaca     360
tataaaggga cggtgacaag tgatgggggc acatatgata tctatacgac catgcggcac     420
aacgcgcctt ccattgacgg aactcaaacg tttgcccagt actggagtgt tcgacaatcg     480
aaaagagcga ccggggtcaa ctcctccatt acgttcagca accacgtgaa cgcatgggct     540
agcaagggaa tgaatctggg aagcagctgg tcatatcagg tgttagctac agagggttat     600
caaagtagcg gaagctctaa cgtaacagtg tggtaa                               636
```

<210> 198
<211> 211
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<400> 198

```
Met Phe Lys Phe Ser Lys Lys Met Met Thr Val Ile Leu Ala Ala Thr
1               5                   10                  15
Met Ser Phe Gly Leu Phe Ala Thr Thr Ser Ser Ala Ala Thr Asp Tyr
            20                  25                  30
Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr Val Asn Ala Val Asn Gly
        35                  40                  45
Ser Gly Gly Asn Tyr Ser Val Thr Trp Gln Asn Thr Gly Asn Phe Val
    50                  55                  60
Val Gly Lys Gly Trp Asn Thr Gly Ser Pro Asn Arg Thr Ile Asn Tyr
65                  70                  75                  80
Asn Ala Gly Val Trp Ala Pro Ser Gly Asn Gly Tyr Leu Thr Leu Tyr
                85                  90                  95
Gly Trp Thr Arg Asn Ala Leu Ile Glu Tyr Tyr Val Val Asp Ser Trp
            100                 105                 110
Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys Gly Thr Val Thr Ser Asp
        115                 120                 125
Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Met Arg His Asn Ala Pro Ser
    130                 135                 140
Ile Asp Gly Thr Gln Thr Phe Ala Gln Tyr Trp Ser Val Arg Gln Ser
145                 150                 155                 160
Lys Arg Ala Thr Gly Val Asn Ser Ser Ile Thr Phe Ser Asn His Val
                165                 170                 175
```

```
Asn Ala Trp Ala Ser Lys Gly Met Asn Leu Gly Ser Ser Trp Ser Tyr
            180                 185                 190
Gln Val Leu Ala Thr Glu Gly Tyr Gln Ser Ser Gly Ser Ser Asn Val
        195                 200                 205
Thr Val Trp
    210
```

<210> 199
<211> 1074
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 199

```
atgattttcg gtctaaagtc gatcacgggc aggcgcgccg tcgcggcgct ggcctgcctt      60
gccggcctct acatggcgcc ggcgaatgcg caaacctgca tcacgtcgag ccagacgggc     120
accaacaacg gcaactactt ttcgttctgg aaagacagcc cgggcacggt gaacttctgc     180
atgtactccg gcggccgcta cacgtccaac tggagcggca tcaacaactg ggtgggcggc     240
aagggctggc agacgggctc gtcccgcacc gtctcctact ccggcagctt caattcgccg     300
ggtaacggct acctgacgct ctacggctgg accaccaatc cgctcatcga gtactacatc     360
gtcgacaact ggggcagcta tcgtccgccg ggtggccagg gcttcatggg cacggtgaac     420
accgacggcg gcacgtacga catctatcgc acgcaacggg tcaaccagcc gtcgatcatc     480
ggcaccgcga cgttctacca gtactggagc gtgcggcagt cgaagcgcac cggcggcacc     540
atcaccacgg ccaaccactt caatgcctgg gccagcctcg gcatgaacct gggacagcac     600
aactaccagg tgatggccac cgagggctac cagagcagcg gcagctccga catcacggtg     660
tgggaaggca cgagcagcgg cggaagcagc aatggcggca gcagcaacgg cggcagcagc     720
aatggtggca gcggcggcac gaagagcttc acggtgcgcg cgcgcggcac tgcgggcggc     780
gagtccatca cgctgcgggt caacaaccag aacgtgcaga cctggacgct gggtaccagc     840
atgcagaact acacggcctc gacctcgctg agcggcggca tcacggtggc gttcaccaac     900
gacggcggca gccgcgacgt gcaggtggac tacatcatcg tgaatggcca gacccgccag     960
tccgaacagc agagctacaa cactggcctc tacgccaatg gaagctgtgg tggcggttcg    1020
aacagcgagt ggatgcattg caacggcgcc atcggctacg gcaatacgcc ctga          1074
```

<210> 200
<211> 354
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(30)

<400> 200

```
Met Ile Phe Gly Leu Lys Ser Ile Thr Gly Arg Arg Ala Val Ala Ala
 1               5                  10                  15
Leu Ala Cys Leu Ala Gly Leu Tyr Met Ala Pro Ala Asn Ala Gln Thr
            20                  25                  30
Cys Ile Thr Ser Ser Gln Thr Gly Thr Asn Asn Gly Asn Tyr Phe Ser
        35                  40                  45
Phe Trp Lys Asp Ser Pro Gly Thr Val Asn Phe Cys Met Tyr Ser Gly
    50                  55                  60
Gly Arg Tyr Thr Ser Asn Trp Ser Gly Ile Asn Asn Trp Val Gly Gly
65                  70                  75                  80
Lys Gly Trp Gln Thr Gly Ser Ser Arg Thr Val Ser Tyr Ser Gly Ser
                85                  90                  95
Phe Asn Ser Pro Gly Asn Gly Tyr Leu Thr Leu Tyr Gly Trp Thr Thr
            100                 105                 110
Asn Pro Leu Ile Glu Tyr Tyr Ile Val Asp Asn Trp Gly Ser Tyr Arg
        115                 120                 125
Pro Pro Gly Gly Gln Gly Phe Met Gly Thr Val Asn Thr Asp Gly Gly
    130                 135                 140
Thr Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile
145                 150                 155                 160
Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Gln Ser Lys Arg
                165                 170                 175
```

Thr Gly Gly Thr Ile Thr Thr Ala Asn His Phe Asn Ala Trp Ala Ser
180 185 190
Leu Gly Met Asn Leu Gly Gln His Asn Tyr Gln Val Met Ala Thr Glu
195 200 205
Gly Tyr Gln Ser Ser Gly Ser Ser Asp Ile Thr Val Trp Glu Gly Thr
210 215 220
Ser Ser Gly Gly Ser Ser Asn Gly Gly Ser Ser Asn Gly Gly Ser Ser
225 230 235 240
Asn Gly Gly Ser Gly Gly Thr Lys Ser Phe Thr Val Arg Ala Arg Gly
245 250 255
Thr Ala Gly Gly Glu Ser Ile Thr Leu Arg Val Asn Asn Gln Asn Val
260 265 270
Gln Thr Trp Thr Leu Gly Thr Ser Met Gln Asn Tyr Thr Ala Ser Thr
275 280 285
Ser Leu Ser Gly Gly Ile Thr Val Ala Phe Thr Asn Asp Gly Gly Ser
290 295 300
Arg Asp Val Gln Val Asp Tyr Ile Ile Val Asn Gly Gln Thr Arg Gln
305 310 315 320
Ser Glu Gln Gln Ser Tyr Asn Thr Gly Leu Tyr Ala Asn Gly Ser Cys
325 330 335
Gly Gly Gly Ser Asn Ser Glu Trp Met His Cys Asn Gly Ala Ile Gly
340 345 350
Tyr Gly

<210> 201
<211> 1002
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 201
atgaagatga acagctccct cccctccctc cgcgatgtat tcgcgaatga tttccgcatc 60
ggggcggcgg tcaatcctgt gacgatcgag atgcaaaaac agttgttgat cgatcatgtc 120
aacagtatta cggcagagaa ccatatgaag tttgagcatc ttcagccgga agaagggaaa 180
tttacctttc aggaagcgga tcggattgtg gattttgctt gttcgcaccg aatggcggtt 240
cgagggcaca cacttgtatg gcacaaccag actccggatt gggtgtttca agatggtcaa 300
ggccatttcg tcagtcggga tgtgttgctt gagcggatga aatgtcacat ttcaactgtt 360
gtacggcgat acaagggaaa aatatattgt tgggatgtca tcaacgaagc ggtagccgac 420
gaaggagacg aattgttgag gccgtcgaag tggcgacaaa tcatcgggga cgattttatg 480
gaacaagcat ttctctacgc ttatgaagct gacccagatg cactgctttt ttacaatgac 540
tataatgaat gttttccgga aaagagagaa aaaatttttg cacttgtcaa atcgctgcgt 600
gataaaggca ttccgattca tggcatcggc atgcaggcgc actggagcct gacccgcccg 660
tcgcttgatg aaattcgtgc ggcgattgaa cggtatgcgt cccttggtgt tgttcttcat 720
attacggaac tcgatgtatc catgtttgaa tttcacgatc gtcgaaccga tttggctgtc 780
ccgacgaacg aaatgatcga acagcaagca gaacggtatg ggcaaatttt tgctttgttt 840
aaggagtatc gcgatgttat tcaaagtgtc acattttggg gaattgctga tgaccataca 900
tggctcgata actttccagt gcacgggaga aaaaactggc cgcttttgtt cgatgaacag 960
cataaaccga aaccagcttt ttggcgggca gtgagtgtct ga 1002

<210> 202
<211> 333
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 202
Met Lys Met Asn Ser Ser Leu Pro Ser Leu Arg Asp Val Phe Ala Asn
1 5 10 15
Asp Phe Arg Ile Gly Ala Ala Val Asn Pro Val Thr Ile Glu Met Gln
20 25 30
Lys Gln Leu Leu Ile Asp His Val Asn Ser Ile Thr Ala Glu Asn His
35 40 45
Met Lys Phe Glu His Leu Gln Pro Glu Glu Gly Lys Phe Thr Phe Gln
50 55 60

Glu Ala Asp Arg Ile Val Asp Phe Ala Cys Ser His Arg Met Ala Val
65 70 75 80
Arg Gly His Thr Leu Val Trp His Asn Gln Thr Pro Asp Trp Val Phe
85 90 95
Gln Asp Gly Gln Gly His Phe Val Ser Arg Asp Val Leu Leu Glu Arg
100 105 110
Met Lys Cys His Ile Ser Thr Val Val Arg Arg Tyr Lys Gly Lys Ile
115 120 125
Tyr Cys Trp Asp Val Ile Asn Glu Ala Val Ala Asp Glu Gly Asp Glu
130 135 140
Leu Leu Arg Pro Ser Lys Trp Arg Gln Ile Ile Gly Asp Asp Phe Met
145 150 155 160
Glu Gln Ala Phe Leu Tyr Ala Tyr Glu Ala Asp Pro Asp Ala Leu Leu
165 170 175
Phe Tyr Asn Asp Tyr Asn Glu Cys Phe Pro Glu Lys Arg Glu Lys Ile
180 185 190
Phe Ala Leu Val Lys Ser Leu Arg Asp Lys Gly Ile Pro Ile His Gly
195 200 205
Ile Gly Met Gln Ala His Trp Ser Leu Thr Arg Pro Ser Leu Asp Glu
210 215 220
Ile Arg Ala Ala Ile Glu Arg Tyr Ala Ser Leu Gly Val Val Leu His
225 230 235 240
Ile Thr Glu Leu Asp Val Ser Met Phe Glu Phe His Asp Arg Arg Thr
245 250 255
Asp Leu Ala Val Pro Thr Asn Glu Met Ile Glu Gln Gln Ala Glu Arg
260 265 270
Tyr Gly Gln Ile Phe Ala Leu Phe Lys Glu Tyr Arg Asp Val Ile Gln
275 280 285
Ser Val Thr Phe Trp Gly Ile Ala Asp Asp His Thr Trp Leu Asp Asn
290 295 300
Phe Pro Val His Gly Arg Lys Asn Trp Pro Leu Leu Phe Asp Glu Gln
305 310 315 320
His Lys Pro Lys Pro Ala Phe Trp Arg Ala Val Ser Val
325 330

<210> 203
<211> 687
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 203
atgaaatctg cacgcgcact tttggtggcg ctatcacgca tacttccgat cgcacttgtg 60
ctgttgctcg cccccgtccc cgcgcaagcc caacaggtct gcaacaacgg aacgggcacg 120
cataacggct tcttctggac gttttggaag gacggcggca cggcctgcat gacgctcggc 180
tcgggcggca attatagcac gacgttcaat ctgtccggcg gccgcaacct tgttgcgggc 240
aagggctggc agactggctc caccaaccga gtcgtcggtt acaatgcggg cgtctggaac 300
ccaggcacca attcttatct gacgctctat ggctggtcga cgaatccgct cgtcgaatat 360
tatgtcgtgg accattgggg cagccaattc accccgccag gcaacggcgc gcagagcatg 420
gggaccgtga ccaccgacgg cggcacctac aacatctacc gcacccaacg cgtcaacgcg 480
ccttcgatca tcggcaacgc cacgttctac caatattgga gcgtgcgcac ttcgcgccgc 540
gggcaaggca cgaacaacac gatcaccttc gccaatcacg tcaacgcttg gcgcagccgc 600
ggcatgaacc ttgggaccat gaattatcaa gtcatggcca cggaaggttt cggctcgaac 660
ggaagctcca acctcacagt atggtag 687

<210> 204
<211> 228
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(30)

<400> 204

Met Lys Ser Ala Arg Ala Leu Leu Val Ala Leu Ser Arg Ile Leu Pro
1 5 10 15
Ile Ala Leu Val Leu Leu Leu Ala Pro Val Pro Ala Gln Ala Gln Gln
20 25 30
Val Cys Asn Asn Gly Thr Gly Thr His Asn Gly Phe Phe Trp Thr Phe
35 40 45
Trp Lys Asp Gly Gly Thr Ala Cys Met Thr Leu Gly Ser Gly Gly Asn
50 55 60
Tyr Ser Thr Thr Phe Asn Leu Ser Gly Gly Arg Asn Leu Val Ala Gly
65 70 75 80
Lys Gly Trp Gln Thr Gly Ser Thr Asn Arg Val Val Gly Tyr Asn Ala
85 90 95
Gly Val Trp Asn Pro Gly Thr Asn Ser Tyr Leu Thr Leu Tyr Gly Trp
100 105 110
Ser Thr Asn Pro Leu Val Glu Tyr Tyr Val Val Asp His Trp Gly Ser
115 120 125
Gln Phe Thr Pro Pro Gly Asn Gly Ala Gln Ser Met Gly Thr Val Thr
130 135 140
Thr Asp Gly Gly Thr Tyr Asn Ile Tyr Arg Thr Gln Arg Val Asn Ala
145 150 155 160
Pro Ser Ile Ile Gly Asn Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg
165 170 175
Thr Ser Arg Arg Gly Gln Gly Thr Asn Asn Thr Ile Thr Phe Ala Asn
180 185 190
His Val Asn Ala Trp Arg Ser Arg Gly Met Asn Leu Gly Thr Met Asn
195 200 205
Tyr Gln Val Met Ala Thr Glu Gly Phe Gly Ser Asn Gly Ser Ser Asn
210 215 220
Leu Thr Val Trp
225

<210> 205
<211> 1068
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 205
atgcaaattt tcaaatcacc actgtcatgg gccggatcac tattactgat cctgtccacc 60
gccctgtttt caacagcggc cactgcccag gaatactgct ccaaccagac cggtacacac 120
agcggttttt actttaccca ttggtctgac ggcggcggta ctgcctgcat tactctggga 180
gacgacggaa attacagtta cacctggtcc aacacaggca attttgtcgg tggcaagggc 240
tggagtaccg gcacctccaa tcgggtgatc ggttacaacg ccggagacta ctcgccctcc 300
ggcaactcct acctggcgct gtatggctgg agcaccaatc cactgattga gtactacgtg 360
gtggatagct ggggtagctg gcgtccgccg ggtggcacct cggtaggtac agtcaccagc 420
gatggcggga cttacgacct gtaccgcacc gagcgcgtgc agcagccctc catcgaaggc 480
acggccacct tctatcaata ttggagcgtg cgcacctcac agcgtcccca ggggcagaac 540
aacaccatca cctttcagaa ccacgtggat gcctgggcca atcagggctg gaacctcggc 600
acccacaact atcaggtaat ggcgaccgaa ggctacgaaa gcagcggcag ctccaacgtc 660
acggtttggg attccggcac cagtagcggt aacggtggca acgctggcgg cggtggtggc 720
gaggcaggta acggctccaa ctcactggtc gtgcgtgcgg tgggcacttc gggcaacgaa 780
cagttgcgcg tcaacgtcag cggcaacacg gttgaaaccc tgaacctgtc taccaactgg 840
caggactaca ccatcaacac caacgcttcc ggcgatgtga atgtggagtt gatcaacgat 900
cagggcgagg gctacgaagc ccgggtggaa tacgtcatcg tcaacggcga tacccgctac 960
ggcgctgatc agagctacaa caccagcgcc tggacggcg agtgcggcgg cggttccttt 1020
accatgtgga tgcactgcga aggcatcctc ggttttggcg atatgtaa 1068

<210> 206
<211> 355
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(29)

<400> 206
Met Gln Ile Phe Lys Ser Pro Leu Ser Trp Ala Gly Ser Leu Leu Leu
1   5   10   15
Ile Leu Ser Thr Ala Leu Phe Ser Thr Ala Ala Thr Ala Gln Glu Tyr
            20   25   30
Cys Ser Asn Gln Thr Gly Thr His Ser Gly Phe Tyr Phe Thr His Trp
        35   40   45
Ser Asp Gly Gly Gly Thr Ala Cys Ile Thr Leu Gly Asp Asp Gly Asn
    50   55   60
Tyr Ser Tyr Thr Trp Ser Asn Thr Gly Asn Phe Val Gly Gly Lys Gly
65   70   75   80
Trp Ser Thr Gly Thr Ser Asn Arg Val Ile Gly Tyr Asn Ala Gly Asp
                85   90   95
Tyr Ser Pro Ser Gly Asn Ser Tyr Leu Ala Leu Tyr Gly Trp Ser Thr
            100   105   110
Asn Pro Leu Ile Glu Tyr Tyr Val Val Asp Ser Trp Gly Ser Trp Arg
        115   120   125
Pro Pro Gly Gly Thr Ser Val Gly Thr Val Thr Ser Asp Gly Gly Thr
    130   135   140
Tyr Asp Leu Tyr Arg Thr Glu Arg Val Gln Gln Pro Ser Ile Glu Gly
145   150   155   160
Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Thr Ser Gln Arg Pro
                165   170   175
Gln Gly Gln Asn Asn Thr Ile Thr Phe Gln Asn His Val Asp Ala Trp
            180   185   190
Ala Asn Gln Gly Trp Asn Leu Gly Thr His Asn Tyr Gln Val Met Ala
        195   200   205
Thr Glu Gly Tyr Glu Ser Ser Gly Ser Ser Asn Val Thr Val Trp Asp
    210   215   220
Ser Gly Thr Ser Ser Gly Asn Gly Gly Asn Ala Gly Gly Gly Gly Gly
225   230   235   240
Glu Ala Gly Asn Gly Ser Asn Ser Leu Val Val Arg Ala Val Gly Thr
                245   250   255
Ser Gly Asn Glu Gln Leu Arg Val Asn Val Ser Gly Asn Thr Val Glu
            260   265   270
Thr Leu Asn Leu Ser Thr Asn Trp Gln Asp Tyr Thr Ile Asn Thr Asn
        275   280   285
Ala Ser Gly Asp Val Asn Val Glu Leu Ile Asn Asp Gln Gly Glu Gly
    290   295   300
Tyr Glu Ala Arg Val Glu Tyr Val Ile Val Asn Gly Asp Thr Arg Tyr
305   310   315   320
Gly Ala Asp Gln Ser Tyr Asn Thr Ser Ala Trp Asp Gly Glu Cys Gly
                325   330   335
Gly Gly Ser Phe Thr Met Trp Met His Cys Glu Gly Ile Leu Gly Phe
            340   345   350
Gly Asp Met
        355

<210> 207
<211> 633
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 207
atgaaattaa aaaagaagat gctcacttta ctcctgacgg cttcgatgag tttcggttta 60
tttggggcaa cctcgagtgc agcaacggat tattggcaat attggacgga tggcggcgga 120
acggtgaatg cggttaacgg gtccgggggc aattacagcg taacttggca aaatagcggg 180
aacttcgtgg tcggcaaagg ctggagcgta gggtcgccaa atcggacgat caattacaat 240
gccggcatct gggaaccttc ggggaacggg tacttgaccc tttacggatg gactagaaac 300
tcgctgatcg agtattacgt tgtcgacagt tgggggacgt accggccaac aggtactcac 360
aaaggaacgg tgaacagcga cggaggcacc tacgatattt atacgaccat gcgctataat 420
gcgccttcca ttgatggcac gcagacgttc caacagttct ggagcgtgcg gcaatcgaaa 480
cgaccaaccg gcagcaacgt ctccatcacc ttcagcaatc acgtgaatgc ctggagaagc 540
aagggcatga acctgggcag cagctggtcg taccaggtct tggcgacgga aggctatcag 600
agcagcggaa gatccaacgt cacggtgtgg taa 633

<210> 208
<211> 210
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(27)

<400> 208
Met Lys Leu Lys Lys Lys Met Leu Thr Leu Leu Leu Thr Ala Ser Met
1   5   10   15
Ser Phe Gly Leu Phe Gly Ala Thr Ser Ser Ala Ala Thr Asp Tyr Trp
            20   25   30
Gln Tyr Trp Thr Asp Gly Gly Gly Thr Val Asn Ala Val Asn Gly Ser
        35   40   45
Gly Gly Asn Tyr Ser Val Thr Trp Gln Asn Ser Gly Asn Phe Val Val
    50   55   60
Gly Lys Gly Trp Ser Val Gly Ser Pro Asn Arg Thr Ile Asn Tyr Asn
65   70   75   80
Ala Gly Ile Trp Glu Pro Ser Gly Asn Gly Tyr Leu Thr Leu Tyr Gly
                85   90   95
Trp Thr Arg Asn Ser Leu Ile Glu Tyr Tyr Val Val Asp Ser Trp Gly
            100   105   110
Thr Tyr Arg Pro Thr Gly Thr His Lys Gly Thr Val Asn Ser Asp Gly
        115   120   125
Gly Thr Tyr Asp Ile Tyr Thr Thr Met Arg Tyr Asn Ala Pro Ser Ile
    130   135   140
Asp Gly Thr Gln Thr Phe Gln Gln Phe Trp Ser Val Arg Gln Ser Lys
145   150   155   160
Arg Pro Thr Gly Ser Asn Val Ser Ile Thr Phe Ser Asn His Val Asn
                165   170   175
Ala Trp Arg Ser Lys Gly Met Asn Leu Gly Ser Ser Trp Ser Tyr Gln
            180   185   190
Val Leu Ala Thr Glu Gly Tyr Gln Ser Ser Gly Arg Ser Asn Val Thr
        195   200   205
Val Trp
    210

<210> 209
<211> 1194
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 209
atgaaaacat ttagtgtgac caagtctagc gttgttttcg caatggcttt gggtatggct 60
tcgacagctt ttgctcagga tttctgcagc aatgcgcaac attccggcca aaggtaacg 120
attacttcga accaaactgg taaaatcggc gatatcggtt acgaactctg ggacgaaaac 180
ggtcatggtg gtagtgctac cttctatagc gatggttcca tggactgcaa tatcactggt 240
gctaaggact atctctgccg tgcgggcctt tccctcggca gtaacaagac ctacaaggaa 300
cttggtggtg atatgattgc cgagttcaag cttgtgaaga gcggtgccca gaatgtgggt 360
tactcttata tcggtatcta tggctggatg gaaggtgttt ctggaacgcc tagccagttg 420
gtcgaatact acgtgattga taacaccctc gccaatgaca tgccgggtag ctggattggt 480
aacgaaagaa agggtaccat tacggttgac ggcggtacct atactgttta tcgcaatacc 540
cgtacaggtc cggctattaa gaacagcggt aacgtcacgt tctatcagta tttcagcgtt 600
cgtacctctc cgcgcgattg cggtaccatc aatatttccg aacacatgag acagtgggaa 660
aagatgggca tgaccatggg taagctctac gaagccaagg tgcttggcga agcgggtaac 720
gtgaatggcg aagtccgcgg tggtcacatg gacttcccgc atgctaaggt ttatgtgaaa 780
aacggctctg atccggcttc ttcctcttct gtgaagtcca gctcttctac agtaacgcca 840
aaatccagct cctcgaaggg taacggcaac gtttctggta aaattgacgc ctgcaaggac 900
gctatgggcc atgaaggcaa agaaacgaga actcagggtc agaacaactc tagcgtgacg 960
ggtaacgtcg gcagctctcc gtaccactat gaaatttggt atcagggtgg taacaactcc 1020
atgacgttct acgacaacgg tacttataag gcaagctgga atggtaccaa cgacttcctt 1080

gctcgtgtcg gtttcaagta tgatgaaaag cacacttacg aagaacttgg ccctatcgat 1140
gcctactaca agtggagcaa gcagggtagt gctggtggct acaactacat cggt 1194

<210> 210
<211> 398
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(25)

<400> 210
Met Lys Thr Phe Ser Val Thr Lys Ser Ser Val Val Phe Ala Met Ala
1 5 10 15
Leu Gly Met Ala Ser Thr Ala Phe Ala Gln Asp Phe Cys Ser Asn Ala
20 25 30
Gln His Ser Gly Gln Lys Val Thr Ile Thr Ser Asn Gln Thr Gly Lys
35 40 45
Ile Gly Asp Ile Gly Tyr Glu Leu Trp Asp Glu Asn Gly His Gly Gly
50 55 60
Ser Ala Thr Phe Tyr Ser Asp Gly Ser Met Asp Cys Asn Ile Thr Gly
65 70 75 80
Ala Lys Asp Tyr Leu Cys Arg Ala Gly Leu Ser Leu Gly Ser Asn Lys
85 90 95
Thr Tyr Lys Glu Leu Gly Gly Asp Met Ile Ala Glu Phe Lys Leu Val
100 105 110
Lys Ser Gly Ala Gln Asn Val Gly Tyr Ser Tyr Ile Gly Ile Tyr Gly
115 120 125
Trp Met Glu Gly Val Ser Gly Thr Pro Ser Gln Leu Val Glu Tyr Tyr
130 135 140
Val Ile Asp Asn Thr Leu Ala Asn Asp Met Pro Gly Ser Trp Ile Gly
145 150 155 160
Asn Glu Arg Lys Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Thr Val
165 170 175
Tyr Arg Asn Thr Arg Thr Gly Pro Ala Ile Lys Asn Ser Gly Asn Val
180 185 190
Thr Phe Tyr Gln Tyr Phe Ser Val Arg Thr Ser Pro Arg Asp Cys Gly
195 200 205
Thr Ile Asn Ile Ser Glu His Met Arg Gln Trp Glu Lys Met Gly Met
210 215 220
Thr Met Gly Lys Leu Tyr Glu Ala Lys Val Leu Gly Glu Ala Gly Asn
225 230 235 240
Val Asn Gly Glu Val Arg Gly Gly His Met Asp Phe Pro His Ala Lys
245 250 255
Val Tyr Val Lys Asn Gly Ser Asp Pro Ala Ser Ser Ser Ser Val Lys
260 265 270
Ser Ser Ser Ser Thr Val Thr Pro Lys Ser Ser Ser Ser Lys Gly Asn
275 280 285
Gly Asn Val Ser Gly Lys Ile Asp Ala Cys Lys Asp Ala Met Gly His
290 295 300
Glu Gly Lys Glu Thr Arg Thr Gln Gly Gln Asn Asn Ser Ser Val Thr
305 310 315 320
Gly Asn Val Gly Ser Ser Pro Tyr His Tyr Glu Ile Trp Tyr Gln Gly
325 330 335
Gly Asn Asn Ser Met Thr Phe Tyr Asp Asn Gly Thr Tyr Lys Ala Ser
340 345 350
Trp Asn Gly Thr Asn Asp Phe Leu Ala Arg Val Gly Phe Lys Tyr Asp
355 360 365
Glu Lys His Thr Tyr Glu Glu Leu Gly Pro Ile Asp Ala Tyr Tyr Lys
370 375 380
Trp Ser Lys Gln Gly Ser Ala Gly Gly Tyr Asn Tyr Ile Gly
385 390 395

<210> 211
<211> 1086
<212> DNA

<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 211
atgataagtt ctaaagcatc acagtcatgg ggctggtcac tattggtggc cctgtccgcc 60
gttctgcttt cggcgacagc ttccgcccag caacactgct ccaaccaaac cggtacgcac 120
aacggttttt actttaccca ttggtcagac ggtggcggta ccgcctgcat gactctgggg 180
gacgacggca actacagcta tacctggtcc aacactggca attttgtcgg tggtaagggc 240
tggagcacag gtacatccaa ccgggtgatt ggttacaacg ccggagacta ctcgccctcc 300
ggcaactcct acctggcact gtatggctgg agcaccaatc cgctgattga atattacgtg 360
gtcgacagtt ggggcagctg gcgtccgccg ggtggcacct ctgtgggcac ggtaaccagc 420
gacggtggca cttacgacct gtaccgaacc cagcgtgtgc agcagccctc cattgagggt 480
acggccacct tctatcaata ctggagcgtg cgcacctcac agcggcctca ggggcaaaac 540
aacaccatca cctttcagaa ccacgtgaat gcctgggcca atcagggctg gaatctgggc 600
acccacaact atcaggtgat ggcgaccgaa ggctacgaaa gcagcggcag ctccaacgtc 660
accgtttggg attccggcac cagtagcggt ggcggtggcg gtggcaacgc gggcggcggc 720
ggagcccccg gtggtggtga ggctggaggc ggctccaact cactggttgt gcgtgcggtg 780
ggcacttcgg gcaatgaaca gttgcgcgtc aacgtcagtg gcaacacggt ggaaaccctg 840
aacctgtcta ccaactggca ggactacacc atcaacacca acgcctccgg cgatgtcaat 900
gtggaattga tcaacgacca gggcgaaggc tacgaggccc gcgtcgagta cgtcatcatc 960
aacggcgata cccgctacgg cgccgaccag agctacaaca ccagcgcctg ggacggcgag 1020
tgcggtagcg gttcctttac catgtggatg cactgcgaag gcatcctcgg ttttggcgat 1080
atgtaa 1086

<210> 212
<211> 361
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(29)

<400> 212
Met Ile Ser Ser Lys Ala Ser Gln Ser Trp Gly Trp Ser Leu Leu Val
1 5 10 15
Ala Leu Ser Ala Val Leu Leu Ser Ala Thr Ala Ser Ala Gln Gln His
20 25 30
Cys Ser Asn Gln Thr Gly Thr His Asn Gly Phe Tyr Phe Thr His Trp
35 40 45
Ser Asp Gly Gly Gly Thr Ala Cys Met Thr Leu Gly Asp Asp Gly Asn
50 55 60
Tyr Ser Tyr Thr Trp Ser Asn Thr Gly Asn Phe Val Gly Gly Lys Gly
65 70 75 80
Trp Ser Thr Gly Thr Ser Asn Arg Val Ile Gly Tyr Asn Ala Gly Asp
85 90 95
Tyr Ser Pro Ser Gly Asn Ser Tyr Leu Ala Leu Tyr Gly Trp Ser Thr
100 105 110
Asn Pro Leu Ile Glu Tyr Tyr Val Val Asp Ser Trp Gly Ser Trp Arg
115 120 125
Pro Pro Gly Gly Thr Ser Val Gly Thr Val Thr Ser Asp Gly Gly Thr
130 135 140
Tyr Asp Leu Tyr Arg Thr Gln Arg Val Gln Gln Pro Ser Ile Glu Gly
145 150 155 160
Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Thr Ser Gln Arg Pro
165 170 175
Gln Gly Gln Asn Asn Thr Ile Thr Phe Gln Asn His Val Asn Ala Trp
180 185 190
Ala Asn Gln Gly Trp Asn Leu Gly Thr His Asn Tyr Gln Val Met Ala
195 200 205
Thr Glu Gly Tyr Glu Ser Ser Gly Ser Ser Asn Val Thr Val Trp Asp
210 215 220
Ser Gly Thr Ser Ser Gly Gly Gly Gly Gly Gly Asn Ala Gly Gly Gly
225 230 235 240
Gly Ala Pro Gly Gly Gly Glu Ala Gly Gly Gly Ser Asn Ser Leu Val

```
                        245                 250                 255
Val Arg Ala Val Gly Thr Ser Gly Asn Glu Gln Leu Arg Val Asn Val
            260                 265                 270
Ser Gly Asn Thr Val Glu Thr Leu Asn Leu Ser Thr Asn Trp Gln Asp
        275                 280                 285
Tyr Thr Ile Asn Thr Asn Ala Ser Gly Asp Val Asn Val Glu Leu Ile
    290                 295                 300
Asn Asp Gln Gly Glu Gly Tyr Glu Ala Arg Val Glu Tyr Val Ile Ile
305                 310                 315                 320
Asn Gly Asp Thr Arg Tyr Gly Ala Asp Gln Ser Tyr Asn Thr Ser Ala
                325                 330                 335
Trp Asp Gly Glu Cys Gly Ser Gly Ser Phe Thr Met Trp Met His Cys
            340                 345                 350
Glu Gly Ile Leu Gly Phe Gly Asp Met
        355                 360
```

<210> 213
<211> 912
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 213

```
gtgaacgcac aacaaaccct tacgtctaac tccaccggta ctcatggtgg tcactactat      60
tctttctgga aggactccgg caatgcgtcc ttcactctct acgatggcgg acgttacggc     120
tcgcaatgga atagcggcac caacaattgg gtgggcggta aaggctggaa cccgggcggc     180
gcaaaagtcg ttaactacga aggttattac ggcgttaaca attcccagaa ttcttacctg     240
gcactctacg ggtggacccg caatccgctg atcgagtact acataatcga aagttacggt     300
tcgtacaacc catcgagctg tagtggcggt actaactacg gtagcttcca aagcgatggt     360
gcgacctata acgtccgccg ttgccagcgc gtacagcagc catcgattga tggaacgcaa     420
acgttctatc agtatttcag cgttcgctca cccaaaaagg gcttcggcca aatcagcggc     480
actatcaatg taggcaacca ctttaattat tgggccagca aagggctgaa tttgggtagc     540
cacgattaca tggttctggc gactgaaggc tatcagagca gcggcaattc agatatttcc     600
gtgtccgaag gcagcagcgg cggctcttcc tcaggcggtt cgacctccag cggaagctcc     660
tccggtagta cgaccagttc ttcaggaggc ggtggcggcg gcatcacagt acgtgctcgc     720
ggcactaatg gtgatgagcg tatcagcctg cgtgtcggcg gttctgcggt agccagttgg     780
acactcagta ccagcgcaca aagctatagc tacacaggcg gcgcctctgg cgatatccag     840
gtggaattcg atatcaagct tatcgatacc gtcgacctcg agggggggcc cggtacccaa     900
ttcgccctat ag                                                         912
```

<210> 214
<211> 303
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 214

```
Val Asn Ala Gln Gln Thr Leu Thr Ser Asn Ser Thr Gly Thr His Gly
1               5                   10                  15
Gly His Tyr Tyr Ser Phe Trp Lys Asp Ser Gly Asn Ala Ser Phe Thr
            20                  25                  30
Leu Tyr Asp Gly Gly Arg Tyr Gly Ser Gln Trp Asn Ser Gly Thr Asn
        35                  40                  45
Asn Trp Val Gly Gly Lys Gly Trp Asn Pro Gly Gly Ala Lys Val Val
    50                  55                  60
Asn Tyr Glu Gly Tyr Tyr Gly Val Asn Asn Ser Gln Asn Ser Tyr Leu
65                  70                  75                  80
Ala Leu Tyr Gly Trp Thr Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Ile
                85                  90                  95
Glu Ser Tyr Gly Ser Tyr Asn Pro Ser Ser Cys Ser Gly Gly Thr Asn
            100                 105                 110
Tyr Gly Ser Phe Gln Ser Asp Gly Ala Thr Tyr Asn Val Arg Arg Cys
        115                 120                 125
Gln Arg Val Gln Gln Pro Ser Ile Asp Gly Thr Gln Thr Phe Tyr Gln
    130                 135                 140
```

Tyr Phe Ser Val Arg Ser Pro Lys Lys Gly Phe Gly Gln Ile Ser Gly
145 150 155 160
Thr Ile Asn Val Gly Asn His Phe Asn Tyr Trp Ala Ser Lys Gly Leu
165 170 175
Asn Leu Gly Ser His Asp Tyr Met Val Leu Ala Thr Glu Gly Tyr Gln
180 185 190
Ser Ser Gly Asn Ser Asp Ile Ser Val Ser Glu Gly Ser Ser Gly Gly
195 200 205
Ser Ser Ser Gly Gly Ser Thr Ser Ser Gly Ser Ser Ser Gly Ser Thr
210 215 220
Thr Ser Ser Ser Gly Gly Gly Gly Gly Gly Ile Thr Val Arg Ala Arg
225 230 235 240
Gly Thr Asn Gly Asp Glu Arg Ile Ser Leu Arg Val Gly Gly Ser Ala
245 250 255
Val Ala Ser Trp Thr Leu Ser Thr Ser Ala Gln Ser Tyr Ser Tyr Thr
260 265 270
Gly Gly Ala Ser Gly Asp Ile Gln Val Glu Phe Asp Ile Lys Leu Ile
275 280 285
Asp Thr Val Asp Leu Glu Gly Gly Pro Gly Thr Gln Phe Ala Leu
290 295 300

<210> 215
<211> 1065
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 215
atgtttgcaa gattcgagaa actggccgcg gcgggtaaag ccgtcgtggc cctggcaggg 60
ctcgcccttt tgggcacggc gcctgccaat gcacagacct gtctcacgaa caattccacc 120
ggcaccaaca acggctacta ctactcgttc tggaaggaca gcggcaacgt gaccttctgc 180
atgtacgggg gcggccgcta tacctcgcag tggagcaaca tcaacaactg ggtgggcggc 240
aagggctgga atccgggcgg tcgtcggacc gtcacctatt cggggacgtt caacccgaac 300
ggcaattcct atctcacgct gtacggctgg accaccaatc cactggtcga gtactacatc 360
gtcgacagct ggggcagctg gcgtccgccg ggttccggct acatgggttc cgtcacgagc 420
gacggcggca cctacgacat ctatcgcacg cagcgcgtca accagccctc gatcatcggc 480
accgcgacgt tctaccagta ctggagcgtg cggcagcaga agcgcgtggg tggcaccatc 540
accaccggca accacttcga tgcctgggct tcgctgggca tgaacctcgg ccagcacaac 600
tacatggtca tggccaccga gggctaccag agcagcggca gctccgacat cacggtgggc 660
ggcaccagca gctcctcgtc gtcgagcggg ggcagcagca gcagtagcag cagcagcggg 720
ggtggcggct cgaagagctt caccgtgcgc gcgcggggtt cgacgggcgg tgagcagatc 780
agtttgcgcg tgaacaacca gaccgtgcag aactggacgc tgggcaccag catgcagaac 840
tacaccgcgt ccaccaacct gagcggcggc atcaccgtgc acttcaccaa tgacagcggc 900
aaccgcgacg tgcaggtgga ctacatccag gtgaacggcc agacgcgtca atccgagcag 960
cagagctaca acaccgggct gtatgccaac ggcagctgtg gcggcggcgg ctacagcgag 1020
tggatgcatt gcaatggcgc gatcggttac ggcaacacgc cgtag 1065

<210> 216
<211> 354
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(31)

<400> 216
Met Phe Ala Arg Phe Glu Lys Leu Ala Ala Ala Gly Lys Ala Val Val
1 5 10 15
Ala Leu Ala Gly Leu Ala Leu Leu Gly Thr Ala Pro Ala Asn Ala Gln
20 25 30
Thr Cys Leu Thr Asn Asn Ser Thr Gly Thr Asn Asn Gly Tyr Tyr Tyr
35 40 45
Ser Phe Trp Lys Asp Ser Gly Asn Val Thr Phe Cys Met Tyr Gly Gly
50 55 60

Gly Arg Tyr Thr Ser Gln Trp Ser Asn Ile Asn Asn Trp Val Gly Gly
65 70 75 80
Lys Gly Trp Asn Pro Gly Gly Arg Arg Thr Val Thr Tyr Ser Gly Thr
85 90 95
Phe Asn Pro Asn Gly Asn Ser Tyr Leu Thr Leu Tyr Gly Trp Thr Thr
100 105 110
Asn Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp Gly Ser Trp Arg
115 120 125
Pro Pro Gly Ser Gly Tyr Met Gly Ser Val Thr Ser Asp Gly Gly Thr
130 135 140
Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly
145 150 155 160
Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Gln Gln Lys Arg Val
165 170 175
Gly Gly Thr Ile Thr Thr Gly Asn His Phe Asp Ala Trp Ala Ser Leu
180 185 190
Gly Met Asn Leu Gly Gln His Asn Tyr Met Val Met Ala Thr Glu Gly
195 200 205
Tyr Gln Ser Ser Gly Ser Ser Asp Ile Thr Val Gly Gly Thr Ser Ser
210 215 220
Ser Ser Ser Ser Ser Gly Gly Ser Ser Ser Ser Ser Ser Ser Ser Gly
225 230 235 240
Gly Gly Gly Ser Lys Ser Phe Thr Val Arg Ala Arg Gly Ser Thr Gly
245 250 255
Gly Glu Gln Ile Ser Leu Arg Val Asn Asn Gln Thr Val Gln Asn Trp
260 265 270
Thr Leu Gly Thr Ser Met Gln Asn Tyr Thr Ala Ser Thr Asn Leu Ser
275 280 285
Gly Gly Ile Thr Val His Phe Thr Asn Asp Ser Gly Asn Arg Asp Val
290 295 300
Gln Val Asp Tyr Ile Gln Val Asn Gly Gln Thr Arg Gln Ser Glu Gln
305 310 315 320
Gln Ser Tyr Asn Thr Gly Leu Tyr Ala Asn Gly Ser Cys Gly Gly Gly
325 330 335
Gly Tyr Ser Glu Trp Met His Cys Asn Gly Ala Ile Gly Tyr Gly Asn
340 345 350
Thr Pro

<210> 217
<211> 1083
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 217
atgactttcg tcaagacgat caccggcaga cgcgccatcg cggcgttcct ctgcctcgcc 60
ggcctctaca tggcgccggc aaacgcgcaa acctgcatca cgtccagcca gaccggcacc 120
aacaacggga actacttttc gttctggaaa gacagcccgg gcacggtgaa cttctgcatg 180
tacccgaatg gccgctacac ctcgaactgg agcggcatca acaactgggt cggcggcaag 240
ggctggtcga ccggctccag ccgcaccgtc agctattcgg gcagcttcaa ttcgcccggc 300
aacggctacc tgactctcta cgggtggacc accaacccgc tcatcgagta ctacatcgtc 360
gagaactggg gtaactaccg cccgccgggc ggccaggggt acatggggac cgtcaattcc 420
gacggggcga cctatgacat ctaccggacc ttccgggaca accagccctg catcacgggc 480
aactcctgcg acttctacca gtactggagc gtgcgccagt ccaagcgcag cagcggcacc 540
atcaccacgg ccaatcactt cgcggcgtgg aacagcctcg gcatgaacct gggccagcac 600
aactaccagg tcatggccac cgagggttac cagagcagcg gcagctccga catcacggtc 660
acggaaggcg gcggcggcag cagcaatggt ggcagcagca acggcggcag cagcaatggc 720
ggcagcagca atggcggcgg cggcggcacc aagagcttca cggtccgcgc ccgtggcacc 780
gcgggtggcg agtccatcac gctgcgtgtc aacaaccaga acgtgcagac ctggacgctg 840
ggcaccggca tgcagaacta cacggcctcg acctcgctga gcggtggcat cacggtgcac 900
ttcaccaacg acggcggaag ccgcgacgtg caggtggact acatccaggt gaacggcagc 960
acgcgccagt ccgaggcaca gagctacaac accggcgcct acctgaacgg ccgttgcggc 1020
ggtggcggca acagcgaatg gatgcattgc aacggcgcca tcggctacgg caatacgccc 1080
tga 1083

<210> 218

<211> 360
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(29)

<400> 218
```
Met Thr Phe Val Lys Thr Ile Thr Gly Arg Arg Ala Ile Ala Ala Phe
 1               5                  10                  15
Leu Cys Leu Ala Gly Leu Tyr Met Ala Pro Ala Asn Ala Gln Thr Cys
            20                  25                  30
Ile Thr Ser Ser Gln Thr Gly Thr Asn Asn Gly Asn Tyr Phe Ser Phe
        35                  40                  45
Trp Lys Asp Ser Pro Gly Thr Val Asn Phe Cys Met Tyr Pro Asn Gly
    50                  55                  60
Arg Tyr Thr Ser Asn Trp Ser Gly Ile Asn Asn Trp Val Gly Gly Lys
65                  70                  75                  80
Gly Trp Ser Thr Gly Ser Ser Arg Thr Val Ser Tyr Ser Gly Ser Phe
                85                  90                  95
Asn Ser Pro Gly Asn Gly Tyr Leu Thr Leu Tyr Gly Trp Thr Thr Asn
            100                 105                 110
Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Trp Gly Asn Tyr Arg Pro
        115                 120                 125
Pro Gly Gly Gln Gly Tyr Met Gly Thr Val Asn Ser Asp Gly Ala Thr
    130                 135                 140
Tyr Asp Ile Tyr Arg Thr Phe Arg Asp Asn Gln Pro Cys Ile Thr Gly
145                 150                 155                 160
Asn Ser Cys Asp Phe Tyr Gln Tyr Trp Ser Val Arg Gln Ser Lys Arg
                165                 170                 175
Ser Ser Gly Thr Ile Thr Thr Ala Asn His Phe Ala Ala Trp Asn Ser
            180                 185                 190
Leu Gly Met Asn Leu Gly Gln His Asn Tyr Gln Val Met Ala Thr Glu
        195                 200                 205
Gly Tyr Gln Ser Ser Gly Ser Ser Asp Ile Thr Val Thr Glu Gly Gly
    210                 215                 220
Gly Gly Ser Ser Asn Gly Gly Ser Ser Asn Gly Gly Ser Ser Asn Gly
225                 230                 235                 240
Gly Ser Ser Asn Gly Gly Gly Gly Gly Thr Lys Ser Phe Thr Val Arg
                245                 250                 255
Ala Arg Gly Thr Ala Gly Gly Glu Ser Ile Thr Leu Arg Val Asn Asn
            260                 265                 270
Gln Asn Val Gln Thr Trp Thr Leu Gly Thr Gly Met Gln Asn Tyr Thr
        275                 280                 285
Ala Ser Thr Ser Leu Ser Gly Gly Ile Thr Val His Phe Thr Asn Asp
    290                 295                 300
Gly Gly Ser Arg Asp Val Gln Val Asp Tyr Ile Gln Val Asn Gly Ser
305                 310                 315                 320
Thr Arg Gln Ser Glu Ala Gln Ser Tyr Asn Thr Gly Ala Tyr Leu Asn
                325                 330                 335
Gly Arg Cys Gly Gly Gly Gly Asn Ser Glu Trp Met His Cys Asn Gly
            340                 345                 350
Ala Ile Gly Tyr Gly Asn Thr Pro
        355                 360
```

<210> 219
<211> 1029
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 219
```
atgacatcag gtctcaagaa agtgatggca ttcgtctgtc tcgccaccct tggcgtttcg      60
gcgcatgccc agacatgtat tcagtccagt cagaccggca ccaacaacgg attctatttc     120
```

```
tccttctgga aggacaaccc gggcacggtg cagttctgcc tgcagagcgg cggtcgttac     180
acctccaact ggaacggcat caacaactgg gtgggcggca aggggtggca gaccggcgca     240
cgccgcacgg tgaactactc gggctcgttc aactcgccgg gcaacggcta tctggcgctg     300
tacggctgga ccaccaatcc gctggtcgag tactacatcg tcgacagctg ggcagcttc      360
cgtccgccgg gcaacactgc aggcctgtgg gtactggtga acagcgatgg cggcacctac     420
gacatctatc gcgcgcatcg cagtaacgcg ccctgcatca ccggcagcag ctgcgacttc     480
gaccagtact ggagcgtgcg acagtcgaag cgcgtcggcg gcaccatcac caccggcaac     540
cacttcgatg cctgggcgaa ccaccagatg aatctgggcc agttcaacta ccagatcatg     600
gctaccgagg gtttccagag caacggcagc tccgacatca ccgtcagtga atgcaccagc     660
aattgcggcg gtggcggcgg cggcgggggt ggcagcaaca gcatcacggt gcgcgcgcgc     720
ggcacgggcg gcggcgagca gatccggctg cgggtgaaca acaccacggt gcaaacctgg     780
acgctgacca ccagctacca gaacttcacg gcttcgacct cgctgagcgg cggcaccatc     840
gtcgagtact tcaacgacag ttccggccat gacgtgcagg tcgactacat catcgtgaat     900
ggcgtgaccc gccagtccga atcgcagagc tacaacaccg ggctgtatgc caacgggcgt     960
tgcggcggcg gctccaacag cgagtggatg cattgcaacg gtgccattgg atacggaaat    1020
accccgtaa                                                            1029
```

<210> 220
<211> 342
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(23)

<400> 220

```
Met Thr Ser Gly Leu Lys Lys Val Met Ala Phe Val Cys Leu Ala Thr
 1               5                  10                  15
Leu Gly Val Ser Ala His Ala Gln Thr Cys Ile Gln Ser Ser Gln Thr
            20                  25                  30
Gly Thr Asn Asn Gly Phe Tyr Phe Ser Phe Trp Lys Asp Asn Pro Gly
        35                  40                  45
Thr Val Gln Phe Cys Leu Gln Ser Gly Gly Arg Tyr Thr Ser Asn Trp
    50                  55                  60
Asn Gly Ile Asn Asn Trp Val Gly Gly Lys Gly Trp Gln Thr Gly Ala
65                  70                  75                  80
Arg Arg Thr Val Asn Tyr Ser Gly Ser Phe Asn Ser Pro Gly Asn Gly
                85                  90                  95
Tyr Leu Ala Leu Tyr Gly Trp Thr Thr Asn Pro Leu Val Glu Tyr Tyr
            100                 105                 110
Ile Val Asp Ser Trp Gly Ser Phe Arg Pro Pro Gly Asn Thr Ala Gly
        115                 120                 125
Leu Trp Val Leu Val Asn Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Arg
    130                 135                 140
Ala His Arg Ser Asn Ala Pro Cys Ile Thr Gly Ser Ser Cys Asp Phe
145                 150                 155                 160
Asp Gln Tyr Trp Ser Val Arg Gln Ser Lys Arg Val Gly Gly Thr Ile
                165                 170                 175
Thr Thr Gly Asn His Phe Asp Ala Trp Ala Asn His Gln Met Asn Leu
            180                 185                 190
Gly Gln Phe Asn Tyr Gln Ile Met Ala Thr Glu Gly Phe Gln Ser Asn
        195                 200                 205
Gly Ser Ser Asp Ile Thr Val Ser Glu Cys Thr Ser Asn Cys Gly Gly
    210                 215                 220
Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ile Thr Val Arg Ala Arg
225                 230                 235                 240
Gly Thr Gly Gly Gly Glu Gln Ile Arg Leu Arg Val Asn Asn Thr Thr
                245                 250                 255
Val Gln Thr Trp Thr Leu Thr Thr Ser Tyr Gln Asn Phe Thr Ala Ser
            260                 265                 270
Thr Ser Leu Ser Gly Gly Thr Ile Val Glu Tyr Phe Asn Asp Ser Ser
        275                 280                 285
Gly His Asp Val Gln Val Asp Tyr Ile Ile Val Asn Gly Val Thr Arg
    290                 295                 300
Gln Ser Glu Ser Gln Ser Tyr Asn Thr Gly Leu Tyr Ala Asn Gly Arg
305                 310                 315                 320
```

Cys Gly Gly Gly Ser Asn Ser Glu Trp Met His Cys Asn Gly Ala Ile
325 330 335
Gly Tyr Gly Asn Thr Pro
340

<210> 221
<211> 1044
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 221
atgattgtta gtttcaagag cgtgaaggca ctcgcgtgcc tggccgtgct cggcgtgacc 60
gccgcgcagg cgcaaacctg catcaattcc agccagaccg gcaccaacaa cggcaattat 120
ttttcattct ggaaagacaa cccgggcacg gtgaccttct gcatgtatgc caacggccgc 180
tacacctcca actggagcgg catcaacaac tgggtgggtg gcaagggctg gcagaccggc 240
tcgaatcgca cggtgaccta ctccggttcg ttcaactcgc ccggcaacgg ctacctcacc 300
ctgtacgggt ggaccacgaa tccgctgatc gagtactaca tcgtcgacag ttggggcagt 360
tatcgaccgc ccggcggcca gggcttcatg ggcaccgtga cgaccgacgg cggcacctac 420
gacatctatc gcacgcagcg cgtgaaccag ccttccatca tcggcaccgc gacgttctac 480
cagtactgga gcgtgcggca gtcgaagcgc gtgggggca ccatcaccac cgccaaccac 540
ttcaatgcct gggcgacgct gggcatgaac ctgggccagc acaactacca ggtcatggcc 600
accgagggtt accagagcag cggcagctcc gacatcaccg tgaccgaagg cggcggcagc 660
tcgtcgtcgt cgagcggcgg cggcagcacc agcagcggcg gtggcggcag caagagcttc 720
acggtgcgcg cccgcggcac ggtcggcggc gaaaacatcc agctgcaggt caacaaccag 780
acggtggcga gctggaacct gaccaccagc atgcagaact acaacgcctc gaccagcctg 840
agtggcggca tcaccgtggt ctacaccaac gacggcggta accgcgacgt ccaggtcgac 900
tacatcaccg tgaacggcca gacccgccag tccgaagcgc agagtttcaa caccgggctg 960
tatgccaacg gacgttgtgg cggcggctcg aacagcgagt ggatgcattg caatggcgcg 1020
atcggctacg gcaacacgcc gtaa 1044

<210> 222
<211> 347
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(24)

<400> 222
Met Ile Val Ser Phe Lys Ser Val Lys Ala Leu Ala Cys Leu Ala Val
1 5 10 15
Leu Gly Val Thr Ala Ala Gln Ala Gln Thr Cys Ile Asn Ser Ser Gln
20 25 30
Thr Gly Thr Asn Asn Gly Asn Tyr Phe Ser Phe Trp Lys Asp Asn Pro
35 40 45
Gly Thr Val Thr Phe Cys Met Tyr Ala Asn Gly Arg Tyr Thr Ser Asn
50 55 60
Trp Ser Gly Ile Asn Asn Trp Val Gly Gly Lys Gly Trp Gln Thr Gly
65 70 75 80
Ser Asn Arg Thr Val Thr Tyr Ser Gly Ser Phe Asn Ser Pro Gly Asn
85 90 95
Gly Tyr Leu Thr Leu Tyr Gly Trp Thr Thr Asn Pro Leu Ile Glu Tyr
100 105 110
Tyr Ile Val Asp Ser Trp Gly Ser Tyr Arg Pro Pro Gly Gly Gln Gly
115 120 125
Phe Met Gly Thr Val Thr Thr Asp Gly Gly Thr Tyr Asp Ile Tyr Arg
130 135 140
Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly Thr Ala Thr Phe Tyr
145 150 155 160
Gln Tyr Trp Ser Val Arg Gln Ser Lys Arg Val Gly Gly Thr Ile Thr
165 170 175
Thr Ala Asn His Phe Asn Ala Trp Ala Thr Leu Gly Met Asn Leu Gly
180 185 190

Gln His Asn Tyr Gln Val Met Ala Thr Glu Gly Tyr Gln Ser Ser Gly
195 200 205
Ser Ser Asp Ile Thr Val Thr Glu Gly Gly Gly Ser Ser Ser Ser Ser
210 215 220
Ser Gly Gly Gly Ser Thr Ser Ser Gly Gly Gly Gly Ser Lys Ser Phe
225 230 235 240
Thr Val Arg Ala Arg Gly Thr Val Gly Gly Glu Asn Ile Gln Leu Gln
245 250 255
Val Asn Asn Gln Thr Val Ala Ser Trp Asn Leu Thr Thr Ser Met Gln
260 265 270
Asn Tyr Asn Ala Ser Thr Ser Leu Ser Gly Gly Ile Thr Val Val Tyr
275 280 285
Thr Asn Asp Gly Gly Asn Arg Asp Val Gln Val Asp Tyr Ile Thr Val
290 295 300
Asn Gly Gln Thr Arg Gln Ser Glu Ala Gln Ser Phe Asn Thr Gly Leu
305 310 315 320
Tyr Ala Asn Gly Arg Cys Gly Gly Gly Ser Asn Ser Glu Trp Met His
325 330 335
Cys Asn Gly Ala Ile Gly Tyr Gly Asn Thr Pro
340 345

<210> 223
<211> 642
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 223
atgtttaagt ttaaaaagaa tttcttagtt ggattatcgg cagctttaat gagtattagc 60
ttgttttcgg caaccgcctc tgcagctagc acagactact ggcaaaattg gactgatggg 120
ggcggtatag taaacgctgt caatgggtct ggcgggaatt acagtgttaa ttggtctaat 180
accggaaatt tcgttgttgg taaaggttgg actacaggtt cgccatttag gacgataaac 240
tataatgccg gagtttgggc accgaatgga aatggatatt taactttata tggttggacg 300
agatcacctc tcatagaata ttatgtagtg gattcatggg gtacttatag acctactgga 360
acgtataaag gtactgtaaa aagtgatggg ggtacatatg acatatatac aactacacgt 420
tataacgcac cttccattga tggcgatcgc actactttta cgcagtactg gagtgttcgc 480
caaacgaaga gaccaaccgg aagcaacgct acaatcactt tcagcaatca tgttaacgca 540
tggaagagcc atggaatgaa tctgggcagt aattgggctt accaagtcat ggcgacagaa 600
ggatatcaaa gtagtggaag ttctaacgta acagtgtggt aa 642

<210> 224
<211> 213
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<400> 224
Met Phe Lys Phe Lys Lys Asn Phe Leu Val Gly Leu Ser Ala Ala Leu
1 5 10 15
Met Ser Ile Ser Leu Phe Ser Ala Thr Ala Ser Ala Ala Ser Thr Asp
20 25 30
Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Ile Val Asn Ala Val Asn
35 40 45
Gly Ser Gly Gly Asn Tyr Ser Val Asn Trp Ser Asn Thr Gly Asn Phe
50 55 60
Val Val Gly Lys Gly Trp Thr Thr Gly Ser Pro Phe Arg Thr Ile Asn
65 70 75 80
Tyr Asn Ala Gly Val Trp Ala Pro Asn Gly Asn Gly Tyr Leu Thr Leu
85 90 95
Tyr Gly Trp Thr Arg Ser Pro Leu Ile Glu Tyr Tyr Val Val Asp Ser
100 105 110
Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys Gly Thr Val Lys Ser

115 120 125
Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr Arg Tyr Asn Ala Pro
130 135 140
Ser Ile Asp Gly Asp Arg Thr Thr Phe Thr Gln Tyr Trp Ser Val Arg
145 150 155 160
Gln Thr Lys Arg Pro Thr Gly Ser Asn Ala Thr Ile Thr Phe Ser Asn
165 170 175
His Val Asn Ala Trp Lys Ser His Gly Met Asn Leu Gly Ser Asn Trp
180 185 190
Ala Tyr Gln Val Met Ala Thr Glu Gly Tyr Gln Ser Ser Gly Ser Ser
195 200 205
Asn Val Thr Val Trp
210

<210> 225
<211> 1059
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 225
atgtttgtta gtctcaggaa gacggcttgg gcgtgcctgt tgctcgccgg cctcggaatc 60
tcgacttcac aagcccagac ctgcatcacg tccagcggga cgggcaccaa caacggccac 120
tactattcct tctggaagga cagtggcggc accgtcaact tctgcatgta cgcgaacggc 180
cgctacacct ccaactggag cggcatcaac aactgggtgg gcggcaaggg ctggcagacc 240
ggctcacgcc ggacgatcag ctactcgggc tcgttcaact cacccggcaa tggttatctc 300
accctgtacg gttggaccac caatccattg atcgagtact acatcgtcga caactggggc 360
acgtaccggc cgccgggagg ctcgggctac atgggcacgg tgacgagcga cggcggcacc 420
tacgacgtct atcgcaccca gcgcgtaaac cagccttcca tcatcggcac cgcgacgttc 480
tatcaatact ggagcgtgcg ccagcagaag cggaccggcg ggaccatcac caccggcaat 540
cacttcgacg cctgggccgc atacggaatg aacctcggca cccacaacta ccagatcatg 600
gcgaccgagg gttaccagag cagcggcagt tcggacatca cggtgagcga gggcggtggc 660
agttcatcga gcagcagctc gtcgagcagc agcagttcgt cctcttcgag cggcggcggc 720
ggcacgaaga gcttcacggt ccgcgcgcgc ggcacggcgg gcggtgaatc catcacgctg 780
cgcgtgaaca accagaacgt gcagacctgg acgctgggca cgtcgatgca gaactacacc 840
gcatcgacca cgctctccgg tggcatcacc gtcgcgtaca ccaacgacag cggcaatcgc 900
gacgtgcagg tggactacat cgtcgtgaac ggcgccaccc gccagtccga ggcgcagagc 960
tacaacaccg gtctctatgc caacggtcgt tgcggcggcg gctccaacag cgagtggatg 1020
cactgcaacg ggcagatcgg ctacgggaat actccctag 1059

<210> 226
<211> 352
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(25)

<400> 226
Met Phe Val Ser Leu Arg Lys Thr Ala Trp Ala Cys Leu Leu Leu Ala
1 5 10 15
Gly Leu Gly Ile Ser Thr Ser Gln Ala Gln Thr Cys Ile Thr Ser Ser
20 25 30
Gly Thr Gly Thr Asn Asn Gly His Tyr Tyr Ser Phe Trp Lys Asp Ser
35 40 45
Gly Gly Thr Val Asn Phe Cys Met Tyr Ala Asn Gly Arg Tyr Thr Ser
50 55 60
Asn Trp Ser Gly Ile Asn Asn Trp Val Gly Gly Lys Gly Trp Gln Thr
65 70 75 80
Gly Ser Arg Arg Thr Ile Ser Tyr Ser Gly Ser Phe Asn Ser Pro Gly
85 90 95
Asn Gly Tyr Leu Thr Leu Tyr Gly Trp Thr Thr Asn Pro Leu Ile Glu
100 105 110
Tyr Tyr Ile Val Asp Asn Trp Gly Thr Tyr Arg Pro Pro Gly Gly Ser

115 120 125
Gly Tyr Met Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Val Tyr
130 135 140
Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly Thr Ala Thr Phe
145 150 155 160
Tyr Gln Tyr Trp Ser Val Arg Gln Gln Lys Arg Thr Gly Gly Thr Ile
165 170 175
Thr Thr Gly Asn His Phe Asp Ala Trp Ala Ala Tyr Gly Met Asn Leu
180 185 190
Gly Thr His Asn Tyr Gln Ile Met Ala Thr Glu Gly Tyr Gln Ser Ser
195 200 205
Gly Ser Ser Asp Ile Thr Val Ser Glu Gly Gly Gly Ser Ser Ser Ser
210 215 220
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Gly Gly Gly
225 230 235 240
Gly Thr Lys Ser Phe Thr Val Arg Ala Arg Gly Thr Ala Gly Gly Glu
245 250 255
Ser Ile Thr Leu Arg Val Asn Asn Gln Asn Val Gln Thr Trp Thr Leu
260 265 270
Gly Thr Ser Met Gln Asn Tyr Thr Ala Ser Thr Thr Leu Ser Gly Gly
275 280 285
Ile Thr Val Ala Tyr Thr Asn Asp Ser Gly Asn Arg Asp Val Gln Val
290 295 300
Asp Tyr Ile Val Val Asn Gly Ala Thr Arg Gln Ser Glu Ala Gln Ser
305 310 315 320
Tyr Asn Thr Gly Leu Tyr Ala Asn Gly Arg Cys Gly Gly Gly Ser Asn
325 330 335
Ser Glu Trp Met His Cys Asn Gly Gln Ile Gly Tyr Gly Asn Thr Pro
340 345 350

<210> 227
<211> 747
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 227
atgggcggca cgactggtag tggcggctca gccgccgccg gcgcaggcac gagtggaagc 60
gcgggcggta ccgccggagc gctcggcccc ggcggtaccc agggcagcgg tggcgcagcc 120
ggtggtacga gcggaacggg cggggccatc agcagcagct gcacggaagc tgacaagacg 180
gtctgcaaca acgaaaccgg tcgccactgc aattacacgt acgagtattg gaaggaccag 240
ggaagcggtt gcctcgtgaa caaagccgac ggcttcagcg tcaactggaa caacatcaac 300
aatctgctgg gtcgcaaggg tctgaggccc ggatcgtcga atcagacggt gacctaccag 360
gcaaactacc agccgaacgg caattcatac ctgtgcgtat atggatggac gcaaaacccc 420
ctcgtcgaat actacatcgt cgatagctgg ggcagctggc gcccgccggg gggaacgtcc 480
atgggcaccg tcaacgcgga cggcggcacc tacgacatct accgcaccca gcgcgtcaac 540
cagccttcca tcgaaggcac caagaccttc tatcaatact ggagcgttcg cactcagaag 600
cgcacgagcg gaacgatcac ggttgccgct cacttcgacg cctgggcgac gaaggggatg 660
aacatgggga gtctgtacga ggtgtcgatg accgtcgagg gctatcaaag cagcgggacc 720
gccgacgtga gcttctcgat gaagtga 747

<210> 228
<211> 248
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(39)

<400> 228
Met Gly Gly Thr Thr Gly Ser Gly Gly Ser Ala Ala Ala Gly Ala Gly
1 5 10 15
Thr Ser Gly Ser Ala Gly Gly Thr Ala Gly Ala Leu Gly Pro Gly Gly
20 25 30

Thr Gln Gly Ser Gly Gly Ala Ala Gly Gly Thr Ser Gly Thr Gly Gly
35 40 45
Ala Ile Ser Ser Ser Cys Thr Glu Ala Asp Lys Thr Val Cys Asn Asn
50 55 60
Glu Thr Gly Arg His Cys Asn Tyr Thr Tyr Glu Tyr Trp Lys Asp Gln
65 70 75 80
Gly Ser Gly Cys Leu Val Asn Lys Ala Asp Gly Phe Ser Val Asn Trp
85 90 95
Asn Asn Ile Asn Asn Leu Leu Gly Arg Lys Gly Leu Arg Pro Gly Ser
100 105 110
Ser Asn Gln Thr Val Thr Tyr Gln Ala Asn Tyr Gln Pro Asn Gly Asn
115 120 125
Ser Tyr Leu Cys Val Tyr Gly Trp Thr Gln Asn Pro Leu Val Glu Tyr
130 135 140
Tyr Ile Val Asp Ser Trp Gly Ser Trp Arg Pro Pro Gly Gly Thr Ser
145 150 155 160
Met Gly Thr Val Asn Ala Asp Gly Gly Thr Tyr Asp Ile Tyr Arg Thr
165 170 175
Gln Arg Val Asn Gln Pro Ser Ile Glu Gly Thr Lys Thr Phe Tyr Gln
180 185 190
Tyr Trp Ser Val Arg Thr Gln Lys Arg Thr Ser Gly Thr Ile Thr Val
195 200 205
Ala Ala His Phe Asp Ala Trp Ala Thr Lys Gly Met Asn Met Gly Ser
210 215 220
Leu Tyr Glu Val Ser Met Thr Val Glu Gly Tyr Gln Ser Ser Gly Thr
225 230 235 240
Ala Asp Val Ser Phe Ser Met Lys
245

<210> 229
<211> 642
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 229
atgtttaagt ttacaaagaa attcttagtt gggttaacgg cagctttgat gagtattagc 60
ttgttttcgg caaacgcctc tgcagctaac acagactact ggcaaaattg gactgatggg 120
ggcggaacag taaacgctgt caatgggtct ggcgggaatt acagtgtgaa ttggtctaat 180
accgggaatt tcgttgttgg taaaggttgg actacaggtt cgccatttag gacgataaac 240
tataatgccg gagtttgggc gccgaatggc aatgcatatt tgactttata tggttggacg 300
cgatcacccc tcatagaata ttatgtagtg gattcatggg gtacttatag acctactgga 360
acgtataaag gtacggttta cagtgatggg ggtacatatg acgtgtacac aactacacgt 420
tatgatgcac cttccattga tggcgataaa actactttta cgcagtactg gagtgttcgc 480
cagtcgaaga gaccaactgg aagcaacgct acaatcactt tcagcaatca cgttaacgca 540
tggaagagat atgggatgaa tctgggtagt aattggtctt accaagtctt agcgacagag 600
ggatatcaaa gtagtggaag ttctaacgta acagtgtggt aa 642

<210> 230
<211> 213
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<400> 230
Met Phe Lys Phe Thr Lys Lys Phe Leu Val Gly Leu Thr Ala Ala Leu
1 5 10 15
Met Ser Ile Ser Leu Phe Ser Ala Asn Ala Ser Ala Ala Asn Thr Asp
20 25 30
Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr Val Asn Ala Val Asn
35 40 45
Gly Ser Gly Gly Asn Tyr Ser Val Asn Trp Ser Asn Thr Gly Asn Phe

```
    50                  55                  60
Val Val Gly Lys Gly Trp Thr Thr Gly Ser Pro Phe Arg Thr Ile Asn
65                  70                  75                  80
Tyr Asn Ala Gly Val Trp Ala Pro Asn Gly Asn Ala Tyr Leu Thr Leu
                85                  90                  95
Tyr Gly Trp Thr Arg Ser Pro Leu Ile Glu Tyr Tyr Val Val Asp Ser
            100                 105                 110
Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys Gly Thr Val Tyr Ser
        115                 120                 125
Asp Gly Gly Thr Tyr Asp Val Tyr Thr Thr Thr Arg Tyr Asp Ala Pro
    130                 135                 140
Ser Ile Asp Gly Asp Lys Thr Thr Phe Thr Gln Tyr Trp Ser Val Arg
145                 150                 155                 160
Gln Ser Lys Arg Pro Thr Gly Ser Asn Ala Thr Ile Thr Phe Ser Asn
                165                 170                 175
His Val Asn Ala Trp Lys Arg Tyr Gly Met Asn Leu Gly Ser Asn Trp
            180                 185                 190
Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln Ser Ser Gly Ser Ser
        195                 200                 205
Asn Val Thr Val Trp
    210
```

<210> 231
<211> 1008
<212> DNA
<213> Bacteria

<400> 231
```
atgaacctgc tcgtccagcc gaggcgtcgc agacgcggtc cggtcacctt gctcgtcagg      60
agcgcgtggg ccgtcgcgct ggcggcgctc gccgcgctga tgctgccggg caccgcccag     120
gccgacacgg tcgtcacgac caaccaggag ggcaccaaca acggctacta ctactcgttc     180
tggaccgaca gccagggcac cgtctccatg aacatgggct ccggcggtca gtacagcacc     240
tcgtggcgca acaccggcaa cttcgtcgcg ggcaagggct gggccaacgg cggccgccgg     300
accgtgcagt actcgggcag cttcaacccc tccggcaacg cgtacctggc gctctacgga     360
tggacgtcga acccgctcgt cgagtactac atcgtcgaca actggggcac ctaccggccc     420
acgggcgagt acaagggcac cgtcaccagc gacggcggca cctacgacat ctacaagacg     480
acccgcgtca acaagccctc cgtcgagggc acccgcacct tcgaccagta ctggagcgtc     540
cggcaggcga agcggaccgg cggcaccatc acgaccggca accacttcga cgcgtggcc      600
cgggccggga tgccgctcgg caacttcagc tactacatga tcatggccac cgagggctac     660
cagagcagcg gcagctccag catcaacgtc ggcgggaccg gccgcggcga caacggcggc     720
ggcgacaacg gggcggtgg cggcgggtgc accgccacgg tgtccgccgg gcagaagtgg      780
ggcgaccggt acaacctcga cgtctccgtc agcggcgcca gcgactggac ggtgacgatg     840
aacgtgccgt ccccggcgaa ggtcctgtcg acctggaacg tcaacgccag ctatcccagt     900
gcgcagacgc tgaccgccag gtcgaacggc agcggcaaca actggggcgc caccatccag     960
gccaacggca actggacctg gcccagcgtg tcctgcagcg cgggctga                 1008
```

<210> 232
<211> 335
<212> PRT
<213> Bacteria

<220>
<221> SIGNAL
<222> (1)...(41)

<400> 232
```
Met Asn Leu Leu Val Gln Pro Arg Arg Arg Arg Arg Gly Pro Val Thr
 1               5                  10                  15
Leu Leu Val Arg Ser Ala Trp Ala Val Ala Leu Ala Ala Leu Ala Ala
            20                  25                  30
Leu Met Leu Pro Gly Thr Ala Gln Ala Asp Thr Val Val Thr Thr Asn
        35                  40                  45
Gln Glu Gly Thr Asn Asn Gly Tyr Tyr Tyr Ser Phe Trp Thr Asp Ser
    50                  55                  60
Gln Gly Thr Val Ser Met Asn Met Gly Ser Gly Gly Gln Tyr Ser Thr
65                  70                  75                  80
Ser Trp Arg Asn Thr Gly Asn Phe Val Ala Gly Lys Gly Trp Ala Asn
                85                  90                  95
Gly Gly Arg Arg Thr Val Gln Tyr Ser Gly Ser Phe Asn Pro Ser Gly
```

```
                100                 105                 110
Asn Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Ser Asn Pro Leu Val Glu
            115                 120                 125
Tyr Tyr Ile Val Asp Asn Trp Gly Thr Tyr Arg Pro Thr Gly Glu Tyr
    130                 135                 140
Lys Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Lys Thr
145                 150                 155                 160
Thr Arg Val Asn Lys Pro Ser Val Glu Gly Thr Arg Thr Phe Asp Gln
                165                 170                 175
Tyr Trp Ser Val Arg Gln Ala Lys Arg Thr Gly Gly Thr Ile Thr Thr
            180                 185                 190
Gly Asn His Phe Asp Ala Trp Ala Arg Ala Gly Met Pro Leu Gly Asn
        195                 200                 205
Phe Ser Tyr Tyr Met Ile Met Ala Thr Glu Gly Tyr Gln Ser Ser Gly
    210                 215                 220
Ser Ser Ser Ile Asn Val Gly Gly Thr Gly Arg Gly Asp Asn Gly Gly
225                 230                 235                 240
Gly Asp Asn Gly Gly Gly Gly Gly Gly Cys Thr Ala Thr Val Ser Ala
                245                 250                 255
Gly Gln Lys Trp Gly Asp Arg Tyr Asn Leu Asp Val Ser Val Ser Gly
            260                 265                 270
Ala Ser Asp Trp Thr Val Thr Met Asn Val Pro Ser Pro Ala Lys Val
        275                 280                 285
Leu Ser Thr Trp Asn Val Asn Ala Ser Tyr Pro Ser Ala Gln Thr Leu
    290                 295                 300
Thr Ala Arg Ser Asn Gly Ser Gly Asn Asn Trp Gly Ala Thr Ile Gln
305                 310                 315                 320
Ala Asn Gly Asn Trp Thr Trp Pro Ser Val Ser Cys Ser Ala Gly
                325                 330                 335
```

<210> 233
<211> 1071
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 233

```
atgtctatgt ttttgagtct caaaagagtg gcggcgctcg tctgcgtcgc agggtttggc    60
atttcggcgg cgaacgctca gtgcgtcact tcgagccaga caggaaccaa caacgggttc   120
tatttttcgt tctggaaaga tagtccggga accgtgaatt tctgcaacca gagcggtggc   180
cgctacacat ccaattggag cggtatcaac aactgggtcg gtggcaaggg ttggcagacc   240
ggctcgcgaa gggtcgtgag ctactccggt tcgttcaatt cgccgggcaa cgggtatctg   300
accctctatg ggtggaccac caatccgctc atcgagtact acatcgtcga caactggggc   360
tcgtatcgcc cgccgggcgg acaggggttc atgggcacgg tgaccagcga cggcggcacg   420
tacgatgtct accgcacaca gcgcgtcaat caaccctgca tcaccggcag cagttgcacc   480
ttctatcaat actggagcgt gcggcagtcg aagagaacgg gcggcacgat cacgacgggc   540
aatcactttg acgcgtgggc gagttacggc atgaacctgg gcgctcacaa ctaccagatc   600
atggcgaccg agggttatca aagcagcggg agctctgaca tcacggtcag tgaaggcagc   660
agcagtagca gcagtagcag cagttcgagc agtagctcga gcagcagctc cagcagcagc   720
agcggcggcg gtggcaccaa gagcttcacg gtccgcgcgc gcggcgtggc cggcggggaa   780
tccatcacgt tgcgcgtgaa caatcagaac gtgcagacct ggactctcgg caccggcatg   840
cagaactaca cggcgtcgac gtctttgagt ggcggcatca cggttgcgta taccaacgat   900
ggcggcagtc gcgacgtgca ggttgactac atcatcgtga acggccagac gcgtcagtcg   960
gaagcgcaga gctacaacac cggctttat gccaacggcc gttgcggtgg cggcggcaac   1020
agcgaatgga tgcattgcaa tggcgccatt ggctacggga acacgccgta g            1071
```

<210> 234
<211> 356
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(26)

<400> 234
Met Ser Met Phe Leu Ser Leu Lys Arg Val Ala Ala Leu Val Cys Val
1 5 10 15
Ala Gly Phe Gly Ile Ser Ala Ala Asn Ala Gln Cys Val Thr Ser Ser
20 25 30
Gln Thr Gly Thr Asn Asn Gly Phe Tyr Phe Ser Phe Trp Lys Asp Ser
35 40 45
Pro Gly Thr Val Asn Phe Cys Asn Gln Ser Gly Gly Arg Tyr Thr Ser
50 55 60
Asn Trp Ser Gly Ile Asn Asn Trp Val Gly Gly Lys Gly Trp Gln Thr
65 70 75 80
Gly Ser Arg Arg Val Val Ser Tyr Ser Gly Ser Phe Asn Ser Pro Gly
85 90 95
Asn Gly Tyr Leu Thr Leu Tyr Gly Trp Thr Thr Asn Pro Leu Ile Glu
100 105 110
Tyr Tyr Ile Val Asp Asn Trp Gly Ser Tyr Arg Pro Pro Gly Gly Gln
115 120 125
Gly Phe Met Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Val Tyr
130 135 140
Arg Thr Gln Arg Val Asn Gln Pro Cys Ile Thr Gly Ser Ser Cys Thr
145 150 155 160
Phe Tyr Gln Tyr Trp Ser Val Arg Gln Ser Lys Arg Thr Gly Gly Thr
165 170 175
Ile Thr Thr Gly Asn His Phe Asp Ala Trp Ala Ser Tyr Gly Met Asn
180 185 190
Leu Gly Ala His Asn Tyr Gln Ile Met Ala Thr Glu Gly Tyr Gln Ser
195 200 205
Ser Gly Ser Ser Asp Ile Thr Val Ser Glu Gly Ser Ser Ser Ser Ser
210 215 220
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
225 230 235 240
Ser Gly Gly Gly Gly Thr Lys Ser Phe Thr Val Arg Ala Arg Gly Val
245 250 255
Ala Gly Gly Glu Ser Ile Thr Leu Arg Val Asn Asn Gln Asn Val Gln
260 265 270
Thr Trp Thr Leu Gly Thr Gly Met Gln Asn Tyr Thr Ala Ser Thr Ser
275 280 285
Leu Ser Gly Gly Ile Thr Val Ala Tyr Thr Asn Asp Gly Gly Ser Arg
290 295 300
Asp Val Gln Val Asp Tyr Ile Ile Val Asn Gly Gln Thr Arg Gln Ser
305 310 315 320
Glu Ala Gln Ser Tyr Asn Thr Gly Leu Tyr Ala Asn Gly Arg Cys Gly
325 330 335
Gly Gly Gly Asn Ser Glu Trp Met His Cys Asn Gly Ala Ile Gly Tyr
340 345 350
Gly Asn Thr Pro
355

<210> 235
<211> 1539
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 235
atgtcgaata acagatttgt gctgaatcgt gttgctgcag gtttgctgct gggtttctcg 60
ctgctgtcat cagcagccat cgcccagaat gtggtggtaa atccttctac ggtccatcag 120
accgtgcgcg gctttggcgg catgaacgcg ccgggctgga ttgatgacct taccaccgcc 180
caggtcaata aggcctatgg cagtggcgat ggccaggtcg ggctctccat catgcgcatg 240
cgcattgatc cgaactcggc agcctggaat atccaggtgc cggctgccaa gcgggccaag 300
gagctgggtg cgatcctgtt tgccacgccc tggtcgccgc ccgcctacat gaaatccaac 360
aaaagcctga ataacggcgg caagctgctg cccgagtatt acagcgccta caccacccac 420
ctgctggatt ttgcgagttt catgtcgcgc aacggcgcac cgctgtatgc gatttcaatc 480
cagaacgaac cggactggct gccggattat gagtcgtgtg cctggactgg tactgatttc 540
gtcaattatc tgaataccca gggctcgcgt tttggtgatc tgaaagtgat tgcgccggaa 600
tccctgggtt tcacgacctc gtattccgac cccatcctca acagcgccac ggcagcgccg 660
catgtcgaca tcatcggcgg ccacctctac ggcgtgctgc ccaaggacta cccgctggcg 720

cgccagaagg gcaaggaaat ctggatgacc gagcattaca ccgagagcaa gaactcgggt 780
gatgcctggc cgctggcgct ggacgtaggc accgagctgc accagagcat ggtggccaac 840
tacaacgcct acgtgtggtg gtatgtgcgc cgcagctacg gcctgctgct ggagaacggc 900
aatgtgagca agcgcggcta catcatgtcg cagtacgcac gcttcgtccg ccccggctcc 960
aagcgcatcg gcgcgacgga aaagccgcac gccgacgtgg cggtgacggc ctacaagacg 1020
ccggataacc gcattgtgct ggtggcggtg aataccggtg cggcgcaccg tcagctgaac 1080
atcacggtgc cgagcggcag cgtgggttct ttcagcaagt tctccacttc cggcacgctg 1140
aatgtgggca gtggtggcag ctacaaggtc aacaacggcg cggtgagcct gtacatcgat 1200
ccgcagagcg tggccacgct ggtgggtgat ctgcccggca cggcctccag ctcttcggcg 1260
gcgtcctcgt cctcttccag tgcagccagc tctgcttcga gcagtgctag cggcgcaccg 1320
gccctgtctg gcagcagcga ttaccccacg ggcttcagca agtgcgctga tctgggtggt 1380
acttgtgccg tgccttcggg ctcgggctgg acggctttcg ggcgcaaggg caagtgggtt 1440
gccaagtacg tcggtgtggg caagagcatt gcctgcacgg tgacggcttt cggcagcgat 1500
cccggtggtg cacccaacaa gtgttcttac cagaagtaa 1539

<210> 236
<211> 512
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<400> 236
Met Ser Asn Asn Arg Phe Val Leu Asn Arg Val Ala Ala Gly Leu Leu
1 5 10 15
Leu Gly Phe Ser Leu Leu Ser Ser Ala Ala Ile Ala Gln Asn Val Val
20 25 30
Val Asn Pro Ser Thr Val His Gln Thr Val Arg Gly Phe Gly Gly Met
35 40 45
Asn Ala Pro Gly Trp Ile Asp Asp Leu Thr Thr Ala Gln Val Asn Lys
50 55 60
Ala Tyr Gly Ser Gly Asp Gly Gln Val Gly Leu Ser Ile Met Arg Met
65 70 75 80
Arg Ile Asp Pro Asn Ser Ala Ala Trp Asn Ile Gln Val Pro Ala Ala
85 90 95
Lys Arg Ala Lys Glu Leu Gly Ala Ile Leu Phe Ala Thr Pro Trp Ser
100 105 110
Pro Pro Ala Tyr Met Lys Ser Asn Lys Ser Leu Asn Asn Gly Gly Lys
115 120 125
Leu Leu Pro Glu Tyr Tyr Ser Ala Tyr Thr Thr His Leu Leu Asp Phe
130 135 140
Ala Ser Phe Met Ser Arg Asn Gly Ala Pro Leu Tyr Ala Ile Ser Ile
145 150 155 160
Gln Asn Glu Pro Asp Trp Leu Pro Asp Tyr Glu Ser Cys Ala Trp Thr
165 170 175
Gly Thr Asp Phe Val Asn Tyr Leu Asn Thr Gln Gly Ser Arg Phe Gly
180 185 190
Asp Leu Lys Val Ile Ala Pro Glu Ser Leu Gly Phe Thr Thr Ser Tyr
195 200 205
Ser Asp Pro Ile Leu Asn Ser Ala Thr Ala Ala Pro His Val Asp Ile
210 215 220
Ile Gly Gly His Leu Tyr Gly Val Leu Pro Lys Asp Tyr Pro Leu Ala
225 230 235 240
Arg Gln Lys Gly Lys Glu Ile Trp Met Thr Glu His Tyr Thr Glu Ser
245 250 255
Lys Asn Ser Gly Asp Ala Trp Pro Leu Ala Leu Asp Val Gly Thr Glu
260 265 270
Leu His Gln Ser Met Val Ala Asn Tyr Asn Ala Tyr Val Trp Trp Tyr
275 280 285
Val Arg Arg Ser Tyr Gly Leu Leu Leu Glu Asn Gly Asn Val Ser Lys
290 295 300
Arg Gly Tyr Ile Met Ser Gln Tyr Ala Arg Phe Val Arg Pro Gly Ser
305 310 315 320
Lys Arg Ile Gly Ala Thr Glu Lys Pro His Ala Asp Val Ala Val Thr
325 330 335

Ala Tyr Lys Thr Pro Asp Asn Arg Ile Val Leu Val Ala Val Asn Thr
340 345 350
Gly Ala Ala His Arg Gln Leu Asn Ile Thr Val Pro Ser Gly Ser Val
355 360 365
Gly Ser Phe Ser Lys Phe Ser Thr Ser Gly Thr Leu Asn Val Gly Ser
370 375 380
Gly Gly Ser Tyr Lys Val Asn Asn Gly Ala Val Ser Leu Tyr Ile Asp
385 390 395 400
Pro Gln Ser Val Ala Thr Leu Val Gly Asp Leu Pro Gly Thr Ala Ser
405 410 415
Ser Ser Ser Ala Ala Ser Ser Ser Ser Ser Ser Ala Ala Ser Ser Ala
420 425 430
Ser Ser Ser Ala Ser Gly Ala Pro Ala Leu Ser Gly Ser Ser Asp Tyr
435 440 445
Pro Thr Gly Phe Ser Lys Cys Ala Asp Leu Gly Gly Thr Cys Ala Val
450 455 460
Pro Ser Gly Ser Gly Trp Thr Ala Phe Gly Arg Lys Gly Lys Trp Val
465 470 475 480
Ala Lys Tyr Val Gly Val Gly Lys Ser Ile Ala Cys Thr Val Thr Ala
485 490 495
Phe Gly Ser Asp Pro Gly Gly Ala Pro Asn Lys Cys Ser Tyr Gln Lys
500 505 510

<210> 237
<211> 1269
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 237
atgattccac gcataaaaaa aacaatttgt gtactattag tatgtttcac tatgctgtca 60
gtcatgttag ggccaggcgc tactgaagtt ttggcagcaa gtgatgtaac agttaatgta 120
tctgcagaga aacaagtgat tcgcggtttt ggagggatga atcatccggc ttgggctggg 180
gatcttacag cagctcaaag agaaactgct tttggcaatg gacagaacca gttaggattt 240
tcaatcttaa gaattcatgt agatgaaaat cgaaataatt ggtataaaga ggtggagact 300
gcaaagagtg cggtcaaaca cggagcaatc gtttttgctt ctccttggaa tcctccaagt 360
gatatggttg agacctttaa tcggaatggt gacacatcgg ctaaacggct gaaatacaac 420
aagtacgcag catacgcgca gcatcttaac gattttgtta ccttcatgaa gaataatggt 480
gtgaatcttt acgcgatttc ggtccaaaac gagcctgatt acgctcacga gtggacgtgg 540
tggacgccgc aagaaatact tcgctttatg agagaaaacg ccggctcgat caatgcccgc 600
gtcattgcgc ctgagtcatt tcaatacttg aagaatttgt cggacccgat cttgaacgat 660
ccgcaggctc ttgccaatat ggatattctc ggaactcacc tgtacggcac ccaggtcagc 720
caattccctt atcctctttt caaacaaaaa ggagcgggga aggacctttg gatgacggaa 780
gtatactatc caaacagtga taccaactcg gcggatcgat ggcctgaggc attggatgtt 840
tcacagcata ttcacaatgc gatggtagag ggggactttc aagcttatgt atggtggtac 900
atccgaagat catatggacc tatgaaagaa gatggtacga tcagcaaacg cggctacaat 960
atggctcatt tctcaaagtt tgtgcgtccc ggctatgtaa ggattgatgc aacgaaaaac 1020
cctaatgcga acgtttacgt gtcagcctat aaaggtgaca acaaggtcgt tattgttgcc 1080
atcaataaaa gcaacacagg agtcaaccaa aactttgttt tgcagaatgg atctgcttca 1140
aacgtatcta gatggatcac gagcagcagc agcaatctac aacctggaac gaatctcact 1200
gtatcaggca atcatttttg ggctcatctt ccagctcaaa gcgtgacaac atttgttgta 1260
aatcgttaa 1269

<210> 238
<211> 422
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(32)

<400> 238
Met Ile Pro Arg Ile Lys Lys Thr Ile Cys Val Leu Leu Val Cys Phe
1 5 10 15

Thr Met Leu Ser Val Met Leu Gly Pro Gly Ala Thr Glu Val Leu Ala
20 25 30
Ala Ser Asp Val Thr Val Asn Val Ser Ala Glu Lys Gln Val Ile Arg
35 40 45
Gly Phe Gly Gly Met Asn His Pro Ala Trp Ala Gly Asp Leu Thr Ala
50 55 60
Ala Gln Arg Glu Thr Ala Phe Gly Asn Gly Gln Asn Gln Leu Gly Phe
65 70 75 80
Ser Ile Leu Arg Ile His Val Asp Glu Asn Arg Asn Asn Trp Tyr Lys
85 90 95
Glu Val Glu Thr Ala Lys Ser Ala Val Lys His Gly Ala Ile Val Phe
100 105 110
Ala Ser Pro Trp Asn Pro Pro Ser Asp Met Val Glu Thr Phe Asn Arg
115 120 125
Asn Gly Asp Thr Ser Ala Lys Arg Leu Lys Tyr Asn Lys Tyr Ala Ala
130 135 140
Tyr Ala Gln His Leu Asn Asp Phe Val Thr Phe Met Lys Asn Asn Gly
145 150 155 160
Val Asn Leu Tyr Ala Ile Ser Val Gln Asn Glu Pro Asp Tyr Ala His
165 170 175
Glu Trp Thr Trp Trp Thr Pro Gln Glu Ile Leu Arg Phe Met Arg Glu
180 185 190
Asn Ala Gly Ser Ile Asn Ala Arg Val Ile Ala Pro Glu Ser Phe Gln
195 200 205
Tyr Leu Lys Asn Leu Ser Asp Pro Ile Leu Asn Asp Pro Gln Ala Leu
210 215 220
Ala Asn Met Asp Ile Leu Gly Thr His Leu Tyr Gly Thr Gln Val Ser
225 230 235 240
Gln Phe Pro Tyr Pro Leu Phe Lys Gln Lys Gly Ala Gly Lys Asp Leu
245 250 255
Trp Met Thr Glu Val Tyr Tyr Pro Asn Ser Asp Thr Asn Ser Ala Asp
260 265 270
Arg Trp Pro Glu Ala Leu Asp Val Ser Gln His Ile His Asn Ala Met
275 280 285
Val Glu Gly Asp Phe Gln Ala Tyr Val Trp Trp Tyr Ile Arg Arg Ser
290 295 300
Tyr Gly Pro Met Lys Glu Asp Gly Thr Ile Ser Lys Arg Gly Tyr Asn
305 310 315 320
Met Ala His Phe Ser Lys Phe Val Arg Pro Gly Tyr Val Arg Ile Asp
325 330 335
Ala Thr Lys Asn Pro Asn Ala Asn Val Tyr Val Ser Ala Tyr Lys Gly
340 345 350
Asp Asn Lys Val Val Ile Val Ala Ile Asn Lys Ser Asn Thr Gly Val
355 360 365
Asn Gln Asn Phe Val Leu Gln Asn Gly Ser Ala Ser Asn Val Ser Arg
370 375 380
Trp Ile Thr Ser Ser Ser Ser Asn Leu Gln Pro Gly Thr Asn Leu Thr
385 390 395 400
Val Ser Gly Asn His Phe Trp Ala His Leu Pro Ala Gln Ser Val Thr
405 410 415
Thr Phe Val Val Asn Arg
420

<210> 239
<211> 1281
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 239
atgaatcgtt tcttgatttc acgttataag aaagccataa gtgcatgttt ggcccttgtc 60
cttgcgttgt ctctcatggc ggcacctggc gatgttgccg cagccagcga cgccgttata 120
aatgtatcgt cggagaaaca agtgatacgc ggtttcggag gcatcaacca cccggcatgg 180
atcggagatt tgacggcagc acagagagaa accgcatttg ggaacgggcc aaatcagtta 240
ggcttctcga tattaagaat ctacgtgcat gaagaccgaa atcagtggca ccgtgaactg 300
gatacggcca aacgagcgat tgcccttgga gctatcgtat tcgcttcgcc atggaatccg 360
cccgccgaca tggtcgagac cttcaaccgc aacggcgata cgtcggcaaa gcgacttcgt 420

tacgacaagt ataccgccta tgcccagcat cttaacgatt tcgtaaccta catgagaaac 480
aatggcgtga atctctacgc gatttccgtc cagaacgagc ccgattatgc gcatgactgg 540
acgtggtgga ctccgcagga aatgcttcgc tttatgaaag aaaatgccgg atcgatcaac 600
agcagagtga tcgcaccgga atcgttccaa tatctgaaaa atatgtcgga cccgattcta 660
aatgatcccc aggcgcttgc caatatggat attcttggcg ctcatctgta cggtacccaa 720
gttagcaatt tcgcgtatcc actattcaaa caaaaaggag cgggaaaaga cctctggatg 780
accgaggtgt attacccgaa cagcgacaac aactcggcgg atcgctggcc cgaagccctg 840
gatgtgtctt accatatcca caatgcgatg gtagagggag attttcaagc ttatgtatgg 900
tggtatatcc gcagatccta tggtccaatg aaagaggacg gcacgatcag caaacgcggc 960
tacaatatgg ctcatttctc caagtttgtc cgtcccggct atgtcagggt ggatgcttcg 1020
aaaaatccag aaacgaacgt ttacgtatcc gcatataaag gcgacaacaa aatcgttatc 1080
gttgccataa accggaacaa ctccggggtc aatcagaact ttgtccttca gaatggatcc 1140
gtttcgcagg tatcaaggtg gatcacgagc agcagcagca atctccagcc aggaacgtct 1200
ctcaatgtaa cagggagcaa tttctgggct catcttcccg cgcaaagcgt tacgactttt 1260
gtgggtgaac tcggaaggta a 1281

<210> 240
<211> 426
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(30)

<400> 240
Met Asn Arg Phe Leu Ile Ser Arg Tyr Lys Lys Ala Ile Ser Ala Cys
1 5 10 15
Leu Ala Leu Val Leu Ala Leu Ser Leu Met Ala Ala Pro Gly Asp Val
20 25 30
Ala Ala Ala Ser Asp Ala Val Ile Asn Val Ser Ser Glu Lys Gln Val
35 40 45
Ile Arg Gly Phe Gly Gly Ile Asn His Pro Ala Trp Ile Gly Asp Leu
50 55 60
Thr Ala Ala Gln Arg Glu Thr Ala Phe Gly Asn Gly Pro Asn Gln Leu
65 70 75 80
Gly Phe Ser Ile Leu Arg Ile Tyr Val His Glu Asp Arg Asn Gln Trp
85 90 95
His Arg Glu Leu Asp Thr Ala Lys Arg Ala Ile Ala Leu Gly Ala Ile
100 105 110
Val Phe Ala Ser Pro Trp Asn Pro Pro Ala Asp Met Val Glu Thr Phe
115 120 125
Asn Arg Asn Gly Asp Thr Ser Ala Lys Arg Leu Arg Tyr Asp Lys Tyr
130 135 140
Thr Ala Tyr Ala Gln His Leu Asn Asp Phe Val Thr Tyr Met Arg Asn
145 150 155 160
Asn Gly Val Asn Leu Tyr Ala Ile Ser Val Gln Asn Glu Pro Asp Tyr
165 170 175
Ala His Asp Trp Thr Trp Trp Thr Pro Gln Glu Met Leu Arg Phe Met
180 185 190
Lys Glu Asn Ala Gly Ser Ile Asn Ser Arg Val Ile Ala Pro Glu Ser
195 200 205
Phe Gln Tyr Leu Lys Asn Met Ser Asp Pro Ile Leu Asn Asp Pro Gln
210 215 220
Ala Leu Ala Asn Met Asp Ile Leu Gly Ala His Leu Tyr Gly Thr Gln
225 230 235 240
Val Ser Asn Phe Ala Tyr Pro Leu Phe Lys Gln Lys Gly Ala Gly Lys
245 250 255
Asp Leu Trp Met Thr Glu Val Tyr Tyr Pro Asn Ser Asp Asn Asn Ser
260 265 270
Ala Asp Arg Trp Pro Glu Ala Leu Asp Val Ser Tyr His Ile His Asn
275 280 285
Ala Met Val Glu Gly Asp Phe Gln Ala Tyr Val Trp Trp Tyr Ile Arg
290 295 300
Arg Ser Tyr Gly Pro Met Lys Glu Asp Gly Thr Ile Ser Lys Arg Gly
305 310 315 320
Tyr Asn Met Ala His Phe Ser Lys Phe Val Arg Pro Gly Tyr Val Arg

```
                    325                                     330                                     335
Val Asp Ala Ser Lys Asn Pro Glu Thr Asn Val Tyr Val Ser Ala Tyr
            340                                     345                                     350
Lys Gly Asp Asn Lys Ile Val Ile Val Ala Ile Asn Arg Asn Asn Ser
        355                                     360                                     365
Gly Val Asn Gln Asn Phe Val Leu Gln Asn Gly Ser Val Ser Gln Val
    370                                     375                                     380
Ser Arg Trp Ile Thr Ser Ser Ser Ser Asn Leu Gln Pro Gly Thr Ser
385                                     390                                     395                                     400
Leu Asn Val Thr Gly Ser Asn Phe Trp Ala His Leu Pro Ala Gln Ser
                    405                                     410                                     415
Val Thr Thr Phe Val Gly Glu Leu Gly Arg
            420                                     425
```

<210> 241
<211> 1695
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 241
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gtgaagatat tgaaatttaa gatgaattta aaaaaatcgg ttcatgttct gttggcctgt     60
ttaacagccc tgcctctcat gttaacgccg acacacgtat cagcagcaag tgatgccaac    120
attaatttgt cctccgaaaa acagcttatc aaggggtttg gaggtattaa ccacccagcc    180
tggattggcg acttgacggc agctcagcgt gaaacagcct ttggcaacgg agcgaaccag    240
cttggttttt ccatactaag aatctatgtc gatgaaaatc caaacaactg gtacagggag    300
gtggctactg ccaaaagagc catagagcaa ggtgccatcg tattcgcttc tccctggaat    360
ccaccaagtg acatggtcga aaccttcaat cggaacgggg atacgaacgc caaacgattg    420
agatacgaca aatatgctgc gtacgcgcag catctgaacg actttgtcag ttatatgaaa    480
aataacggtg tggatctgta tgccatttcg gtacaaaatg agccggatta tgcccatgaa    540
tggacctggt ggactccgca ggagatcctt cgtttcatga aggagaatgc gggatccatt    600
cagaatacca aagtcatggc acctgaatcg ttccagtatt tgaaaaacat gtctgacccg    660
attctgaatg atcctcaggc actcgccaat atggacattc tgggagctca tacgtacggg    720
acacagttca aagatttcgc atacccgctc tttaagcaaa agggagccgg caaagaactg    780
tggatgacag aagtgtatta cccgaacagc gataacaact cgtcggaccg ttggcctgag    840
gcattggacg tatcttacca tatgcataat gccatggttg aaggagattt tcaggcttac    900
gtatggtggt atattcggag acagtacggt ccgatgaatg agaacgggac tattagcaaa    960
cgtggttaca atatggccca tttctccaaa tttgtgcgac caggctatta ccgtgtcgat   1020
gcaaccaaaa atccggatac caataccttc gtctcagcct ataaaggtga taataaggca   1080
gtcattgtgg cgattaatcg cggcacctcg gctgtaagcc aaaaattcgt tcttcagaat   1140
ggtaacgctt ctactgtatc ctcttgggtt acggatagca gccgaaacct ggcaagcgga   1200
gcgccgatta cgatgtcagg tggagccttt acagcacaac tgccagccca aagcgtaaca   1260
acgtttgtag ccaacattac tggtggtagt gtcactccag gcagcggaac cacgtacgag   1320
gcggaaacgg gcactacact taccgatgcc gtgatcgaga ctctctaccc gggatacact   1380
gggaccggat acgtgaactt taatgcgtat actggttcgg ccattcaatg gaatgccatc   1440
aataacacga taacaggtac caaaaatgtg aaatttcgtt acgcccagga aagcggaacg   1500
cgtaatctcg acattttcgt taacggaact aaagtcatca gcaacgaacc tttcccggca   1560
acaggcagct ggtcgacctg gagtgaaaaa actattcagg tccccatgaa cgcgggaacc   1620
aatacgatta aagtggtcac aaccggtaca gaagggccaa atattgataa catcaatgtc   1680
actgcagtcc aataa                                                    1695
```

<210> 242
<211> 564
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<400> 242
```
Val Lys Ile Leu Lys Phe Lys Met Asn Leu Lys Lys Ser Val His Val
 1                  5                                     10                                     15
Leu Leu Ala Cys Leu Thr Ala Leu Pro Leu Met Leu Thr Pro Thr His
            20                                      25                                      30
```

Val Ser Ala Ala Ser Asp Ala Asn Ile Asn Leu Ser Ser Glu Lys Gln
35 40 45
Leu Ile Lys Gly Phe Gly Gly Ile Asn His Pro Ala Trp Ile Gly Asp
50 55 60
Leu Thr Ala Ala Gln Arg Glu Thr Ala Phe Gly Asn Gly Ala Asn Gln
65 70 75 80
Leu Gly Phe Ser Ile Leu Arg Ile Tyr Val Asp Glu Asn Pro Asn Asn
85 90 95
Trp Tyr Arg Glu Val Ala Thr Ala Lys Arg Ala Ile Glu Gln Gly Ala
100 105 110
Ile Val Phe Ala Ser Pro Trp Asn Pro Pro Ser Asp Met Val Glu Thr
115 120 125
Phe Asn Arg Asn Gly Asp Thr Asn Ala Lys Arg Leu Arg Tyr Asp Lys
130 135 140
Tyr Ala Ala Tyr Ala Gln His Leu Asn Asp Phe Val Ser Tyr Met Lys
145 150 155 160
Asn Asn Gly Val Asp Leu Tyr Ala Ile Ser Val Gln Asn Glu Pro Asp
165 170 175
Tyr Ala His Glu Trp Thr Trp Trp Thr Pro Gln Glu Ile Leu Arg Phe
180 185 190
Met Lys Glu Asn Ala Gly Ser Ile Gln Asn Thr Lys Val Met Ala Pro
195 200 205
Glu Ser Phe Gln Tyr Leu Lys Asn Met Ser Asp Pro Ile Leu Asn Asp
210 215 220
Pro Gln Ala Leu Ala Asn Met Asp Ile Leu Gly Ala His Thr Tyr Gly
225 230 235 240
Thr Gln Phe Lys Asp Phe Ala Tyr Pro Leu Phe Lys Gln Lys Gly Ala
245 250 255
Gly Lys Glu Leu Trp Met Thr Glu Val Tyr Tyr Pro Asn Ser Asp Asn
260 265 270
Asn Ser Ser Asp Arg Trp Pro Glu Ala Leu Asp Val Ser Tyr His Met
275 280 285
His Asn Ala Met Val Glu Gly Asp Phe Gln Ala Tyr Val Trp Trp Tyr
290 295 300
Ile Arg Arg Gln Tyr Gly Pro Met Asn Glu Asn Gly Thr Ile Ser Lys
305 310 315 320
Arg Gly Tyr Asn Met Ala His Phe Ser Lys Phe Val Arg Pro Gly Tyr
325 330 335
Tyr Arg Val Asp Ala Thr Lys Asn Pro Asp Thr Asn Thr Phe Val Ser
340 345 350
Ala Tyr Lys Gly Asp Asn Lys Ala Val Ile Val Ala Ile Asn Arg Gly
355 360 365
Thr Ser Ala Val Ser Gln Lys Phe Val Leu Gln Asn Gly Asn Ala Ser
370 375 380
Thr Val Ser Ser Trp Val Thr Asp Ser Ser Arg Asn Leu Ala Ser Gly
385 390 395 400
Ala Pro Ile Thr Met Ser Gly Gly Ala Phe Thr Ala Gln Leu Pro Ala
405 410 415
Gln Ser Val Thr Thr Phe Val Ala Asn Ile Thr Gly Gly Ser Val Thr
420 425 430
Pro Gly Ser Gly Thr Thr Tyr Glu Ala Glu Thr Gly Thr Thr Leu Thr
435 440 445
Asp Ala Val Ile Glu Thr Leu Tyr Pro Gly Tyr Thr Gly Thr Gly Tyr
450 455 460
Val Asn Phe Asn Ala Tyr Thr Gly Ser Ala Ile Gln Trp Asn Ala Ile
465 470 475 480
Asn Asn Thr Ile Thr Gly Thr Lys Asn Val Lys Phe Arg Tyr Ala Gln
485 490 495
Glu Ser Gly Thr Arg Asn Leu Asp Ile Phe Val Asn Gly Thr Lys Val
500 505 510
Ile Ser Asn Glu Pro Phe Pro Ala Thr Gly Ser Trp Ser Thr Trp Ser
515 520 525
Glu Lys Thr Ile Gln Val Pro Met Asn Ala Gly Thr Asn Thr Ile Lys
530 535 540
Val Val Thr Thr Gly Thr Glu Gly Pro Asn Ile Asp Asn Ile Asn Val
545 550 555 560
Thr Ala Val Gln

<210> 243
<211> 1272
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 243
atgatttcaa gcgtaaaaaa accaatttgt gtattattgg tatgtttcac tatgctgtca 60
gtcatgttag ccgggccagg tgctactgaa gttttagcag caagtgatgt aacaattaat 120
ttatctgcag aaaaacaagt gatccgcggt tttggaggca tgaaccaccc ggcttggatt 180
ggagatttga cagcagctca aagagaaacc gcttttggca atggacagaa tcagttaggt 240
ttttcaatct taagaattca tgtggatgaa aatagaaata attggtacag agaagtggag 300
actgcaaaga gtgcgatcaa acatggagca atcgttttttg cttctccctg gaatcctcca 360
agcgatatgg ttgagacttt caatcgtaat ggtgacacat cagctaaacg gctaagatac 420
gataagtacg ccgcatacgc gcagcatctt aacgattttg ttacctacat gaagaataat 480
ggcgtgaatc tttatgcgat ttctgttcaa aacgagcctg attatgcgca cgaatggacg 540
tggtggactc cgcaagaaat acttcgtttc atgagagaaa atgccggttc cattaatgca 600
cgtgtcattg caccagaatc ttttcagtac tttaaaaata tatcggaccc cattttgaac 660
gatccacagg cgcttaggaa tatggatatt ctcggaactc acctgtacgg tactcaggtc 720
agtcagtttc cttatcctct attcaaacaa aaaggagcag ggaaagagct atggatgacg 780
gaagtatact atccaaacag tgacaacaat tcagcggatc gctggcccga ggcattaggc 840
gtttcagagc atattcacca ttcaatggtg gagggagatt ttcaatctta tgtttggtgg 900
tacatccgca gatcttacgg tcctatgaaa gaggacggta cgatcagcaa acgcggttac 960
aatatggctc atttctcgaa gtttgtgcgt cccggctatg taagggtaga tgcaacgaaa 1020
aatcctaatg cgaacgttta cgtgtcagcc tataaaggtg acaacaaggt cgttattgtt 1080
gccattaaca aaagcaatac aggggtcaac caaaactttg tgttgcagaa tggatctgct 1140
tctcaggtat ctaggtggat aacaagcgga agcagcaatc ttcaacctgg aacgaatctc 1200
aatgtaacgg gcaatcattt ttgggcccat cttccagctc aaagcgtgac aacatttgtc 1260
gcaaatcgtt aa 1272

<210> 244
<211> 423
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(33)

<400> 244
Met Ile Ser Ser Val Lys Lys Pro Ile Cys Val Leu Leu Val Cys Phe
1 5 10 15
Thr Met Leu Ser Val Met Leu Ala Gly Pro Gly Ala Thr Glu Val Leu
20 25 30
Ala Ala Ser Asp Val Thr Ile Asn Leu Ser Ala Glu Lys Gln Val Ile
35 40 45
Arg Gly Phe Gly Gly Met Asn His Pro Ala Trp Ile Gly Asp Leu Thr
50 55 60
Ala Ala Gln Arg Glu Thr Ala Phe Gly Asn Gly Gln Asn Gln Leu Gly
65 70 75 80
Phe Ser Ile Leu Arg Ile His Val Asp Glu Asn Arg Asn Asn Trp Tyr
85 90 95
Arg Glu Val Glu Thr Ala Lys Ser Ala Ile Lys His Gly Ala Ile Val
100 105 110
Phe Ala Ser Pro Trp Asn Pro Pro Ser Asp Met Val Glu Thr Phe Asn
115 120 125
Arg Asn Gly Asp Thr Ser Ala Lys Arg Leu Arg Tyr Asp Lys Tyr Ala
130 135 140
Ala Tyr Ala Gln His Leu Asn Asp Phe Val Thr Tyr Met Lys Asn Asn
145 150 155 160
Gly Val Asn Leu Tyr Ala Ile Ser Val Gln Asn Glu Pro Asp Tyr Ala
165 170 175
His Glu Trp Thr Trp Trp Thr Pro Gln Glu Ile Leu Arg Phe Met Arg
180 185 190
Glu Asn Ala Gly Ser Ile Asn Ala Arg Val Ile Ala Pro Glu Ser Phe

195 200 205
Gln Tyr Phe Lys Asn Ile Ser Asp Pro Ile Leu Asn Asp Pro Gln Ala
210 215 220
Leu Arg Asn Met Asp Ile Leu Gly Thr His Leu Tyr Gly Thr Gln Val
225 230 235 240
Ser Gln Phe Pro Tyr Pro Leu Phe Lys Gln Lys Gly Ala Gly Lys Glu
245 250 255
Leu Trp Met Thr Glu Val Tyr Tyr Pro Asn Ser Asp Asn Asn Ser Ala
260 265 270
Asp Arg Trp Pro Glu Ala Leu Gly Val Ser Glu His Ile His His Ser
275 280 285
Met Val Glu Gly Asp Phe Gln Ser Tyr Val Trp Trp Tyr Ile Arg Arg
290 295 300
Ser Tyr Gly Pro Met Lys Glu Asp Gly Thr Ile Ser Lys Arg Gly Tyr
305 310 315 320
Asn Met Ala His Phe Ser Lys Phe Val Arg Pro Gly Tyr Val Arg Val
325 330 335
Asp Ala Thr Lys Asn Pro Asn Ala Asn Val Tyr Val Ser Ala Tyr Lys
340 345 350
Gly Asp Asn Lys Val Val Ile Val Ala Ile Asn Lys Ser Asn Thr Gly
355 360 365
Val Asn Gln Asn Phe Val Leu Gln Asn Gly Ser Ala Ser Gln Val Ser
370 375 380
Arg Trp Ile Thr Ser Gly Ser Ser Asn Leu Gln Pro Gly Thr Asn Leu
385 390 395 400
Asn Val Thr Gly Asn His Phe Trp Ala His Leu Pro Ala Gln Ser Val
405 410 415
Thr Thr Phe Val Ala Asn Arg
420

<210> 245
<211> 1263
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 245
atgtcaatga tcaaaaaacc aatctgcact ttattgatct gcttcaccat gctgtctgtc 60
atgttcatcg gacctggcgt gactgaggtt tcagcagcag atgccaatat taatatcaat 120
gcggaaagac aagtgattcg cggctttggc ggaatgaacc atccggcttg gattggtgat 180
ttgaccgcac ctcaaaggga aaccgccttt ggcaatgggc agaatcaatt aggattttcc 240
attctaagaa tttttgtaga tgagaaccga aataattggc acagagaggt cgctactgcc 300
aaaagagcaa tagagcatgg agctttggtg atcgcttcac catggaatcc tccaagcaat 360
atggtagaga ccttcaaccg gaatggtaca tctgcaaagc ggctcagata caaccaatac 420
gccgcatatg ctcagcatct gaacgatttt gtgacgtata tgaaaaataa tggcgtcaat 480
ctctatgcta tatctgtaca aaatgagccc gattatgcac acgaatggac atggtggact 540
cctcaggaaa tcctgcgttt catgagagaa aatgctggct ccattaatgc ccgcgtgatc 600
gcaccagaat cctttcaata ccttaaaaat atatcagatc ctatcctaaa cgatccgcag 660
gcgcttggaa acatggacat tctcggagcc catttgtacg gaacccaaat cagccagctt 720
ccgtatcctc ttttcaaaca aaagggaggg ggaaaggagc tttggatgac agaggtctac 780
tacccgaata gcgataacaa ttcagcggac cgctggcctg aagcattagg ggtttcagag 840
catattcacc attcgatggt agaaggggac tttcaggcat atgtttggtg gtacattcgc 900
agatcctacg gccctatgaa agaagacggt ctaatcagca aacgtggtta caacatggcg 960
catttctcca agtttgtacg cccaggatac atcagaattg atgcaacgaa aagtcctgaa 1020
ccgaatgttt tcgtatcagc ctataaagga aacaatcaag tcgtcattgt cgcgattaac 1080
aaaaacaata caggagtcaa tcagcacttt gtgatgcaaa acggaactgc ttcacaagcg 1140
tcaagatgga tcacaagtag caacagcaac cttcagcctg gtacagactt aaatatatca 1200
ggtaatcaat tttgggctca tctcccggct caaagtgtga caacatttgt ggtcaaacgc 1260
tag 1263

<210> 246
<211> 401
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(32)

<400> 246
Met Ser Met Ile Lys Lys Pro Ile Cys Thr Leu Leu Ile Cys Phe Thr
1 5 10 15
Met Leu Ser Val Met Phe Ile Gly Pro Gly Val Thr Glu Val Ser Ala
20 25 30
Ala Asp Ala Asn Ile Asn Ile Asn Ala Glu Arg Gln Val Ile Arg Gly
35 40 45
Phe Gly Gly Met Asn His Pro Ala Trp Ile Gly Asp Leu Thr Ala Pro
50 55 60
Gln Arg Glu Thr Ala Phe Gly Asn Gly Gln Asn Gln Leu Gly Phe Ser
65 70 75 80
Ile Leu Arg Ile Phe Val Asp Glu Asn Arg Asn Asn Trp His Arg Glu
85 90 95
Val Ala Thr Ala Lys Arg Ala Ile Glu His Gly Ala Leu Val Ile Ala
100 105 110
Ser Pro Trp Asn Pro Pro Ser Asn Met Val Glu Thr Phe Asn Arg Asn
115 120 125
Gly Thr Ser Ala Lys Arg Leu Arg Tyr Asn Gln Tyr Ala Ala Tyr Ala
130 135 140
Gln His Leu Asn Asp Phe Val Thr Tyr Met Lys Asn Asn Gly Val Asn
145 150 155 160
Leu Tyr Ala Ile Ser Val Gln Asn Glu Pro Asp Tyr Ala His Glu Trp
165 170 175
Thr Trp Trp Thr Pro Gln Glu Ile Leu Arg Phe Met Arg Glu Asn Ala
180 185 190
Gly Ser Ile Asn Ala Arg Val Ile Ala Pro Glu Ser Phe Gln Tyr Leu
195 200 205
Lys Asn Ile Ser Asp Pro Ile Leu Asn Asp Pro Gln Ala Leu Gly Asn
210 215 220
Met Asp Ile Leu Gly Ala His Leu Tyr Gly Thr Gln Ile Ser Gln Leu
225 230 235 240
Pro Tyr Pro Leu Phe Lys Gln Lys Gly Gly Gly Lys Glu Leu Trp Met
245 250 255
Thr Glu Val Tyr Tyr Pro Asn Ser Asp Asn Asn Ser Ala Asp Arg Trp
260 265 270
Pro Glu Ala Leu Gly Val Ser Glu His Ile His His Ser Met Val Glu
275 280 285
Gly Asp Phe Gln Ala Tyr Val Trp Trp Tyr Ile Arg Arg Ser Tyr Gly
290 295 300
Pro Met Lys Glu Asp Gly Leu Ile Ser Lys Arg Gly Tyr Asn Met Ala
305 310 315 320
His Phe Ser Lys Phe Val Arg Pro Gly Tyr Ile Arg Ile Asp Ala Thr
325 330 335
Lys Ser Pro Glu Pro Asn Val Phe Val Ser Ala Tyr Lys Gly Asn Asn
340 345 350
Gln Val Val Ile Val Ala Ile Asn Lys Asn Asn Thr Gly Val Asn Gln
355 360 365
His Phe Val Met Gln Asn Gly Thr Ala Ser Gln Ala Ser Arg Trp Ile
370 375 380
Thr Ser Ser Asn Ser Asn Leu Gln Pro Gly Thr Asp Leu Asn Ile Ser
385 390 395 400
Gly

<210> 247
<211> 1044
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 247
gtgtttgcca acgatttcct gataggcgtg gcgctcaact cacggcaggt cgccggggaa 60
tccgaggccg gaaaactagc tggcgcgcaa ttttcgtcgg tgacggcgga gaatgagatg 120

aagtggcagt cgctccatcc ccagcccgac cgctatcagt tcggcgcggc ggactcctac 180
atcgattttg ccaaaaaaca caagatggcg gtgatcggcc acacgctcgt gtggcacagc 240
cagacacccg gctgggtgtt cgagggcaag gacggcaagc cggcgacccg cgaggatctg 300
ctcaagcgca tgcgcgatca catccacacc gtggccggac gctacaaggg caaggtgcgc 360
ggctgggacg tggtcaacga ggccttgtcc gacggcggtc ccgaaatcct gcgggattct 420
ccgtggcggc gcatcatcgg cgatgacttc atcgaccacg cgttccgttt cgcccgtgag 480
gccgatccga aagccgaact ctactacaac gactacggtc tcgagaacga aaggaagcgg 540
agcaactgca tcaagctcgt caagggcatg aaacaacgcg gcgtgccgat cgacggggtg 600
ggcacccagt cgcatttcca cttgaaacat ccctcgctcc aggaaatcga aaagaccatc 660
aaggactttt ccgaactcgg actcaaggtg atgatcaccg agctggatgt cgatgtgctg 720
ccgtcgcgtg gcaatttcgg caacgccgac atcagccgcc gcgagcaggg cggtgacgca 780
ctcaatcctt acaccggcgg cttgcccgat gaggtccaac aggaacttgc gaaacgctat 840
gcggacattt ttgatatcta tctgcgccac cggaaggcgg tcacccgcgt aaccttctgg 900
ggactcgatg acgggcatac ctggttgaac ggtttcccga tccgcggacg caccaactat 960
ccgctgttgt tcgaccgcgc cctcaagccg aagcccgcgt tcgaggcggt catcaaaaaa 1020
gggcttgaac ccaggaaacg ttga 1044

<210> 248
<211> 347
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 248
Val Phe Ala Asn Asp Phe Leu Ile Gly Val Ala Leu Asn Ser Arg Gln
1 5 10 15
Val Ala Gly Glu Ser Glu Ala Gly Lys Leu Ala Gly Ala Gln Phe Ser
20 25 30
Ser Val Thr Ala Glu Asn Glu Met Lys Trp Gln Ser Leu His Pro Gln
35 40 45
Pro Asp Arg Tyr Gln Phe Gly Ala Ala Asp Ser Tyr Ile Asp Phe Ala
50 55 60
Lys Lys His Lys Met Ala Val Ile Gly His Thr Leu Val Trp His Ser
65 70 75 80
Gln Thr Pro Gly Trp Val Phe Glu Gly Lys Asp Gly Lys Pro Ala Thr
85 90 95
Arg Glu Asp Leu Leu Lys Arg Met Arg Asp His Ile His Thr Val Ala
100 105 110
Gly Arg Tyr Lys Gly Lys Val Arg Gly Trp Asp Val Val Asn Glu Ala
115 120 125
Leu Ser Asp Gly Gly Pro Glu Ile Leu Arg Asp Ser Pro Trp Arg Arg
130 135 140
Ile Ile Gly Asp Asp Phe Ile Asp His Ala Phe Arg Phe Ala Arg Glu
145 150 155 160
Ala Asp Pro Lys Ala Glu Leu Tyr Tyr Asn Asp Tyr Gly Leu Glu Asn
165 170 175
Glu Arg Lys Arg Ser Asn Cys Ile Lys Leu Val Lys Gly Met Lys Gln
180 185 190
Arg Gly Val Pro Ile Asp Gly Val Gly Thr Gln Ser His Phe His Leu
195 200 205
Lys His Pro Ser Leu Gln Glu Ile Glu Lys Thr Ile Lys Asp Phe Ser
210 215 220
Glu Leu Gly Leu Lys Val Met Ile Thr Glu Leu Asp Val Asp Val Leu
225 230 235 240
Pro Ser Arg Gly Asn Phe Gly Asn Ala Asp Ile Ser Arg Arg Glu Gln
245 250 255
Gly Gly Asp Ala Leu Asn Pro Tyr Thr Gly Gly Leu Pro Asp Glu Val
260 265 270
Gln Gln Glu Leu Ala Lys Arg Tyr Ala Asp Ile Phe Asp Ile Tyr Leu
275 280 285
Arg His Arg Lys Ala Val Thr Arg Val Thr Phe Trp Gly Leu Asp Asp
290 295 300
Gly His Thr Trp Leu Asn Gly Phe Pro Ile Arg Gly Arg Thr Asn Tyr
305 310 315 320
Pro Leu Leu Phe Asp Arg Ala Leu Lys Pro Lys Pro Ala Phe Glu Ala
325 330 335
Val Ile Lys Lys Gly Leu Glu Pro Arg Lys Arg

340 345

<210> 249
<211> 1439
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 249
tgatcaatcc agtgaaggat cttcgtgaag atttcatctt tggaatggac gtttcaatgc 60
tctacgagat agagcggctc ggtggtaagt tcttcgatgg tggtgtggag aaagatcttt 120
tccagatact gaaggatcat gagataaact ggatcagatt gagagtgtgg aacgatccaa 180
gggatgaaaa cggaaatccg ctcggtgggg gaaactgtga ttatctgaaa atgacagaga 240
tcgcaaaaag ggccaaaaag tacggaatga aggttcttct tgactttcac tacagcgact 300
ggtgggcaga tcccggcaag cagtacaaac caaaagagtg ggatcacctt catggagaac 360
ttctggaaag ggcggtgtat tcctacacga aactcgtgct gaatcatatg agaagaaacg 420
gtgcactgcc ggacatggtc caggtgggaa acgaggtgaa caacggcttt ctctggccgg 480
atggaatgat tgccggaaag gatgcaggag gattcgacgg attcacaaaa cttttgaagg 540
cggccatcaa agccgtcagg gaagttgatc ccgatatcaa gatagtcatt catttggcag 600
aaggtggaaa caactcactt ttcaggtggt tcttcgacga gatcacaaga agagacgtgg 660
attttgatgt gatcggtgta tcgtactatc cgtactggca tggtaccctg gatgacctga 720
agaacaacct gtacgacata gcgaaaagat acaacaaaga cgtgctcatc gttgaaacgg 780
cgtatgcctg gacactcgag gacggggacg gttaccccaa catcttcagt ggtgaagaga 840
tggagctcac gggtggttac aaagcaacgg ttcagggaca ggcaacgttc ttgagggatc 900
tcatagaagt ggtgaacagt gttcctgacg gtcacggtct tgggatcttc tattgggaag 960
gagactggat tcctgtgaaa ggagccggct ggaaaaccgg cgaaggaaat ccatgggaga 1020
atcaggccat gtttgatttc aatggaaatg ctctcccatc cctggatgtt ttcaagctcg 1080
tgaggacagt cactcctatg gaaataaaaa tcgaagagat tctgcctgtg gagatctcga 1140
cgaatttggg agagattccg aagtttccgg atgctgtgaa agtgctgttc agcgatgatt 1200
ccatcagatc cctgaaagtt acatggaatt ttgatccttc tcttgttgaa acacccggtg 1260
tctacagagt ggaaggatac gtggaaagta tagaccagaa gatcttcgca accttgactg 1320
tgaagggaag tagaaactac ctgaagaacc ctgggtttga aacgggtgag ttttctccct 1380
ggaaggtgtt cggtaacgga aaacgcagtg aaggtggtaa aggccgatcc tccgagtaa 1439

<210> 250
<211> 479
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(33)

<400> 250
Met Ile Asn Pro Val Lys Asp Leu Arg Glu Asp Phe Ile Phe Gly Met
1 5 10 15
Asp Val Ser Met Leu Tyr Glu Ile Glu Arg Leu Gly Gly Lys Phe Phe
20 25 30
Asp Gly Gly Val Glu Lys Asp Leu Phe Gln Ile Leu Lys Asp His Glu
35 40 45
Ile Asn Trp Ile Arg Leu Arg Val Trp Asn Asp Pro Arg Asp Glu Asn
50 55 60
Gly Asn Pro Leu Gly Gly Gly Asn Cys Asp Tyr Leu Lys Met Thr Glu
65 70 75 80
Ile Ala Lys Arg Ala Lys Lys Tyr Gly Met Lys Val Leu Leu Asp Phe
85 90 95
His Tyr Ser Asp Trp Trp Ala Asp Pro Gly Lys Gln Tyr Lys Pro Lys
100 105 110
Glu Trp Asp His Leu His Gly Glu Leu Leu Glu Arg Ala Val Tyr Ser
115 120 125
Tyr Thr Lys Leu Val Leu Asn His Met Arg Arg Asn Gly Ala Leu Pro
130 135 140
Asp Met Val Gln Val Gly Asn Glu Val Asn Asn Gly Phe Leu Trp Pro
145 150 155 160
Asp Gly Met Ile Ala Gly Lys Asp Ala Gly Gly Phe Asp Gly Phe Thr

```
                165                     170                     175
Lys Leu Leu Lys Ala Ala Ile Lys Ala Val Arg Glu Val Asp Pro Asp
            180                     185                     190
Ile Lys Ile Val Ile His Leu Ala Glu Gly Gly Asn Asn Ser Leu Phe
        195                     200                     205
Arg Trp Phe Phe Asp Glu Ile Thr Arg Arg Asp Val Asp Phe Asp Val
    210                     215                     220
Ile Gly Val Ser Tyr Tyr Pro Tyr Trp His Gly Thr Leu Asp Asp Leu
225                     230                     235                     240
Lys Asn Asn Leu Tyr Asp Ile Ala Lys Arg Tyr Asn Lys Asp Val Leu
                245                     250                     255
Ile Val Glu Thr Ala Tyr Ala Trp Thr Leu Glu Asp Gly Asp Gly Tyr
            260                     265                     270
Pro Asn Ile Phe Ser Gly Glu Glu Met Glu Leu Thr Gly Gly Tyr Lys
        275                     280                     285
Ala Thr Val Gln Gly Gln Ala Thr Phe Leu Arg Asp Leu Ile Glu Val
    290                     295                     300
Val Asn Ser Val Pro Asp Gly His Gly Leu Gly Ile Phe Tyr Trp Glu
305                     310                     315                     320
Gly Asp Trp Ile Pro Val Lys Gly Ala Gly Trp Lys Thr Gly Glu Gly
                325                     330                     335
Asn Pro Trp Glu Asn Gln Ala Met Phe Asp Phe Asn Gly Asn Ala Leu
            340                     345                     350
Pro Ser Leu Asp Val Phe Lys Leu Val Arg Thr Val Thr Pro Met Glu
        355                     360                     365
Ile Lys Ile Glu Glu Ile Leu Pro Val Glu Ile Ser Thr Asn Leu Gly
    370                     375                     380
Glu Ile Pro Lys Phe Pro Asp Ala Val Lys Val Leu Phe Ser Asp Asp
385                     390                     395                     400
Ser Ile Arg Ser Leu Lys Val Thr Trp Asn Phe Asp Pro Ser Leu Val
                405                     410                     415
Glu Thr Pro Gly Val Tyr Arg Val Glu Gly Tyr Val Glu Ser Ile Asp
            420                     425                     430
Gln Lys Ile Phe Ala Thr Leu Thr Val Lys Gly Ser Arg Asn Tyr Leu
        435                     440                     445
Lys Asn Pro Gly Phe Glu Thr Gly Glu Phe Ser Pro Trp Lys Val Phe
    450                     455                     460
Gly Asn Gly Lys Arg Ser Glu Gly Gly Lys Gly Arg Ser Ser Glu
465                     470                     475
```

<210> 251
<211> 555
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 251

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atggctacgg attattggca atattggacg gatggcggcg gaacggtgaa tgcggttaac      60
gggtccgggg gcaattacag cgtaacttgg caaaatagcg gggacttcgt ggtcggcaaa     120
ggctggagcg tagggtcgcc aaatcggacg atcaattaca atgccggcat ctgggaacct     180
tcggggaacg ggtacttgac cctttacgga tggactagaa actcgctgat cgagtattac     240
gttgtcgaca gttgggggac gtaccggcca acaggtactc acaaaggaac ggtgaacagc     300
gacggaggca cctacgatat ttatacgacc atgcgctata atgcgccttc cattgatggc     360
acgcagacgt tccaacagtt ctggagcgtg cggcaatcga aacgaccaac cggcagcaac     420
gtctccatca ccttcagcaa tcacgtgaat gcctggagaa gcaagggcat gaacctgggc     480
agcagctggt cgtaccaggt cttggcgacg gaaggctatc agagcagcgg aagatccaac     540
gtcacggtgt ggtaa                                                      555
```

<210> 252
<211> 184
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 252

Met Ala Thr Asp Tyr Trp Gln Tyr Trp Thr Asp Gly Gly Gly Thr Val
1 5 10 15
Asn Ala Val Asn Gly Ser Gly Gly Asn Tyr Ser Val Thr Trp Gln Asn
20 25 30
Ser Gly Asp Phe Val Val Gly Lys Gly Trp Ser Val Gly Ser Pro Asn
35 40 45
Arg Thr Ile Asn Tyr Asn Ala Gly Ile Trp Glu Pro Ser Gly Asn Gly
50 55 60
Tyr Leu Thr Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr Tyr
65 70 75 80
Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr His Lys Gly
85 90 95
Thr Val Asn Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Met Arg
100 105 110
Tyr Asn Ala Pro Ser Ile Asp Gly Thr Gln Thr Phe Gln Gln Phe Trp
115 120 125
Ser Val Arg Gln Ser Lys Arg Pro Thr Gly Ser Asn Val Ser Ile Thr
130 135 140
Phe Ser Asn His Val Asn Ala Trp Arg Ser Lys Gly Met Asn Leu Gly
145 150 155 160
Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln Ser Ser
165 170 175
Gly Arg Ser Asn Val Thr Val Trp
180

<210> 253
<211> 1047
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 253
atgattgtta gcttcaagag cctgaaggca ctcgcgtgcc tcggcgtgct cggcatcacc 60
gccgcgcacg cgcaaacctg catcacgtcg agccagacgg gcaccaacaa cggcaattac 120
ttttcgttct ggaaagacag tccgggcacg gtgaacttct gcatgtatgc gaatggccgc 180
tatacctcca actggagcgg catcaacaac tgggtgggcg gcaagggctg ggctaccggc 240
tccagccaca cgatcagcta ctccggcacg ttcaattcgc cgggcaacgg ttacctggcc 300
ctgtatggct ggaccaccaa tccattggtc gagtactaca tcgtcgacag ctggggtacc 360
taccgtccgc cgggcggcca gggtttcatg ggcacggtag ttagcgacgg gggcacgtac 420
gacgtgtacc ggacgcaacg cgtgaaccag ccatccatca tcggcaacgc cacgttctac 480
cagtactgga gcgtgcggca gtcgaagcgc gtgggcggca ccatcaccat cgccaaccat 540
ttcaacgcct gggccacgct gggcatgaac ctgggccagc acaactacca ggtcatggcc 600
accgagggtt accagagcag cggcagctcc gacatcaccg tgaccgaagg tggcggcagy 660
tcctcgtcgt cctcgggcgg cggcagcacc agcagcagtg gtggcggcgg caacaagagc 720
ttcacggtgc gtgcgcgcgg cacggccgga ggcgagaaca tccagctgca ggtgaacaac 780
cagacggtcg cgagctggaa cctcaccacc agcatgcaga actacaccgc ctcgaccagc 840
ctgagcggcg gcatcaccgt gctctacacc aacgacggcg gcagccgcga cgtgcaggtg 900
gactacatca tcgtgaacgg ccagacccgc cagtccgaag cgcagagcta caacaccggg 960
ttgtatgcga atggacgctg cggcggtggc tcgaacagcg agtggatgca ttgcaacggc 1020
gcgatcggct acggcaatac gccctga 1047

<210> 254
<211> 347
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(24)

<400> 254
Met Ile Val Ser Phe Lys Ser Leu Lys Ala Leu Ala Cys Leu Gly Val
1 5 10 15
Leu Gly Ile Thr Ala Ala His Ala Gln Thr Cys Ile Thr Ser Ser Gln
20 25 30

Thr Gly Thr Asn Asn Gly Asn Tyr Phe Ser Phe Trp Lys Asp Ser Pro
35 40 45
Gly Thr Val Asn Phe Cys Met Tyr Ala Asn Gly Arg Tyr Thr Ser Asn
50 55 60
Trp Ser Gly Ile Asn Asn Trp Val Gly Gly Lys Gly Trp Ala Thr Gly
65 70 75 80
Ser Ser His Thr Ile Ser Tyr Ser Gly Thr Phe Asn Ser Pro Gly Asn
85 90 95
Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Thr Asn Pro Leu Val Glu Tyr
100 105 110
Tyr Ile Val Asp Ser Trp Gly Thr Tyr Arg Pro Pro Gly Gly Gln Gly
115 120 125
Phe Met Gly Thr Val Val Ser Asp Gly Gly Thr Tyr Asp Val Tyr Arg
130 135 140
Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly Asn Ala Thr Phe Tyr
145 150 155 160
Gln Tyr Trp Ser Val Arg Gln Ser Lys Arg Val Gly Gly Thr Ile Thr
165 170 175
Ile Ala Asn His Phe Asn Ala Trp Ala Thr Leu Gly Met Asn Leu Gly
180 185 190
Gln His Asn Tyr Gln Val Met Ala Thr Glu Gly Tyr Gln Ser Ser Gly
195 200 205
Ser Ser Asp Ile Thr Val Thr Glu Gly Gly Gly Ser Ser Ser Ser Ser
210 215 220
Gly Gly Gly Ser Thr Ser Ser Ser Gly Gly Gly Gly Asn Lys Ser Phe
225 230 235 240
Thr Val Arg Ala Arg Gly Thr Ala Gly Gly Glu Asn Ile Gln Leu Gln
245 250 255
Val Asn Asn Gln Thr Val Ala Ser Trp Asn Leu Thr Thr Ser Met Gln
260 265 270
Asn Tyr Thr Ala Ser Thr Ser Leu Ser Gly Gly Ile Thr Val Leu Tyr
275 280 285
Thr Asn Asp Gly Gly Ser Arg Asp Val Gln Val Asp Tyr Ile Ile Val
290 295 300
Asn Gly Gln Thr Arg Gln Ser Glu Ala Gln Ser Tyr Asn Thr Gly Leu
305 310 315 320
Tyr Ala Asn Gly Arg Cys Gly Gly Gly Ser Asn Ser Glu Trp Met His
325 330 335
Cys Asn Gly Ala Ile Gly Tyr Gly Asn Thr Pro
340 345

<210> 255
<211> 1137
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 255
ttgatctttt ccgtcagtgg ttccgcgtct cggcggcgcc ctggcatcca caagggggat 60
tccatgattt tcggtctaaa gtcgatcacg ggcaggcgcg ccgtcgcggc gctggcctgc 120
cttgccggcc tctacatggc gccggcgaat gcgcaaacct gcatcacgtc gagccagacg 180
ggcaccaaca acggcaacta cttttcgttc tggaaagaca gcccgggcac ggtgaacttc 240
tgcatgtact ccggcggccg ctacacgtcc aactggagcg gcatcaacaa ctgggtgggc 300
ggcaagggct ggcagacggg ctcgtcccgc accgtctcct actccggcag cttcaattcg 360
ccgggtaacg gctacctgac gctctacggc tggaccacca atccgctcat cgagtactac 420
atcgtcgaca actggggcag ctatcgtccg ccgggtggcc agggcttcat gggcacggtg 480
aacaccgacg gcggcacgta cgacatctat cgcacgcaac gggtcaacca gccgtcgatc 540
atcggcaccg cgacgttcta ccagtactgg agcgtgcggc agtcgaagcg caccggcggc 600
accatcacca cggccaacca cttcaatgcc tgggccagcc tcggcatgaa cctgggacag 660
cacaactacc aggtgatggc caccgagggc taccagagca gcggcagctc cgacatcacg 720
gtgtgggaag gcacgagcag cggcggaagc agcaatggcg gcagcagcaa cggcggcagc 780
agcaatggtg gcagcggcgg cacgaagagc ttcacggtgc gcgcgcgcgg cactgcgggc 840
ggcgagtcca tcacgctgcg ggtcaacaac cagaacgtgc agacctggac gctgggtacc 900
agcatgcaga actacacggc ctcgacctcg ctgagcggcg gcatcacggt ggcgttcacc 960
aacgacggcg gcagccgcga cgtgcaggtg gactacatca tcgtgaatgg ccagacccgc 1020
cagtccgaac agcagagcta caacactggc ctctacgcca atggaagctg tggtggcggt 1080
tcgaacagcg agtggatgca ttgcaacggc gccatcggct acggcaatac gccctga 1137

<210> 256
<211> 378
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(51)

<400> 256
Leu Ile Phe Ser Val Ser Gly Ser Ala Ser Arg Arg Arg Pro Gly Ile
1   5   10   15
His Lys Gly Asp Ser Met Ile Phe Gly Leu Lys Ser Ile Thr Gly Arg
            20   25   30
Arg Ala Val Ala Ala Leu Ala Cys Leu Ala Gly Leu Tyr Met Ala Pro
        35   40   45
Ala Asn Ala Gln Thr Cys Ile Thr Ser Ser Gln Thr Gly Thr Asn Asn
    50   55   60
Gly Asn Tyr Phe Ser Phe Trp Lys Asp Ser Pro Gly Thr Val Asn Phe
65   70   75   80
Cys Met Tyr Ser Gly Gly Arg Tyr Thr Ser Asn Trp Ser Gly Ile Asn
                85   90   95
Asn Trp Val Gly Gly Lys Gly Trp Gln Thr Gly Ser Ser Arg Thr Val
            100   105   110
Ser Tyr Ser Gly Ser Phe Asn Ser Pro Gly Asn Gly Tyr Leu Thr Leu
        115   120   125
Tyr Gly Trp Thr Thr Asn Pro Leu Ile Glu Tyr Tyr Ile Val Asp Asn
    130   135   140
Trp Gly Ser Tyr Arg Pro Pro Gly Gly Gln Gly Phe Met Gly Thr Val
145   150   155   160
Asn Thr Asp Gly Gly Thr Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn
                165   170   175
Gln Pro Ser Ile Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val
            180   185   190
Arg Gln Ser Lys Arg Thr Gly Gly Thr Ile Thr Thr Ala Asn His Phe
        195   200   205
Asn Ala Trp Ala Ser Leu Gly Met Asn Leu Gly Gln His Asn Tyr Gln
    210   215   220
Val Met Ala Thr Glu Gly Tyr Gln Ser Ser Gly Ser Ser Asp Ile Thr
225   230   235   240
Val Trp Glu Gly Thr Ser Ser Gly Gly Ser Ser Asn Gly Gly Ser Ser
                245   250   255
Asn Gly Gly Ser Ser Asn Gly Gly Ser Gly Gly Thr Lys Ser Phe Thr
            260   265   270
Val Arg Ala Arg Gly Thr Ala Gly Gly Glu Ser Ile Thr Leu Arg Val
        275   280   285
Asn Asn Gln Asn Val Gln Thr Trp Thr Leu Gly Thr Ser Met Gln Asn
    290   295   300
Tyr Thr Ala Ser Thr Ser Leu Ser Gly Gly Ile Thr Val Ala Phe Thr
305   310   315   320
Asn Asp Gly Gly Ser Arg Asp Val Gln Val Asp Tyr Ile Ile Val Asn
                325   330   335
Gly Gln Thr Arg Gln Ser Glu Gln Gln Ser Tyr Asn Thr Gly Leu Tyr
            340   345   350
Ala Asn Gly Ser Cys Gly Gly Gly Ser Asn Ser Glu Trp Met His Cys
        355   360   365
Asn Gly Ala Ile Gly Tyr Gly Asn Thr Pro
    370   375

<210> 257
<211> 2694
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 257
atggctgata tatctaccac accagtcaca gcctcgacag atgctgccaa gaacctgtat 60
gcctatttcc tggaccagta tggcaagaag acgatttcca gcgtcatggc caatgtcaac 120
tggaacaaca cttgtgccga gaaagtctat aaactcacgg gcaagtatcc tgccatgaac 180
tgctacgact tcatccacat ctgtttctcg ccagccaact ggattgacta caccgacatc 240
actcctgcca aggaatggca cgatgcgggc ggtatcgtac agttgatgtg gcatttcaat 300
gtgcctaaga gccagggggc aacagatgtt acctgcacgc ccagcgagac cacctttaag 360
gcttccaatg ctctggttag cggcacgtgg gagaacaaat ggttctacga gcagatggac 420
aaggtcattg ccaccatcct caagttacag gacgctggca ttgccgctac ctggcgacct 480
ttccatgagg cagcaggcaa tgcttgcgcc aagcagcagg ccgactggac caaagcatgg 540
ttctggtggg gctacgacgg tgccgacacc tacaagaaac tgtggattgc catgtacgac 600
tatttcaagc tgaaaggcgt gaacaacctc atctggatgt ggaccaccca gaattataat 660
ggtgacagca gcaaatacaa ccaggacacc gactggtacc ctggcgacga gtatgttgac 720
atcgtggccc gcgacctcta tggctacaat gccgaccaga acctgcagga gttcagcgag 780
attcaggctg cctatcccaa caagatggtg gttctgggtg aatgcggaaa aggtgatagc 840
ggcgaccccg gcaagatgtc cgatgtatgg gcgaaaggtg ccaagtgggg ccacttcatg 900
gtatggtatc aaggcgaaca aggctctacc gacacgatgt gcagcgacga ctggtggaag 960
gatgccatga gcagcgccaa cgtcatcacc cgcgacaagg tggttatccc cgatgtcact 1020
tcaaccatcg agaatgccac ggatgccgtg aagaacatgg gactggggtg gaacctgggg 1080
aacgccctcg acgccaatgc ccagcaatac catgatgcca cccaggacaa ctactgggga 1140
cagcaggaca ttacctctga gagctgctgg ggtcagctac ccaccaaggc agagctgatg 1200
gccatgatga aagaagccgg tttcggagcc atccgcgttc ccgtgacatg gtataaccac 1260
atggacaagg acggcaatgt ggatgcagca tggatgaatc gtgtgcatga ggtggttgac 1320
tatgtcatca gccagggaat gtactgcatc ctcaacgtac accacgacac gggtgccgac 1380
agctacgaca gccagaagaa cctcaccggc taccattgga tcaaggccga cgaaaccaac 1440
tacgccacca acaaggcccg ctatgagaag ctgtggcagc agatagccca ggagttccgc 1500
aactacggcc agctgctgct gttcgagggc tataacgaga tgctcgatgc caacaactcc 1560
tggaattttg cacagagcag ttcagcctac gatgccatca acaaatacgc ccagagcttt 1620
gtcgatgtcg tacgcgccac cggtggcaac aatgcccagc gcaacctcat tgtcagcaca 1680
tacggcgcct gctcaggcaa cggcacgtgg gatgcaagag tgcaagaccc cttgaagaaa 1740
ctgcagattc ccacgggtga aagcaaccat atcatcttcg aggttcacaa ctatccctcc 1800
atcgtcaaca aggacaacgc gggcaactac gtcagcgatc gcaccatcag cgaaatcaag 1860
gcagagattg atgcatggct taagaactta aagacccacc tcgtcagcaa gggcgctccc 1920
gtcatcatcg gcgaatgggg caccaacaac gtcgatgccg gcggtggcaa gacagactac 1980
gacctccata aggacctgat gttcgaattt gtcagctaca tgataaagac catgaagcag 2040
aacgacattg ccaccttcta ctggatggga cttaccgacg gcgctccacg cacctacccc 2100
gccttcacac agcccgacct ggcgctgaag atgctgcagg cctatcacgg cgactcttgg 2160
aatccctacc tgcctgacgc caaggacttt cccgaaggca aaatcacctc ggccacggtg 2220
aatttcaaca gccaatgggg cgaactgacc atccacgatg gagctattga caagaccgtc 2280
tatagaggta tcaaggtgga gctggaagaa aagcctgcca ctggagccct gtctttcaag 2340
gtatatgcca acagtgagaa ggcaacagcc atcaattcca aaaccccaca gttggctttc 2400
ttcagttaca caggcatcca gaaaatcaac ctacagtgga acatagccac caaggggagt 2460
atcaaaatca agagcgtcaa ccttatcaag cacgacgact ccacagaacc ctgtagtctg 2520
aaagtggctt ggggttgtac tctcagcgac cagaactacg ccacgggcat cgaagacatt 2580
actatcactc ctgttcgtca tgacgatgga atcatctaca atctgagcgg acagcctgta 2640
acctctcctc agcgcggcat ctacatcctc aacggaaaga aaatcatcaa atag 2694

<210> 258
<211> 897
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 258
Met Ala Asp Ile Ser Thr Thr Pro Val Thr Ala Ser Thr Asp Ala Ala
1   5   10   15
Lys Asn Leu Tyr Ala Tyr Phe Leu Asp Gln Tyr Gly Lys Lys Thr Ile
            20   25   30
Ser Ser Val Met Ala Asn Val Asn Trp Asn Asn Thr Cys Ala Glu Lys
        35   40   45
Val Tyr Lys Leu Thr Gly Lys Tyr Pro Ala Met Asn Cys Tyr Asp Phe
    50   55   60
Ile His Ile Cys Phe Ser Pro Ala Asn Trp Ile Asp Tyr Thr Asp Ile
65   70   75   80
Thr Pro Ala Lys Glu Trp His Asp Ala Gly Gly Ile Val Gln Leu Met
                85   90   95

Trp His Phe Asn Val Pro Lys Ser Gln Gly Ala Thr Asp Val Thr Cys
100 105 110
Thr Pro Ser Glu Thr Thr Phe Lys Ala Ser Asn Ala Leu Val Ser Gly
115 120 125
Thr Trp Glu Asn Lys Trp Phe Tyr Glu Gln Met Asp Lys Val Ile Ala
130 135 140
Thr Ile Leu Lys Leu Gln Asp Ala Gly Ile Ala Ala Thr Trp Arg Pro
145 150 155 160
Phe His Glu Ala Ala Gly Asn Ala Cys Ala Lys Gln Gln Ala Asp Trp
165 170 175
Thr Lys Ala Trp Phe Trp Trp Gly Tyr Asp Gly Ala Asp Thr Tyr Lys
180 185 190
Lys Leu Trp Ile Ala Met Tyr Asp Tyr Phe Lys Leu Lys Gly Val Asn
195 200 205
Asn Leu Ile Trp Met Trp Thr Thr Gln Asn Tyr Asn Gly Asp Ser Ser
210 215 220
Lys Tyr Asn Gln Asp Thr Asp Trp Tyr Pro Gly Asp Glu Tyr Val Asp
225 230 235 240
Ile Val Ala Arg Asp Leu Tyr Gly Tyr Asn Ala Asp Gln Asn Leu Gln
245 250 255
Glu Phe Ser Glu Ile Gln Ala Ala Tyr Pro Asn Lys Met Val Val Leu
260 265 270
Gly Glu Cys Gly Lys Gly Asp Ser Gly Asp Pro Gly Lys Met Ser Asp
275 280 285
Val Trp Ala Lys Gly Ala Lys Trp Gly His Phe Met Val Trp Tyr Gln
290 295 300
Gly Glu Gln Gly Ser Thr Asp Thr Met Cys Ser Asp Asp Trp Trp Lys
305 310 315 320
Asp Ala Met Ser Ser Ala Asn Val Ile Thr Arg Asp Lys Val Val Ile
325 330 335
Pro Asp Val Thr Ser Thr Ile Glu Asn Ala Thr Asp Ala Val Lys Asn
340 345 350
Met Gly Leu Gly Trp Asn Leu Gly Asn Ala Leu Asp Ala Asn Ala Gln
355 360 365
Gln Tyr His Asp Ala Thr Gln Asp Asn Tyr Trp Gly Gln Gln Asp Ile
370 375 380
Thr Ser Glu Ser Cys Trp Gly Gln Leu Pro Thr Lys Ala Glu Leu Met
385 390 395 400
Ala Met Met Lys Glu Ala Gly Phe Gly Ala Ile Arg Val Pro Val Thr
405 410 415
Trp Tyr Asn His Met Asp Lys Asp Gly Asn Val Asp Ala Ala Trp Met
420 425 430
Asn Arg Val His Glu Val Val Asp Tyr Val Ile Ser Gln Gly Met Tyr
435 440 445
Cys Ile Leu Asn Val His His Asp Thr Gly Ala Asp Ser Tyr Asp Ser
450 455 460
Gln Lys Asn Leu Thr Gly Tyr His Trp Ile Lys Ala Asp Glu Thr Asn
465 470 475 480
Tyr Ala Thr Asn Lys Ala Arg Tyr Glu Lys Leu Trp Gln Gln Ile Ala
485 490 495
Gln Glu Phe Arg Asn Tyr Gly Gln Leu Leu Leu Phe Glu Gly Tyr Asn
500 505 510
Glu Met Leu Asp Ala Asn Asn Ser Trp Asn Phe Ala Gln Ser Ser Ser
515 520 525
Ala Tyr Asp Ala Ile Asn Lys Tyr Ala Gln Ser Phe Val Asp Val Val
530 535 540
Arg Ala Thr Gly Gly Asn Asn Ala Gln Arg Asn Leu Ile Val Ser Thr
545 550 555 560
Tyr Gly Ala Cys Ser Gly Asn Gly Thr Trp Asp Ala Arg Val Gln Asp
565 570 575
Pro Leu Lys Lys Leu Gln Ile Pro Thr Gly Glu Ser Asn His Ile Ile
580 585 590
Phe Glu Val His Asn Tyr Pro Ser Ile Val Asn Lys Asp Asn Ala Gly
595 600 605
Asn Tyr Val Ser Asp Arg Thr Ile Ser Glu Ile Lys Ala Glu Ile Asp
610 615 620
Ala Trp Leu Lys Asn Leu Lys Thr His Leu Val Ser Lys Gly Ala Pro
625 630 635 640
Val Ile Ile Gly Glu Trp Gly Thr Asn Asn Val Asp Ala Gly Gly Gly

```
                645                     650                     655
Lys Thr Asp Tyr Asp Leu His Lys Asp Leu Met Phe Glu Phe Val Ser
            660                     665                     670
Tyr Met Ile Lys Thr Met Lys Gln Asn Asp Ile Ala Thr Phe Tyr Trp
        675                     680                     685
Met Gly Leu Thr Asp Gly Ala Pro Arg Thr Tyr Pro Ala Phe Thr Gln
    690                     695                     700
Pro Asp Leu Ala Leu Lys Met Leu Gln Ala Tyr His Gly Asp Ser Trp
705                     710                     715                     720
Asn Pro Tyr Leu Pro Asp Ala Lys Asp Phe Pro Glu Gly Lys Ile Thr
                725                     730                     735
Ser Ala Thr Val Asn Phe Asn Ser Gln Trp Gly Glu Leu Thr Ile His
            740                     745                     750
Asp Gly Ala Ile Asp Lys Thr Val Tyr Arg Gly Ile Lys Val Glu Leu
        755                     760                     765
Glu Glu Lys Pro Ala Thr Gly Ala Leu Ser Phe Lys Val Tyr Ala Asn
    770                     775                     780
Ser Glu Lys Ala Thr Ala Ile Asn Ser Lys Thr Pro Gln Leu Ala Phe
785                     790                     795                     800
Phe Ser Tyr Thr Gly Ile Gln Lys Ile Asn Leu Gln Trp Asn Ile Ala
                805                     810                     815
Thr Lys Gly Ser Ile Lys Ile Lys Ser Val Asn Leu Ile Lys His Asp
            820                     825                     830
Asp Ser Thr Glu Pro Cys Ser Leu Lys Val Ala Trp Gly Cys Thr Leu
        835                     840                     845
Ser Asp Gln Asn Tyr Ala Thr Gly Ile Glu Asp Ile Thr Ile Thr Pro
    850                     855                     860
Val Arg His Asp Asp Gly Ile Ile Tyr Asn Leu Ser Gly Gln Pro Val
865                     870                     875                     880
Thr Ser Pro Gln Arg Gly Ile Tyr Ile Leu Asn Gly Lys Lys Ile Ile
                885                     890                     895

Lys


<210> 259
<211> 1143
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 259
atgaagaaaa ttcgcttact ccagggtgtt tcgttggcca tgtcaataat gtttcttttg      60
tcatgtcagg cacaaaaacc agttgactct cttaaggaag catttgatgg tttgtttctt     120
ataggtactg ccatgaacac ccctcagatc accggccagg atacacaaac acttgagttg     180
ataaaaaaac acatgaactc catagtggcc gaaaatgtaa tgaaaagtga ggtgcttcaa     240
cccagggaag gagagtttga ttttactctt gccgatcagt ttgttcaatt tggtatcgat     300
aacaatatgc atatagttgg ccataccctt atatggcatt cccaggcgcc acgatggttt     360
tttgtggatg agaacggaaa cgatgtgagc cccgaaattc tgaaacaaag aatgaaagac     420
catatttata ccgtagtagg ccgttataaa ggcaaaattc atggatggga tgtggtgaat     480
gagtgtataa atgacgatgg ttcgtggcgc aatagtaagt tttaccaaat tcttggtgaa     540
gattttgtta aatatgcatt ccagtttgca gctgaagccg atcccgatgc agagctttat     600
tacaatgatt attcgatgtt ccttccagga cgtagggaag gcgtaattaa gatggtgaga     660
aatctgcagg aacagggaat taaaattgat ggtattggga tgcagggcca cctgatgatt     720
gattatccac ccctcgaaga ttttgaaacg agtatactgg cttttgccga tctgggggtg     780
aatgtcatga taaccgaact cgatatatcc gttttgccat ttcctacccg caacgtgggc     840
gccgatgttt ctctgaacat tgcatacaat actgaattaa atccctaccc gaatggctta     900
cccgaagatg tagcgcagaa attacataat cggtgggtgg atctttttcg cctgttcatt     960
aaacaccacg ataaaattac ccgtgtaacc acttggggta cagccgatgc catgtcatgg    1020
aagaataact ggcccattcg tggacgtaca gattatccct tacttttcga tcgcgatttt    1080
cagcccaaac cctttgtcgc tgatataatt aaggaggcat tggcagccaa aagaaaatta    1140
taa                                                                  1143

<210> 260
<211> 380
<212> PRT
<213> Unknown
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<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(24)

<400> 260
Met Lys Lys Ile Arg Leu Leu Gln Gly Val Ser Leu Ala Met Ser Ile
1 5 10 15
Met Phe Leu Leu Ser Cys Gln Ala Gln Lys Pro Val Asp Ser Leu Lys
20 25 30
Glu Ala Phe Asp Gly Leu Phe Leu Ile Gly Thr Ala Met Asn Thr Pro
35 40 45
Gln Ile Thr Gly Gln Asp Thr Gln Thr Leu Glu Leu Ile Lys Lys His
50 55 60
Met Asn Ser Ile Val Ala Glu Asn Val Met Lys Ser Glu Val Leu Gln
65 70 75 80
Pro Arg Glu Gly Glu Phe Asp Phe Thr Leu Ala Asp Gln Phe Val Gln
85 90 95
Phe Gly Ile Asp Asn Asn Met His Ile Val Gly His Thr Leu Ile Trp
100 105 110
His Ser Gln Ala Pro Arg Trp Phe Phe Val Asp Glu Asn Gly Asn Asp
115 120 125
Val Ser Pro Glu Ile Leu Lys Gln Arg Met Lys Asp His Ile Tyr Thr
130 135 140
Val Val Gly Arg Tyr Lys Gly Lys Ile His Gly Trp Asp Val Val Asn
145 150 155 160
Glu Cys Ile Asn Asp Asp Gly Ser Trp Arg Asn Ser Lys Phe Tyr Gln
165 170 175
Ile Leu Gly Glu Asp Phe Val Lys Tyr Ala Phe Gln Phe Ala Ala Glu
180 185 190
Ala Asp Pro Asp Ala Glu Leu Tyr Tyr Asn Asp Tyr Ser Met Phe Leu
195 200 205
Pro Gly Arg Arg Glu Gly Val Ile Lys Met Val Arg Asn Leu Gln Glu
210 215 220
Gln Gly Ile Lys Ile Asp Gly Ile Gly Met Gln Gly His Leu Met Ile
225 230 235 240
Asp Tyr Pro Pro Leu Glu Asp Phe Glu Thr Ser Ile Leu Ala Phe Ala
245 250 255
Asp Leu Gly Val Asn Val Met Ile Thr Glu Leu Asp Ile Ser Val Leu
260 265 270
Pro Phe Pro Thr Arg Asn Val Gly Ala Asp Val Ser Leu Asn Ile Ala
275 280 285
Tyr Asn Thr Glu Leu Asn Pro Tyr Pro Asn Gly Leu Pro Glu Asp Val
290 295 300
Ala Gln Lys Leu His Asn Arg Trp Val Asp Leu Phe Arg Leu Phe Ile
305 310 315 320
Lys His His Asp Lys Ile Thr Arg Val Thr Thr Trp Gly Thr Ala Asp
325 330 335
Ala Met Ser Trp Lys Asn Asn Trp Pro Ile Arg Gly Arg Thr Asp Tyr
340 345 350
Pro Leu Leu Phe Asp Arg Asp Phe Gln Pro Lys Pro Phe Val Ala Asp
355 360 365
Ile Ile Lys Glu Ala Leu Ala Ala Lys Arg Lys Leu
370 375 380

<210> 261
<211> 1629
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 261
atgataaaca aaattggcaa aggttttttt tctgcgttca tttgtgctgc tgcgttgagt 60
gtctccacag ttaatgctca gcaaactgtc accaccaaca cgcaaggcac gcacgatggt 120
tttttctatt cgttttggaa agacagtggt gatgcatcat ttggtttgcg tgagggaggg 180
cgttacacct cgcaatggaa tacttctacc aataactggg tgggtggaaa agggtggaat 240

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cccggtggta gaagggttgt tcactatcaa ggccaatata atgttgataa ttcacaaaac     300
tcttatttgg cattgtatgg ctggacacgc tcaccactga ttgaatatta cgtgattgaa     360
agttacggct cgtataaccc gtcgaattgc acccaaggtc ggcagaccta tggcaccttt     420
cagagtgatg gtgcaaccta tgaaattgtt cgctgtcagc gagttcagca gccctctatc     480
gatggcacac aaactttcta tcaatacttc agtgtgcgtc agccgaagaa aggctttggt     540
agtatcagtg gtacgatcac tgtgggcaac cattttgatg catgggccgc cgccggtttg     600
aacctggggg aacatgatta tatggtgatg gctaccgagg gttatcagag caccggtagt     660
tcggatatta cggtcagtga aattaccggt ggttcaggtg gtggctcttc ctcgggtgct     720
aataccctgg tgattcgtgc tgtgggcacc tctggtaatg aattgctgcg tgtcaatgtg     780
ggtggtagcc ctgtgcagac attgagcctt tcgaccagtt ggcaggattt tactgtcaat     840
acggatgcaa cgggtgacat taacgtagag ttgtttaatg atcagggtca gggttatgag     900
gcgcgtatcg attatgtgct ggttaatggt gagacccgct acgcggccga tcagagttat     960
aacaccagtg cctgggacgg cgaatgtggg ggtggctctt ttacccagtg gatgcattgt    1020
gatggcatga ttggctttgg tgatatgacc ggcggcaatg ccggtggtgg cggttcttcg    1080
ggtggttctg gcgccaatac tctggtggtg cgtgctgtcg gcacttcagg taacgagcag    1140
ttgcgcgtga atgtgggcgg caacacgatt caaacactga acctgtcaag cagttggcaa    1200
gattttactg tcaataccga tgcctcgggc gatattaacg tagagctgtt taatgaccag    1260
ggtcagggct atgaggcgcg tattgattat gtgctggtta atggcgagac ccgctacgcg    1320
gctgaccaga gttataacac cagcgcctgg gatggcgaat gcgggggtgg ctcttttacc    1380
caatggatgc attgtgatgg catgattggt tttggtgata tgtcgggtgg tggttctgct    1440
gtgggtacaa gcagtagcgg taatgccggc agcaatacca gcagtgcctg ttactgtaat    1500
tggtatggca gtgtgatggc ttcttgtgaa aatcaggtga acggctgggg ttgggaaaat    1560
aatcaaagct gtattggtaa taatacctgt aataatcagg gcggtagcgg aggcgtggtg    1620
tgcaattaa                                                            1629
```

<210> 262
<211> 542
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(26)

<400> 262

```
Met Ile Asn Lys Ile Gly Lys Gly Phe Phe Ser Ala Phe Ile Cys Ala
 1               5                  10                  15
Ala Ala Leu Ser Val Ser Thr Val Asn Ala Gln Gln Thr Val Thr Thr
            20                  25                  30
Asn Thr Gln Gly Thr His Asp Gly Phe Phe Tyr Ser Phe Trp Lys Asp
        35                  40                  45
Ser Gly Asp Ala Ser Phe Gly Leu Arg Glu Gly Gly Arg Tyr Thr Ser
    50                  55                  60
Gln Trp Asn Thr Ser Thr Asn Asn Trp Val Gly Gly Lys Gly Trp Asn
65                  70                  75                  80
Pro Gly Gly Arg Arg Val Val His Tyr Gln Gly Gln Tyr Asn Val Asp
                85                  90                  95
Asn Ser Gln Asn Ser Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Ser Pro
            100                 105                 110
Leu Ile Glu Tyr Tyr Val Ile Glu Ser Tyr Gly Ser Tyr Asn Pro Ser
        115                 120                 125
Asn Cys Thr Gln Gly Arg Gln Thr Tyr Gly Thr Phe Gln Ser Asp Gly
    130                 135                 140
Ala Thr Tyr Glu Ile Val Arg Cys Gln Arg Val Gln Gln Pro Ser Ile
145                 150                 155                 160
Asp Gly Thr Gln Thr Phe Tyr Gln Tyr Phe Ser Val Arg Gln Pro Lys
                165                 170                 175
Lys Gly Phe Gly Ser Ile Ser Gly Thr Ile Thr Val Gly Asn His Phe
            180                 185                 190
Asp Ala Trp Ala Ala Ala Gly Leu Asn Leu Gly Glu His Asp Tyr Met
        195                 200                 205
Val Met Ala Thr Glu Gly Tyr Gln Ser Thr Gly Ser Ser Asp Ile Thr
    210                 215                 220
Val Ser Glu Ile Thr Gly Gly Ser Gly Gly Gly Ser Ser Ser Gly Ala
225                 230                 235                 240
Asn Thr Leu Val Ile Arg Ala Val Gly Thr Ser Gly Asn Glu Leu Leu
                245                 250                 255
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Arg Val Asn Val Gly Gly Ser Pro Val Gln Thr Leu Ser Leu Ser Thr
260 265 270
Ser Trp Gln Asp Phe Thr Val Asn Thr Asp Ala Thr Gly Asp Ile Asn
275 280 285
Val Glu Leu Phe Asn Asp Gln Gly Gln Gly Tyr Glu Ala Arg Ile Asp
290 295 300
Tyr Val Leu Val Asn Gly Glu Thr Arg Tyr Ala Ala Asp Gln Ser Tyr
305 310 315 320
Asn Thr Ser Ala Trp Asp Gly Glu Cys Gly Gly Gly Ser Phe Thr Gln
325 330 335
Trp Met His Cys Asp Gly Met Ile Gly Phe Gly Asp Met Thr Gly Gly
340 345 350
Asn Ala Gly Gly Gly Gly Ser Ser Gly Gly Ser Gly Ala Asn Thr Leu
355 360 365
Val Val Arg Ala Val Gly Thr Ser Gly Asn Glu Gln Leu Arg Val Asn
370 375 380
Val Gly Gly Asn Thr Ile Gln Thr Leu Asn Leu Ser Ser Ser Trp Gln
385 390 395 400
Asp Phe Thr Val Asn Thr Asp Ala Ser Gly Asp Ile Asn Val Glu Leu
405 410 415
Phe Asn Asp Gln Gly Gln Gly Tyr Glu Ala Arg Ile Asp Tyr Val Leu
420 425 430
Val Asn Gly Glu Thr Arg Tyr Ala Ala Asp Gln Ser Tyr Asn Thr Ser
435 440 445
Ala Trp Asp Gly Glu Cys Gly Gly Gly Ser Phe Thr Gln Trp Met His
450 455 460
Cys Asp Gly Met Ile Gly Phe Gly Asp Met Ser Gly Gly Gly Ser Ala
465 470 475 480
Val Gly Thr Ser Ser Ser Gly Asn Ala Gly Ser Asn Thr Ser Ser Ala
485 490 495
Cys Tyr Cys Asn Trp Tyr Gly Ser Val Met Ala Ser Cys Glu Asn Gln
500 505 510
Val Asn Gly Trp Gly Trp Glu Asn Asn Gln Ser Cys Ile Gly Asn Asn
515 520 525
Thr Cys Asn Asn Gln Gly Gly Ser Gly Gly Val Val Cys Asn
530 535 540

<210> 263
<211> 1092
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 263
atgaaaacta atcacccatt taaattcggg aaaaaaatat gtatggcatt ggctttgctg 60
gtgcttggca tacaggcttc aatcgcacag gaaatttgta ttaccagcgg cactgaccag 120
atcagagaaa ccacatccaa cggctatacc cacgaactat ggaatcagga cacccggggg 180
acggcctgta tgactattaa tgcaggcacc acttacagtg cgcggtggaa cggtgcattt 240
aactatttgg cccgccgtgg attggcctac gatggttcgt ccctcaccca tgctgaccgg 300
gggaaattca ccataaatta tgcctctaac tacaactgca acaatatgaa tgggctctct 360
tatttaagcg tgtacggatg gacgcgggat tttgccaagg aaaatgccaa tccggcagga 420
tcacaggctc atcaggaagc gctggtggaa tattacattg ttgaaaactg gtgcgactgg 480
aatgtttcac aagaccctaa cgcccagagt ctgggcaccc tgaatgttga tgggtcgatc 540
tatgatatgt atcgcacaga acggatcaac caaccttcta tcaggtgcgg tggtacctgc 600
gataattttt accaatactt cagcattcgc cgcaacacac gtaacagtgg caccattgat 660
gtcagcgctc atttcaacca gtgggaagca ttaaccggcg tccctatggg tggcctgcac 720
gaagtgatga tgaaggtcga aggctacaac tcaaacaatc aatccagtgg caatgtaagc 780
tttactcaat tgctcatgcg tgcccgcttc gaggatggcg ccattgtcga gaaccagaat 840
gcggtcggcc atgcgcacgg tggagaagcg gtgggagatg atcaccgccg tcttgccctg 900
ggccaggccc ttgaagcggg cgaacacctc ggcctcggcc ttggcgtcga gggcggcggt 960
gggttcgtcg agaatgatca actcggcgtc gcgcatatag gcgcgggcga tggctacctt 1020
ctgccactcg ccgcccgaga ggtcgcggcc ctgcttgaaa aggcgcccca attgctccag 1080
agaaacgggt ga 1092

<210> 264
<211> 363
<212> PRT

<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(29)

<400> 264
Met Lys Thr Asn His Pro Phe Lys Phe Gly Lys Lys Ile Cys Met Ala
1 5 10 15
Leu Ala Leu Leu Val Leu Gly Ile Gln Ala Ser Ile Ala Gln Glu Ile
20 25 30
Cys Ile Thr Ser Gly Thr Asp Gln Ile Arg Glu Thr Thr Ser Asn Gly
35 40 45
Tyr Thr His Glu Leu Trp Asn Gln Asp Thr Arg Gly Thr Ala Cys Met
50 55 60
Thr Ile Asn Ala Gly Thr Thr Tyr Ser Ala Arg Trp Asn Gly Ala Phe
65 70 75 80
Asn Tyr Leu Ala Arg Arg Gly Leu Ala Tyr Asp Gly Ser Ser Leu Thr
85 90 95
His Ala Asp Arg Gly Lys Phe Thr Ile Asn Tyr Ala Ser Asn Tyr Asn
100 105 110
Cys Asn Asn Met Asn Gly Leu Ser Tyr Leu Ser Val Tyr Gly Trp Thr
115 120 125
Arg Asp Phe Ala Lys Glu Asn Ala Asn Pro Ala Gly Ser Gln Ala His
130 135 140
Gln Glu Ala Leu Val Glu Tyr Tyr Ile Val Glu Asn Trp Cys Asp Trp
145 150 155 160
Asn Val Ser Gln Asp Pro Asn Ala Gln Ser Leu Gly Thr Leu Asn Val
165 170 175
Asp Gly Ser Ile Tyr Asp Met Tyr Arg Thr Glu Arg Ile Asn Gln Pro
180 185 190
Ser Ile Arg Cys Gly Gly Thr Cys Asp Asn Phe Tyr Gln Tyr Phe Ser
195 200 205
Ile Arg Arg Asn Thr Arg Asn Ser Gly Thr Ile Asp Val Ser Ala His
210 215 220
Phe Asn Gln Trp Glu Ala Leu Thr Gly Val Pro Met Gly Gly Leu His
225 230 235 240
Glu Val Met Met Lys Val Glu Gly Tyr Asn Ser Asn Asn Gln Ser Ser
245 250 255
Gly Asn Val Ser Phe Thr Gln Leu Leu Met Arg Ala Arg Phe Glu Asp
260 265 270
Gly Ala Ile Val Glu Asn Gln Asn Ala Val Gly His Ala His Gly Gly
275 280 285
Glu Ala Val Gly Asp Asp His Arg Arg Leu Ala Leu Gly Gln Ala Leu
290 295 300
Glu Ala Gly Glu His Leu Gly Leu Gly Leu Gly Val Glu Gly Gly Gly
305 310 315 320
Gly Phe Val Glu Asn Asp Gln Leu Gly Val Ala His Ile Gly Ala Gly
325 330 335
Asp Gly Tyr Leu Leu Pro Leu Ala Ala Arg Glu Val Ala Ala Leu Leu
340 345 350
Glu Lys Ala Pro Gln Leu Leu Gln Arg Asn Gly
355 360

<210> 265
<211> 996
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 265
atgaacagct ccctcccctc cctccgcgat gtattcgcga atgatttccg catcggggcg 60
gcggtcaatc ctgtgacgat cgagatgcaa aaacagttgt tgatcgatca tgtcaacagt 120
attacggcag agaaccatat gaagtttgag catcttcagc cggaagaagg gaaatttacc 180
tttcaggaag cggatcggat tgtggatttt gcttgttcgc accgaatggc ggttcgaggg 240

cacacacttg tatggcacaa ccagactccg gattgggtgt ttcaagatgg tcaaggccat 300
ttcgtcagtc gggatgtgtt gcttgagcgg atgaaatgtc acatttcaac tgttgtacgg 360
cgatacaagg gaaaaatata ttgttgggat gtcatcaacg aagcggtagc cgacgaagga 420
gacgaattgt tgaggccgtc gaagtggcga caaatcatcg ggacgattt tatggaacaa 480
gcatttctct acgcttatga agctgaccca gatgcactgc ttttttacaa tgactataat 540
gaatgttttc cggaaaagag agaaaaaatt tttgcacttg tcaaatcgct gcgtgataaa 600
ggcattccga ttcatggcat cggcatgcag gcgcactgga gcctgacccg cccgtcgctt 660
gatgaaattc gtgcggcgat tgaacggtat gcgtcccttg gtgttgttct tcatattacg 720
gaactcgatg tatccatgtt tgaatttcac gatcgtcgaa ccgatttggc tgtcccgacg 780
aacgaaatga tcgaacagca agcagaacgg tatgggcaaa tttttgcttt gtttaaggag 840
tatcgcgatg ttattcaaag tgtcacattt tggggaattg ctgatgacca tacatggctc 900
gataactttc cagtgcacgg gagaaaaaac tggccgcttt tgttcgatga acagcataaa 960
ccgaaaccag ctttttggcg ggcagtgagt gtctga 996

<210> 266
<211> 331
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 266
Met Asn Ser Ser Leu Pro Ser Leu Arg Asp Val Phe Ala Asn Asp Phe
1 5 10 15
Arg Ile Gly Ala Ala Val Asn Pro Val Thr Ile Glu Met Gln Lys Gln
20 25 30
Leu Leu Ile Asp His Val Asn Ser Ile Thr Ala Glu Asn His Met Lys
35 40 45
Phe Glu His Leu Gln Pro Glu Glu Gly Lys Phe Thr Phe Gln Glu Ala
50 55 60
Asp Arg Ile Val Asp Phe Ala Cys Ser His Arg Met Ala Val Arg Gly
65 70 75 80
His Thr Leu Val Trp His Asn Gln Thr Pro Asp Trp Val Phe Gln Asp
85 90 95
Gly Gln Gly His Phe Val Ser Arg Asp Val Leu Leu Glu Arg Met Lys
100 105 110
Cys His Ile Ser Thr Val Val Arg Arg Tyr Lys Gly Lys Ile Tyr Cys
115 120 125
Trp Asp Val Ile Asn Glu Ala Val Ala Asp Glu Gly Asp Glu Leu Leu
130 135 140
Arg Pro Ser Lys Trp Arg Gln Ile Ile Gly Asp Asp Phe Met Glu Gln
145 150 155 160
Ala Phe Leu Tyr Ala Tyr Glu Ala Asp Pro Asp Ala Leu Leu Phe Tyr
165 170 175
Asn Asp Tyr Asn Glu Cys Phe Pro Glu Lys Arg Glu Lys Ile Phe Ala
180 185 190
Leu Val Lys Ser Leu Arg Asp Lys Gly Ile Pro Ile His Gly Ile Gly
195 200 205
Met Gln Ala His Trp Ser Leu Thr Arg Pro Ser Leu Asp Glu Ile Arg
210 215 220
Ala Ala Ile Glu Arg Tyr Ala Ser Leu Gly Val Val Leu His Ile Thr
225 230 235 240
Glu Leu Asp Val Ser Met Phe Glu Phe His Asp Arg Arg Thr Asp Leu
245 250 255
Ala Val Pro Thr Asn Glu Met Ile Glu Gln Gln Ala Glu Arg Tyr Gly
260 265 270
Gln Ile Phe Ala Leu Phe Lys Glu Tyr Arg Asp Val Ile Gln Ser Val
275 280 285
Thr Phe Trp Gly Ile Ala Asp Asp His Thr Trp Leu Asp Asn Phe Pro
290 295 300
Val His Gly Arg Lys Asn Trp Pro Leu Leu Phe Asp Glu Gln His Lys
305 310 315 320
Pro Lys Pro Ala Phe Trp Arg Ala Val Ser Val
325 330

<210> 267
<211> 1956
<212> DNA

<213> Bacteria

<400> 267
atgaagcgta aggttaagaa gatggcagct atggcaacga gtataattat ggctatcatg 60
atcatcctac atagtatacc agtactcgcc gggcgaataa tttacgacaa tgagacaggc 120
acacatggag gctacgacta tgagctctgg aaagactacg gaaatacgat tatggaactt 180
aacgacggtg gtacttttag ttgtcaatgg agtaatatcg gtaatgcact atttagaaaa 240
gggagaaaat ttaattccga caaaacctat caagaattag gagatatagt agttgaatat 300
ggctgtgatt acaatccaaa cggaaattcc tatttgtgtg tttacggttg gacaagaaat 360
ccactggttg aatattacat tgtagaaagc tggggcagct ggcgtccacc tggagcaaca 420
cccaaaggaa ccatcacagt ggatggcggt acttatgaaa tatatgaaac tacccgggta 480
aatcagcctt ccatcgatgg aactgcgaca ttccaacaat attggagtgt tcgtacatcc 540
aagagaacaa gcggaacaat atctgtcact gaacatttta aacagtggga aagaatgggc 600
atgcgaatgg gtaagatgta tgaagttgct cttaccgttg aaggttatca gagcagtggg 660
tacgctaatg tatataagaa tgaaatcaga ataggtgcaa atccaactcc tgccccatct 720
caaagcccaa ttagaagaga tgcattttca ataatcgaag cggaagaata taacagcaca 780
aattcctcca ctttacaagt gattggaacg ccaaataatg gcagaggaat tggttatatt 840
gaaaatggta ataccgtaac ttacagcaat atagattttg gtagtggtgc aacagggttc 900
tctgcaactg ttgcaacgga ggttaatacc tcaattcaaa tccgttctga cagtcctatc 960
ggaactctac ttggtacctt atatgtaagt tctaccggca gctggaatac atatcaaacc 1020
gtatctacaa acatcagcaa aattaccggc gttcatgata ttgtattggt attctcaggt 1080
ccagtcaatg tggacaactt catatttagc agaagttcac cagtgcctgc acctggtgat 1140
aacacaagag acgcatattc tatcattcag gccgaggatt atgacagcag ttatggcccc 1200
aaccttcaaa tctttagctt accaggcggt ggcagcgcca ttggctatat tgaaaatggt 1260
tattccacta cctataataa cgttaatttc gccaacggct taagttctat aacagcaaga 1320
gttgccactc agatctcaac ttccattcag gtgagagcag gaggagcaac cggtacttta 1380
cttggtacaa tatatgttcc ttcgacaaat agttgggatt cttatcagaa tgtaactgcc 1440
aaccttagca atattacagg tgtgcatgat attacccttg tcttttcagg accagtgaat 1500
gtggactact tcgtatttac accagcaaat gtaaattcag ggcctacctc ccctgtcgga 1560
ggtacaagaa gtgcattttc caatattcaa gccgaagatt atgacagcag ttatggtccc 1620
aaccttcaaa tctttagctt accaggtggt ggcagcgcca ttggctatat tgaaaatggt 1680
tattccacta cctataaaaa tattgatttt ggtgacggcg caacgtccgt aacagcaaga 1740
gtagctaccc agaatgctac taccattcag gtaagattgg gaagtccatc gggtacatta 1800
cttggaacaa tttacgtggg gtccacagga agctttgata cttataggga tgtatccgct 1860
accattagta atactgcggg tgtaaaagat attgttcttg tattttcagg tcctgttaat 1920
gttgactggt ttgtattctc aaaatcagga acttaa 1956

<210> 268
<211> 651
<212> PRT
<213> Bacteria

<220>
<221> SIGNAL
<222> (1)...(30)

<400> 268
Met Lys Arg Lys Val Lys Lys Met Ala Ala Met Ala Thr Ser Ile Ile
1 5 10 15
Met Ala Ile Met Ile Ile Leu His Ser Ile Pro Val Leu Ala Gly Arg
20 25 30
Ile Ile Tyr Asp Asn Glu Thr Gly Thr His Gly Gly Tyr Asp Tyr Glu
35 40 45
Leu Trp Lys Asp Tyr Gly Asn Thr Ile Met Glu Leu Asn Asp Gly Gly
50 55 60
Thr Phe Ser Cys Gln Trp Ser Asn Ile Gly Asn Ala Leu Phe Arg Lys
65 70 75 80
Gly Arg Lys Phe Asn Ser Asp Lys Thr Tyr Gln Glu Leu Gly Asp Ile
85 90 95
Val Val Glu Tyr Gly Cys Asp Tyr Asn Pro Asn Gly Asn Ser Tyr Leu
100 105 110
Cys Val Tyr Gly Trp Thr Arg Asn Pro Leu Val Glu Tyr Tyr Ile Val
115 120 125
Glu Ser Trp Gly Ser Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr
130 135 140
Ile Thr Val Asp Gly Gly Thr Tyr Glu Ile Tyr Glu Thr Thr Arg Val
145 150 155 160
Asn Gln Pro Ser Ile Asp Gly Thr Ala Thr Phe Gln Gln Tyr Trp Ser
165 170 175

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Val Arg Thr Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Thr Glu His
            180                 185                 190
Phe Lys Gln Trp Glu Arg Met Gly Met Arg Met Gly Lys Met Tyr Glu
        195                 200                 205
Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Tyr Ala Asn Val
    210                 215                 220
Tyr Lys Asn Glu Ile Arg Ile Gly Ala Asn Pro Thr Pro Ala Pro Ser
225                 230                 235                 240
Gln Ser Pro Ile Arg Arg Asp Ala Phe Ser Ile Ile Glu Ala Glu Glu
                245                 250                 255
Tyr Asn Ser Thr Asn Ser Ser Thr Leu Gln Val Ile Gly Thr Pro Asn
            260                 265                 270
Asn Gly Arg Gly Ile Gly Tyr Ile Glu Asn Gly Asn Thr Val Thr Tyr
        275                 280                 285
Ser Asn Ile Asp Phe Gly Ser Gly Ala Thr Gly Phe Ser Ala Thr Val
    290                 295                 300
Ala Thr Glu Val Asn Thr Ser Ile Gln Ile Arg Ser Asp Ser Pro Ile
305                 310                 315                 320
Gly Thr Leu Leu Gly Thr Leu Tyr Val Ser Ser Thr Gly Ser Trp Asn
                325                 330                 335
Thr Tyr Gln Thr Val Ser Thr Asn Ile Ser Lys Ile Thr Gly Val His
            340                 345                 350
Asp Ile Val Leu Val Phe Ser Gly Pro Val Asn Val Asp Asn Phe Ile
        355                 360                 365
Phe Ser Arg Ser Ser Pro Val Pro Ala Pro Gly Asp Asn Thr Arg Asp
    370                 375                 380
Ala Tyr Ser Ile Ile Gln Ala Glu Asp Tyr Asp Ser Ser Tyr Gly Pro
385                 390                 395                 400
Asn Leu Gln Ile Phe Ser Leu Pro Gly Gly Gly Ser Ala Ile Gly Tyr
                405                 410                 415
Ile Glu Asn Gly Tyr Ser Thr Thr Tyr Asn Asn Val Asn Phe Ala Asn
            420                 425                 430
Gly Leu Ser Ser Ile Thr Ala Arg Val Ala Thr Gln Ile Ser Thr Ser
        435                 440                 445
Ile Gln Val Arg Ala Gly Gly Ala Thr Gly Thr Leu Leu Gly Thr Ile
    450                 455                 460
Tyr Val Pro Ser Thr Asn Ser Trp Asp Ser Tyr Gln Asn Val Thr Ala
465                 470                 475                 480
Asn Leu Ser Asn Ile Thr Gly Val His Asp Ile Thr Leu Val Phe Ser
                485                 490                 495
Gly Pro Val Asn Val Asp Tyr Phe Val Phe Thr Pro Ala Asn Val Asn
            500                 505                 510
Ser Gly Pro Thr Ser Pro Val Gly Gly Thr Arg Ser Ala Phe Ser Asn
        515                 520                 525
Ile Gln Ala Glu Asp Tyr Asp Ser Ser Tyr Gly Pro Asn Leu Gln Ile
    530                 535                 540
Phe Ser Leu Pro Gly Gly Gly Ser Ala Ile Gly Tyr Ile Glu Asn Gly
545                 550                 555                 560
Tyr Ser Thr Thr Tyr Lys Asn Ile Asp Phe Gly Asp Gly Ala Thr Ser
                565                 570                 575
Val Thr Ala Arg Val Ala Thr Gln Asn Ala Thr Thr Ile Gln Val Arg
            580                 585                 590
Leu Gly Ser Pro Ser Gly Thr Leu Leu Gly Thr Ile Tyr Val Gly Ser
        595                 600                 605
Thr Gly Ser Phe Asp Thr Tyr Arg Asp Val Ser Ala Thr Ile Ser Asn
    610                 615                 620
Thr Ala Gly Val Lys Asp Ile Val Leu Val Phe Ser Gly Pro Val Asn
625                 630                 635                 640
Val Asp Trp Phe Val Phe Ser Lys Ser Gly Thr
                645                 650
```

<210> 269
<211> 1110
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 269
atggggtaca ataggatcat acaagcgatc cgcgtaagca agggagatgt tttgggcgtt 60
cataaagttt tttacgctgc acttgcgtgt gtggcgatgg ggtattcgga aacgtgggca 120
cagtgcgcga cctggacccg aagcaccatt cgcaattgcg agggcatcga ctacgagttg 180
tggaaccaga acaaccgcgg cacggtcaac atggaaatca cgggaaacgg aacgttcgcg 240
gcgacgtgga gcggaacgga aaacatcctg tttcgcgccg gcaagaaatg gggttcaac 300
agcaccacga cggcgcggtc ggtcggcgcc atcacgctcg atttcgctgc gacctggacc 360
tccagcgaca acgtgaaaat gctcggcatc tacggctggg cgtattaccc gtcgggaagc 420
gagccgacga aaacggaaag cggtcaaaac acgagctttt ccgatcagat cgagtattac 480
atcatccagg accgcggagg cttcaacccg ggttccggcg gcgtcaacgc caaaaagtac 540
ggcgaggccg tgatcgacgg aatcgcctat gacttttggg tggccgaccg gatcaaccag 600
cccatgctga caggaagagg caacttcaag caatacttca gcgttccacg gaacacgagc 660
agccaccggc aaagcggcat cgtcagcatt tcgaagcact ttgaggagtg ggacaaggcc 720
ggcatgaaga tgctggactg tccgctatac gaagtcgcga tgaaggtgga atcgtatacg 780
ggctcggcga atggcggcgg gtcggcgaac gtgacccgga atattctcac gctcggcggt 840
tcttccgcac cgacccctat cgcgcgcggc cccggccggt ccgccgaaag catgcgggtc 900
gccttcgttc aggaaagagt gctcaaggtc gcgcccgtcg acggaacccg cctgcaagtc 960
aaggtgcggg acgtgaaggg cgtgaaccgg gccgagttca atgccgcggg cgcggcaacg 1020
ttctcgttgt cccatgtccc cgcgggcccg tatttcctgg atgtgacggg gccggatgta 1080
agacagatca cgccgttcgt tttgcgataa 1110

<210> 270
<211> 369
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 270
Met Gly Tyr Asn Arg Ile Ile Gln Ala Ile Arg Val Ser Lys Gly Asp
1 5 10 15
Val Leu Gly Val His Lys Val Phe Tyr Ala Ala Leu Ala Cys Val Ala
20 25 30
Met Gly Tyr Ser Glu Thr Trp Ala Gln Cys Ala Thr Trp Thr Arg Ser
35 40 45
Thr Ile Arg Asn Cys Glu Gly Ile Asp Tyr Glu Leu Trp Asn Gln Asn
50 55 60
Asn Arg Gly Thr Val Asn Met Glu Ile Thr Gly Asn Gly Thr Phe Ala
65 70 75 80
Ala Thr Trp Ser Gly Thr Glu Asn Ile Leu Phe Arg Ala Gly Lys Lys
85 90 95
Trp Gly Phe Asn Ser Thr Thr Thr Ala Arg Ser Val Gly Ala Ile Thr
100 105 110
Leu Asp Phe Ala Ala Thr Trp Thr Ser Ser Asp Asn Val Lys Met Leu
115 120 125
Gly Ile Tyr Gly Trp Ala Tyr Tyr Pro Ser Gly Ser Glu Pro Thr Lys
130 135 140
Thr Glu Ser Gly Gln Asn Thr Ser Phe Ser Asp Gln Ile Glu Tyr Tyr
145 150 155 160
Ile Ile Gln Asp Arg Gly Gly Phe Asn Pro Gly Ser Gly Gly Val Asn
165 170 175
Ala Lys Lys Tyr Gly Glu Ala Val Ile Asp Gly Ile Ala Tyr Asp Phe
180 185 190
Trp Val Ala Asp Arg Ile Asn Gln Pro Met Leu Thr Gly Arg Gly Asn
195 200 205
Phe Lys Gln Tyr Phe Ser Val Pro Arg Asn Thr Ser Ser His Arg Gln
210 215 220
Ser Gly Ile Val Ser Ile Ser Lys His Phe Glu Glu Trp Asp Lys Ala
225 230 235 240
Gly Met Lys Met Leu Asp Cys Pro Leu Tyr Glu Val Ala Met Lys Val
245 250 255
Glu Ser Tyr Thr Gly Ser Ala Asn Gly Gly Gly Ser Ala Asn Val Thr
260 265 270
Arg Asn Ile Leu Thr Leu Gly Gly Ser Ser Ala Pro Thr Pro Ile Ala
275 280 285
Arg Gly Pro Gly Arg Ser Ala Glu Ser Met Arg Val Ala Phe Val Gln
290 295 300
Glu Arg Val Leu Lys Val Ala Pro Val Asp Gly Thr Arg Leu Gln Val

305 310 315 320
Lys Val Arg Asp Val Lys Gly Val Asn Arg Ala Glu Phe Asn Ala Ala
325 330 335
Gly Ala Ala Thr Phe Ser Leu Ser His Val Pro Ala Gly Pro Tyr Phe
340 345 350
Leu Asp Val Thr Gly Pro Asp Val Arg Gln Ile Thr Pro Phe Val Leu
355 360 365
Arg

<210> 271
<211> 1128
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 271
atgttcattc acaacagcat atgcagcgca ctctgcacaa tctttttggc aactgcaaca 60
atgggagaaa acatgacact acaagaagcc tttgccgatc acttttatgt gggagccgcc 120
atcagccaac gcctttttca accagatcgc gccgaaacgc tgcaactggc cgcgcaccaa 180
ttcaacagca tcacagccga aaatgagatg aagtggcagt cgttaaatcc cactcctggc 240
gaataccgtt tcgaaaacgc cgataaattc gtccgctttg gtgtcgaaaa cgatatgtac 300
atcgttgggc acgttctctt ctggcacagc cagacacccg actggctctt caaggatgac 360
gacggtaact tcgtctcccg cgaagtctta ctcgaccgca tgcgcgccca cgtgcgcaat 420
cttgtccagc gctacggcaa ccatgtgcac gcctgggatg ttatcaatga aaccttcaat 480
gataatggtt ccttgcgcga cagcccatgg acgcaaatcc tcggcgagga attcatcgag 540
cacgccttcc ggattgccgg cgaggaactc cccccccatg tcgagctgct ctacaatgat 600
tattcgatga ccattcctgc caagcgcgat gctgttgctg aaatggttcg cgacctcata 660
gccaaaggca tccgcattga cggcgttggc atgcagggac attgggcacg gacccacccg 720
accatagcgg acatagaaaa aagcattctt gccttcgcag gaaccggcgt acaggtacac 780
atcactgagc tcgacatcga catgctgcca cgccatcccc agatgtttac tggtggtgca 840
gacaccatgt tgcgcctaca acaagatccc aaactcgacc cctacactga gggacttcca 900
gcggaagatc agcaggcatt ggcagaacgc tacgcaagca tcttccgttt attcttgaag 960
cacagcgatg ttattcgccg tgtcaccttc tgggggtca ccgatgccca cacctggctc 1020
aacaattggc ccatccgtgg ccgcaccagc catcccctgc tcttcgaccg ccagaacaac 1080
cccaaacccg ccttccacgc cgtcgtcaga ctgaagaccg aagactga 1128

<210> 272
<211> 375
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(22)

<400> 272
Met Phe Ile His Asn Ser Ile Cys Ser Ala Leu Cys Thr Ile Phe Leu
1 5 10 15
Ala Thr Ala Thr Met Gly Glu Asn Met Thr Leu Gln Glu Ala Phe Ala
20 25 30
Asp His Phe Tyr Val Gly Ala Ala Ile Ser Gln Arg Leu Phe Gln Pro
35 40 45
Asp Arg Ala Glu Thr Leu Gln Leu Ala Ala His Gln Phe Asn Ser Ile
50 55 60
Thr Ala Glu Asn Glu Met Lys Trp Gln Ser Leu Asn Pro Thr Pro Gly
65 70 75 80
Glu Tyr Arg Phe Glu Asn Ala Asp Lys Phe Val Arg Phe Gly Val Glu
85 90 95
Asn Asp Met Tyr Ile Val Gly His Val Leu Phe Trp His Ser Gln Thr
100 105 110
Pro Asp Trp Leu Phe Lys Asp Asp Asp Gly Asn Phe Val Ser Arg Glu
115 120 125
Val Leu Leu Asp Arg Met Arg Ala His Val Arg Asn Leu Val Gln Arg
130 135 140

Tyr Gly Asn His Val His Ala Trp Asp Val Ile Asn Glu Thr Phe Asn
145 150 155 160
Asp Asn Gly Ser Leu Arg Asp Ser Pro Trp Thr Gln Ile Leu Gly Glu
165 170 175
Glu Phe Ile Glu His Ala Phe Arg Ile Ala Gly Glu Glu Leu Pro Pro
180 185 190
His Val Glu Leu Leu Tyr Asn Asp Tyr Ser Met Thr Ile Pro Ala Lys
195 200 205
Arg Asp Ala Val Ala Glu Met Val Arg Asp Leu Ile Ala Lys Gly Ile
210 215 220
Arg Ile Asp Gly Val Gly Met Gln Gly His Trp Ala Arg Thr His Pro
225 230 235 240
Thr Ile Ala Asp Ile Glu Lys Ser Ile Leu Ala Phe Ala Gly Thr Gly
245 250 255
Val Gln Val His Ile Thr Glu Leu Asp Ile Asp Met Leu Pro Arg His
260 265 270
Pro Gln Met Phe Thr Gly Gly Ala Asp Thr Met Leu Arg Leu Gln Gln
275 280 285
Asp Pro Lys Leu Asp Pro Tyr Thr Glu Gly Leu Pro Ala Glu Asp Gln
290 295 300
Gln Ala Leu Ala Glu Arg Tyr Ala Ser Ile Phe Arg Leu Phe Leu Lys
305 310 315 320
His Ser Asp Val Ile Arg Arg Val Thr Phe Trp Gly Val Thr Asp Ala
325 330 335
His Thr Trp Leu Asn Asn Trp Pro Ile Arg Gly Arg Thr Ser His Pro
340 345 350
Leu Leu Phe Asp Arg Gln Asn Asn Pro Lys Pro Ala Phe His Ala Val
355 360 365
Val Arg Leu Lys Thr Glu Asp
370 375

<210> 273
<211> 1134
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 273
atggtttcat cgctaatcaa ttcttcatac attcggctca agcactattc gtgctcaagt 60
ttattgctcc tgacattggc agcctgtggc ggccagcagc ctcccccgga tacgggatcc 120
agcacttcaa gttcaagcag ttcttcgagc tccagttcaa gcagctcttc aagttccagc 180
tcaagcagtt cttccagctc cagctcgagc agctcttcga gttcgagctc ttcatcatcc 240
agctcttcag gggcaaaccc gccaccgacc gggggcaagt tcgtcggcaa catcacgacc 300
cgaggcgccg tccaagcgga cttcattcag tactgggatc aaattacgcc ggagaacgag 360
ggcaaatggg gttctgtgga aggaactcgc gaccagtaca actgggcgcc tcttgatcgc 420
atctatgact atgcacgtca gcacaatatc ccagtcaaag cgcatacgct ggtttggggt 480
gcacaggctc caggctggat caacaatctg agtgcggccg agcagcgtga ggaaatcgag 540
gaatggattc gtgattactg cacgcgttac ccagacaccc aaatgatcga cgtagttaac 600
gaggcgcacc caaatcacgc cccgctcgc tatgcgcaga atgccttcgg caatgactgg 660
attaccgaag cgttcaaact ggcgcgccgg cactgcccca acgccatttt gatctacaac 720
gactataatt tcatcacttg ggataccgat gaaatcatgg cgctgattcg cccggctatc 780
gcagcagggg tagtggatgc ggtagggctg caggcgcata gcttgtatcc tgacgaatac 840
gctaacaaga tgtggagtgc cgctgaaata cagcagaagc tcgatctgat ctctaccctt 900
ggcgtgccga tgtatatttc ggaatatgat gtcgccaagt ccaatgacca agagcagttg 960
gcgattttca gcgagcagtt cccggtcctt tacgaacacc ccaatgtcgt aggtgtaacc 1020
ctctggggct atattgatgg agcgacgtgg cgcgccggct cgggcttgat tcgaaacggt 1080
cagcaccggc ccgccatgca atggctgctc gagtacttgg agaacaatcg atag 1134

<210> 274
<211> 377
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(74)

<400> 274
Met Val Ser Ser Leu Ile Asn Ser Ser Tyr Ile Arg Leu Lys His Tyr
1   5   10   15
Ser Cys Ser Ser Leu Leu Leu Leu Thr Leu Ala Ala Cys Gly Gly Gln
            20   25   30
Gln Pro Pro Pro Asp Thr Gly Ser Ser Thr Ser Ser Ser Ser Ser Ser
        35   40   45
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
    50   55   60
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
65   70   75   80
Ser Ser Ser Gly Ala Asn Pro Pro Pro Thr Gly Gly Lys Phe Val Gly
                85   90   95
Asn Ile Thr Thr Arg Gly Ala Val Gln Ala Asp Phe Ile Gln Tyr Trp
            100   105   110
Asp Gln Ile Thr Pro Glu Asn Glu Gly Lys Trp Gly Ser Val Glu Gly
        115   120   125
Thr Arg Asp Gln Tyr Asn Trp Ala Pro Leu Asp Arg Ile Tyr Asp Tyr
    130   135   140
Ala Arg Gln His Asn Ile Pro Val Lys Ala His Thr Leu Val Trp Gly
145   150   155   160
Ala Gln Ala Pro Gly Trp Ile Asn Asn Leu Ser Ala Ala Glu Gln Arg
                165   170   175
Glu Glu Ile Glu Glu Trp Ile Arg Asp Tyr Cys Thr Arg Tyr Pro Asp
            180   185   190
Thr Gln Met Ile Asp Val Val Asn Glu Ala His Pro Asn His Ala Pro
        195   200   205
Ala Arg Tyr Ala Gln Asn Ala Phe Gly Asn Asp Trp Ile Thr Glu Ala
    210   215   220
Phe Lys Leu Ala Arg Arg His Cys Pro Asn Ala Ile Leu Ile Tyr Asn
225   230   235   240
Asp Tyr Asn Phe Ile Thr Trp Asp Thr Asp Glu Ile Met Ala Leu Ile
                245   250   255
Arg Pro Ala Ile Ala Ala Gly Val Val Asp Ala Val Gly Leu Gln Ala
            260   265   270
His Ser Leu Tyr Pro Asp Glu Tyr Ala Asn Lys Met Trp Ser Ala Ala
        275   280   285
Glu Ile Gln Gln Lys Leu Asp Leu Ile Ser Thr Leu Gly Val Pro Met
    290   295   300
Tyr Ile Ser Glu Tyr Asp Val Ala Lys Ser Asn Asp Gln Glu Gln Leu
305   310   315   320
Ala Ile Phe Ser Glu Gln Phe Pro Val Leu Tyr Glu His Pro Asn Val
                325   330   335
Val Gly Val Thr Leu Trp Gly Tyr Ile Asp Gly Ala Thr Trp Arg Ala
            340   345   350
Gly Ser Gly Leu Ile Arg Asn Gly Gln His Arg Pro Ala Met Gln Trp
        355   360   365
Leu Leu Glu Tyr Leu Glu Asn Asn Arg
    370   375

<210> 275
<211> 1401
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 275
ttgggcgctg atccatttgc gctcacctat aacggaagag tgtacattta tatgtcgagt 60
gatgactatg aatatcacag caatggaacg attaaggata attcttttgc caatttgaat 120
agggtctttg tcatctcttc agcagatatg gtgaactgga cagatcatgg cgcgattcca 180
gtagctgggg caaatggcgc aaatggcggc aaaggaattg ccaaatgggc aggtgcttcc 240
tgggctccat cagcagcggt gaaaaaaatc aatgggaagg ataaattttt cctttatttc 300
gcgaacagcg gcggagggat tggcgttctg acagcagact cccccatcgg tccatggaca 360
gatcctatcg gaaaagcact cgtcacgcca aatacaccag ggatggctgg agttgtatgg 420
ctttttgatc ctgccgtttt tgtagatgat gacggcactg gttatctata tgccggcgga 480

ggtgttccag gcggttctaa tccaacgcag ggacaatggg cgaatcctaa aacagcaaga 540
gttctaaaac taggacctga tatgacaagt gtggtaggca gcgcatcaac cattgatgct 600
ccttttatgt ttgaagattc ggggatgcat aagtataacg gaacctatta ctattcctat 660
tgcatcaact ttggcggctc ccacccagca gataaaccac ctggtgagat cggttatatg 720
acgagctcaa gtccgatggg tccctttacg tatagagggc acttcctgaa aaatccgggt 780
gcatttttcg gggaggcgg taataaccat catgctgtgt tcaattttaa aaacgagtgg 840
tatgtcgtgt atcataccca aacggtcagc tctgctttat acggatcagg aaaaggctac 900
agatctccgc atattaataa acttgtgcat aatgctgacg gctcccttcg agaagtcgca 960
gccaattttg aaggggttaa acagctttcc aacctgaatc cttatcagcg tgtagaagct 1020
gaaacattcg catggaatgg acgcattttg acagaggcat cttcagctcc aggcggaccg 1080
gtcaataacc agcatgtcac aaacattcaa aacggagatt gggtggctgc cagtaacgtc 1140
gatttcggat caaacggcgc gaggacattt aaagcgaatg tagcatcaaa tacaggcggg 1200
aaaatagaag tacgcctcgg aagtccagac ggcagactcg tcggaacact gaatgtccct 1260
tccacagggg gaacaaataa ctggcgagaa gtagaaacgg cagtaaatgg agcagcaggc 1320
gtgcacaacg tatttttgt ttttactgga acaggtgcaa atctatttca atttgattcc 1380
tggcagttta ctcaaaggta a 1401

<210> 276
<211> 466
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 276
Met Gly Ala Asp Pro Phe Ala Leu Thr Tyr Asn Gly Arg Val Tyr Ile
1 5 10 15
Tyr Met Ser Ser Asp Asp Tyr Glu Tyr His Ser Asn Gly Thr Ile Lys
20 25 30
Asp Asn Ser Phe Ala Asn Leu Asn Arg Val Phe Val Ile Ser Ser Ala
35 40 45
Asp Met Val Asn Trp Thr Asp His Gly Ala Ile Pro Val Ala Gly Ala
50 55 60
Asn Gly Ala Asn Gly Gly Lys Gly Ile Ala Lys Trp Ala Gly Ala Ser
65 70 75 80
Trp Ala Pro Ser Ala Ala Val Lys Lys Ile Asn Gly Lys Asp Lys Phe
85 90 95
Phe Leu Tyr Phe Ala Asn Ser Gly Gly Gly Ile Gly Val Leu Thr Ala
100 105 110
Asp Ser Pro Ile Gly Pro Trp Thr Asp Pro Ile Gly Lys Ala Leu Val
115 120 125
Thr Pro Asn Thr Pro Gly Met Ala Gly Val Val Trp Leu Phe Asp Pro
130 135 140
Ala Val Phe Val Asp Asp Asp Gly Thr Gly Tyr Leu Tyr Ala Gly Gly
145 150 155 160
Gly Val Pro Gly Gly Ser Asn Pro Thr Gln Gly Gln Trp Ala Asn Pro
165 170 175
Lys Thr Ala Arg Val Leu Lys Leu Gly Pro Asp Met Thr Ser Val Val
180 185 190
Gly Ser Ala Ser Thr Ile Asp Ala Pro Phe Met Phe Glu Asp Ser Gly
195 200 205
Met His Lys Tyr Asn Gly Thr Tyr Tyr Tyr Ser Tyr Cys Ile Asn Phe
210 215 220
Gly Gly Ser His Pro Ala Asp Lys Pro Pro Gly Glu Ile Gly Tyr Met
225 230 235 240
Thr Ser Ser Ser Pro Met Gly Pro Phe Thr Tyr Arg Gly His Phe Leu
245 250 255
Lys Asn Pro Gly Ala Phe Phe Gly Gly Gly Gly Asn Asn His His Ala
260 265 270
Val Phe Asn Phe Lys Asn Glu Trp Tyr Val Val Tyr His Thr Gln Thr
275 280 285
Val Ser Ser Ala Leu Tyr Gly Ser Gly Lys Gly Tyr Arg Ser Pro His
290 295 300
Ile Asn Lys Leu Val His Asn Ala Asp Gly Ser Leu Arg Glu Val Ala
305 310 315 320
Ala Asn Phe Glu Gly Val Lys Gln Leu Ser Asn Leu Asn Pro Tyr Gln
325 330 335
Arg Val Glu Ala Glu Thr Phe Ala Trp Asn Gly Arg Ile Leu Thr Glu

```
                340                 345                 350
Ala Ser Ser Ala Pro Gly Gly Pro Val Asn Asn Gln His Val Thr Asn
        355                 360                 365
Ile Gln Asn Gly Asp Trp Val Ala Ala Ser Asn Val Asp Phe Gly Ser
    370                 375                 380
Asn Gly Ala Arg Thr Phe Lys Ala Asn Val Ala Ser Asn Thr Gly Gly
385                 390                 395                 400
Lys Ile Glu Val Arg Leu Gly Ser Pro Asp Gly Arg Leu Val Gly Thr
                405                 410                 415
Leu Asn Val Pro Ser Thr Gly Gly Thr Asn Asn Trp Arg Glu Val Glu
            420                 425                 430
Thr Ala Val Asn Gly Ala Ala Gly Val His Asn Val Phe Phe Val Phe
        435                 440                 445
Thr Gly Thr Gly Ala Asn Leu Phe Gln Phe Asp Ser Trp Gln Phe Thr
    450                 455                 460
Gln Arg
465
```

<210> 277
<211> 1128
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 277

```
atgcgaaaca cattaatcct tttgattccg gccttgatga tgctttcttg cagtgcggga      60
aatcaggata gagtaccatc cctgcacgcc gagttctcgg atgcattttt gattggaacg     120
gcgctgaatt ctgagcagat attgggtcgg gatacacgcg gactcgaatt gattagaact     180
cattttaacg ccattacgcc cgaaaacatt accaaatggg aggctatcca tcccgaaccc     240
ggtgtctatg attttaaaga ggctgatgca ttcgtcgatt ttggccaaaa atataatatg     300
ttcatggtgg gtcatacact ggtttggcat agtcagacac cgcgctgggt cttcaaagac     360
gaaaatggcg cgttggtatc gcgcgaggta ctgttagagc ggatgcgcga ccacatccac     420
accgttgttg gccgctaccg tggacgtatt cacggctggg atgtcgtaaa cgaagccctc     480
aatgaagacg gttcgtacag agaaacactg tggtaccaaa taattggtac ggactatatt     540
cttaaagcat tcgaatttgc ccgggaggcc gatcccgacg ctgagctata ctataacgat     600
tactcgcttg agaacccctc aaagagagcc ggcgcgatgc gaattgttca atacctgcag     660
gaacatggtg ctccgattac tggggttgga acccaggggc atttcaccct cgactggccc     720
gaactttctg aaattgaaca gaccgtcatt gattttgcct cccttggtat ggatgtaatg     780
attaccgaat tggatatcga tgtactgcct cagccagacg attatactgg cgccgatgtg     840
aattttagcg cagagcttta cgacgaactg aacccatggc ccaacggcct tccaccggaa     900
attgaacagg aattggccaa tcgatatgcc gacatcttcg aaatctattt gcgtcatcgt     960
gataaagtta cgcgagtgtc tttttggggt gtcacagatg gcgactcgtg gaaaaataac    1020
tggcctgtgc caggtcgtac caactatccg ctcatttttg atcgaaactg gaagccaaaa    1080
cccgcttttt tctcgattgt tgatgcagcc agggaggcac tggattaa                1128
```

<210> 278
<211> 375
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(19)

<400> 278

```
Met Arg Asn Thr Leu Ile Leu Leu Ile Pro Ala Leu Met Met Leu Ser
1               5                   10                  15
Cys Ser Ala Gly Asn Gln Asp Arg Val Pro Ser Leu His Ala Glu Phe
            20                  25                  30
Ser Asp Ala Phe Leu Ile Gly Thr Ala Leu Asn Ser Glu Gln Ile Leu
        35                  40                  45
Gly Arg Asp Thr Arg Gly Leu Glu Leu Ile Arg Thr His Phe Asn Ala
    50                  55                  60
Ile Thr Pro Glu Asn Ile Thr Lys Trp Glu Ala Ile His Pro Glu Pro
65                  70                  75                  80
```

```
Gly Val Tyr Asp Phe Lys Glu Ala Asp Ala Phe Val Asp Phe Gly Gln
                85                  90                  95
Lys Tyr Asn Met Phe Met Val Gly His Thr Leu Val Trp His Ser Gln
            100                 105                 110
Thr Pro Arg Trp Val Phe Lys Asp Glu Asn Gly Ala Leu Val Ser Arg
        115                 120                 125
Glu Val Leu Leu Glu Arg Met Arg Asp His Ile His Thr Val Val Gly
    130                 135                 140
Arg Tyr Arg Gly Arg Ile His Gly Trp Asp Val Val Asn Glu Ala Leu
145                 150                 155                 160
Asn Glu Asp Gly Ser Tyr Arg Glu Thr Leu Trp Tyr Gln Ile Ile Gly
                165                 170                 175
Thr Asp Tyr Ile Leu Lys Ala Phe Glu Phe Ala Arg Glu Ala Asp Pro
            180                 185                 190
Asp Ala Glu Leu Tyr Tyr Asn Asp Tyr Ser Leu Glu Asn Pro Ser Lys
        195                 200                 205
Arg Ala Gly Ala Met Arg Ile Val Gln Tyr Leu Gln Glu His Gly Ala
    210                 215                 220
Pro Ile Thr Gly Val Gly Thr Gln Gly His Phe Thr Leu Asp Trp Pro
225                 230                 235                 240
Glu Leu Ser Glu Ile Glu Gln Thr Val Ile Asp Phe Ala Ser Leu Gly
                245                 250                 255
Met Asp Val Met Ile Thr Glu Leu Asp Ile Asp Val Leu Pro Gln Pro
            260                 265                 270
Asp Asp Tyr Thr Gly Ala Asp Val Asn Phe Ser Ala Glu Leu Tyr Asp
        275                 280                 285
Glu Leu Asn Pro Trp Pro Asn Gly Leu Pro Pro Glu Ile Glu Gln Glu
    290                 295                 300
Leu Ala Asn Arg Tyr Ala Asp Ile Phe Glu Ile Tyr Leu Arg His Arg
305                 310                 315                 320
Asp Lys Val Thr Arg Val Ser Phe Trp Gly Val Thr Asp Gly Asp Ser
                325                 330                 335
Trp Lys Asn Asn Trp Pro Val Pro Gly Arg Thr Asn Tyr Pro Leu Ile
            340                 345                 350
Phe Asp Arg Asn Trp Lys Pro Lys Pro Ala Phe Phe Ser Ile Val Asp
        355                 360                 365
Ala Ala Arg Glu Ala Leu Asp
    370                 375
```

<210> 279
<211> 786
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 279
```
atgctttctc cgacaaggaa actcccgccg gccattggac tcaccttcct cttcgccgct      60
tcggcgacgc cggaaaccac gctcaaggac gccttcgcgg accattttct cgtcggggcg     120
gcgctcaatg aatcgcactt tgcggagcac aatccggcgc acgccggtct cgtcgccgca     180
aacttcaatg cgatcaccgc ggagaatgtg atgaaatggg aggccgttca tccccggccg     240
ggagaatata cgttcggcgc cgcggaccgg ttcgttgagt tcggggaaaa gaacggcctg     300
ttcatcgtgg ggcacacgct gatctggcat tctcaaacgc cggcctgggt tttcgaggat     360
gagaatggcg cgccgctcgg ccgcgaggcg ctgctggagc ggatgcgcga tcacattcac     420
accgttgccg gacgttacag gggccgtgtg aaggggtggg acgtggtcaa cgaagccctc     480
gccgaggacg gttccctgcg ggattcgccg tggcgccgca tcataggcga cgactatttc     540
gtgaaggcct ttgagtttgc gcgggaagct gatccggatg cggagttgta ttacaacgat     600
tactcgattg aaaacgaacc gaagcgcaag gggcggtgg cgttggtgag gacgctccag      660
gcggcgggtg ttcccgttgc cggcgtgggg attcagggac acggcaatct ccattggcct     720
tctccgcggc ttgtcgaaga ggcgatccgg gactttgcca gtttggcgt caaggtgatg      780
atctga                                                                786
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<210> 280
<211> 261
<212> PRT
<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(22)

<400> 280
Met Leu Ser Pro Thr Arg Lys Leu Pro Pro Ala Ile Gly Leu Thr Phe
1 5 10 15
Leu Phe Ala Ala Ser Ala Thr Pro Glu Thr Thr Leu Lys Asp Ala Phe
20 25 30
Ala Asp His Phe Leu Val Gly Ala Ala Leu Asn Glu Ser His Phe Ala
35 40 45
Glu His Asn Pro Ala His Ala Gly Leu Val Ala Ala Asn Phe Asn Ala
50 55 60
Ile Thr Ala Glu Asn Val Met Lys Trp Glu Ala Val His Pro Arg Pro
65 70 75 80
Gly Glu Tyr Thr Phe Gly Ala Ala Asp Arg Phe Val Glu Phe Gly Glu
85 90 95
Lys Asn Gly Leu Phe Ile Val Gly His Thr Leu Ile Trp His Ser Gln
100 105 110
Thr Pro Ala Trp Val Phe Glu Asp Glu Asn Gly Ala Pro Leu Gly Arg
115 120 125
Glu Ala Leu Leu Glu Arg Met Arg Asp His Ile His Thr Val Ala Gly
130 135 140
Arg Tyr Arg Gly Arg Val Lys Gly Trp Asp Val Val Asn Glu Ala Leu
145 150 155 160
Ala Glu Asp Gly Ser Leu Arg Asp Ser Pro Trp Arg Arg Ile Ile Gly
165 170 175
Asp Asp Tyr Phe Val Lys Ala Phe Glu Phe Ala Arg Glu Ala Asp Pro
180 185 190
Asp Ala Glu Leu Tyr Tyr Asn Asp Tyr Ser Ile Glu Asn Glu Pro Lys
195 200 205
Arg Lys Gly Ala Val Ala Leu Val Arg Thr Leu Gln Ala Ala Gly Val
210 215 220
Pro Val Ala Gly Val Gly Ile Gln Gly His Gly Asn Leu His Trp Pro
225 230 235 240
Ser Pro Arg Leu Val Glu Glu Ala Ile Arg Asp Phe Ala Ser Leu Gly
245 250 255
Val Lys Val Met Ile
260

<210> 281
<211> 963
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 281
gtgggcacct gcatgagcgg ggccgattcg cgcaaccctg cccgtctgga gctgatcaga 60
acgcagtaca gcatcatcac ccccggaaaac gagctcaagc ccgattccgt tctggatgtg 120
gctgccagcc gtgctctggc caaggaggac gataccgccg tggccgtgca tttcagcgcc 180
gccgctccca tcctgaactt tgcccgtgac aacggcatca aggtgcacgg tcatgtgctg 240
gtctggcaca gccagactcc cgaggagttc ttccacgagg gctataacgc ctccgcgccc 300
tatgtgagcc gcgaggtgat gctggcccgt ctggacaact acatccgtct catctttgaa 360
tatatggatg aaaactatcc cggcctgatc gtgtcctggg atgtggccaa cgaatgcgtg 420
gccgacggct ccaccgccct gcgcacctcc aactggaccc gcgtggtggg gcaggatttt 480
gtggcccgcg ccttcgagat cgccgataaa tacgcgcccg aagatgtgat gctctgctac 540
aacgattatt ccactcccta tgagcccaag ctcaccggca tcgtgaacct gctcaccgag 600
ctgacacagg agggtcatat cgacggctac ggcttccaga gccactacag tgtcggcgat 660
ccctccctgc aggcggtcga gaacgcgttc aaaaagatct ccgccctggg gctcaagctg 720
cgcgtgagcg agctggacat caaggtagat gccgacagcg agcccaaccg cgcccttcag 780
gccgaccggt atgaggccct gctgcgcatc tatatgaaat acggcgtcag cgccgtgcag 840
gtgtggggcg tatgcgacgg caccagctgg atcggcgcga gctatcccct cccctttgac 900
gccgggctgc gtcccaagcc ctccttcttc ggcatactcc gcgcccttga cgaacagaac 960
tga 963

<210> 282

<211> 320
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 282
Met Gly Thr Cys Met Ser Gly Ala Asp Ser Arg Asn Pro Ala Arg Leu
1 5 10 15
Glu Leu Ile Arg Thr Gln Tyr Ser Ile Ile Thr Pro Glu Asn Glu Leu
20 25 30
Lys Pro Asp Ser Val Leu Asp Val Ala Ala Ser Arg Ala Leu Ala Lys
35 40 45
Glu Asp Asp Thr Ala Val Ala Val His Phe Ser Ala Ala Ala Pro Ile
50 55 60
Leu Asn Phe Ala Arg Asp Asn Gly Ile Lys Val His Gly His Val Leu
65 70 75 80
Val Trp His Ser Gln Thr Pro Glu Glu Phe Phe His Glu Gly Tyr Asn
85 90 95
Ala Ser Ala Pro Tyr Val Ser Arg Glu Val Met Leu Ala Arg Leu Asp
100 105 110
Asn Tyr Ile Arg Leu Ile Phe Glu Tyr Met Asp Glu Asn Tyr Pro Gly
115 120 125
Leu Ile Val Ser Trp Asp Val Ala Asn Glu Cys Val Ala Asp Gly Ser
130 135 140
Thr Ala Leu Arg Thr Ser Asn Trp Thr Arg Val Val Gly Gln Asp Phe
145 150 155 160
Val Ala Arg Ala Phe Glu Ile Ala Asp Lys Tyr Ala Pro Glu Asp Val
165 170 175
Met Leu Cys Tyr Asn Asp Tyr Ser Thr Pro Tyr Glu Pro Lys Leu Thr
180 185 190
Gly Ile Val Asn Leu Leu Thr Glu Leu Thr Gln Glu Gly His Ile Asp
195 200 205
Gly Tyr Gly Phe Gln Ser His Tyr Ser Val Gly Asp Pro Ser Leu Gln
210 215 220
Ala Val Glu Asn Ala Phe Lys Lys Ile Ser Ala Leu Gly Leu Lys Leu
225 230 235 240
Arg Val Ser Glu Leu Asp Ile Lys Val Asp Ala Asp Ser Glu Pro Asn
245 250 255
Arg Ala Leu Gln Ala Asp Arg Tyr Glu Ala Leu Leu Arg Ile Tyr Met
260 265 270
Lys Tyr Gly Val Ser Ala Val Gln Val Trp Gly Val Cys Asp Gly Thr
275 280 285
Ser Trp Ile Gly Ala Ser Tyr Pro Leu Pro Phe Asp Ala Gly Leu Arg
290 295 300
Pro Lys Pro Ser Phe Phe Gly Ile Leu Arg Ala Leu Asp Glu Gln Asn
305 310 315 320

<210> 283
<211> 4161
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 283
atgtataaaa gtttcgtcaa gaaagtctcc cttgtattat ctactctttt gctcttagtt 60
tcggcgtttc ctgtctcata tgcacaaatg aattccatcc ccgtttatga agaaacgttt 120
gaaaaccaag gaaactatgt ccaatctggt ggtgcgaccc tcactctagt aaaaaacaaa 180
gtgtttgcag ggaatgaaga tggaactgca ctatatatta gtaatcgatc gaataactgg 240
gacggggcag atttccgttt cacggatctt ggattacaag atggaaaaac atatacgatc 300
aatattatag gatatgtcga tgaaaatgaa gttgttcctt caggagccca agtgtatttg 360
caaactgtag ataaaacata tggatggtta gcaagcgcgg acttaaaaaa cggagagtcg 420
ttcactataa atacaacgtt caccccttgac atgagtaaag gggacacccg tcttcgtata 480
caatccaacg atagtggtaa aaaagtttca ttttacgtcg ggtatttttc aatttcaatt 540
agtgatgtag aaggagaaga tggtgggagc tctatttcaa ggccaccggc tttacctttt 600
gaaactattg actttgaaga tcaaagttta agtggatttg agggacgagc aggcacggaa 660

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acattgaccg ttacgaatga agcaaataga actcctggag gatcttatgc actaaaagtg      720
gaaaatagat ctcaaaattg gcatggacct tccttacgca tcgagaaata tattgattta      780
ggttacgaat atacaatttc tctatgggtt aaacttattt cacccacaag tgcacaaatt      840
cagctttcta cccaagtcgg aagtggaagt ggtgcgagtt ataacaatat tttaagtaaa      900
gtaattagtg ttgatgatgg atgggtactg tatgaaggaa agtatcgcta caatagttcg      960
ggaggggaat atttaacaat ttacgtagaa agcccaaaca atagtactgc atcttttttac    1020
atcgatgata ttcgtttaat aaagagtgga gacccaatct ctgtacaaaa agatcttctc     1080
cctatcaaga gtgtttatga aggtgacttc ttagttggta gtgccgtatc agcgactgat     1140
ttagagggag agagactcga gcttctcaag ttgcattaca atagcataac agcggaaaac     1200
gccatgaaac ctagctattt acaacctact aaaggaaact ttaccttcga agcagcagat     1260
agtattgtaa ataaagccct agaagaagga atgaaagtac atggacatgt tctcgtatgg     1320
catcagcaga cacctgaatg gatgaccact agagaagatg gaagccctct cggcagggaa     1380
gaagcgttag aaaatctaaa aaatcacatt gaaacagtta tgaaacattt tggtgataga     1440
gtaatttcat gggatgttgt caatgaagct atcattgata atccacctaa tcctgataat     1500
tgggaggaat cattaagaaa atcaccatgg tactattcaa tcggttctga ttatgttgag     1560
caagcattcc gaattgcacg acaagttttg gacgaaaatg ggtgggatat taagctatat     1620
tacaatgatt acaatgaaga taatcaaaga aaagcacaag ccatttacca tatggtaaaa     1680
gagcttaatg aaaaatatgc acaagagcat cctggtaaaa gattaatcga tggaattgga     1740
atgcaagggc attacagtat acgaacaaat ccagataatg tgaaaatgtc attagaaaga     1800
tttatttccc ttggtgtgga agttagtatt actgaactcg atattcaagc tggaacggat     1860
aatcatctta cggaagaaca gtcaaaagca caagcatatt tatacgctaa attattcaaa     1920
atattcaaag aaaatgcatc gcatatctcc cgagttacgt tatggggatt aaatgatgcg     1980
gcaagttggc gtgcgtcaac aagtccattg ttatttgatc gaaatttaca ggccaaacca     2040
agttactatg cggtaattga tcctgataca tttatagaag aaaatcctac tgtgacagaa     2100
gagtcgcgga aagcaattgc tttgtatggt atccctgtaa ttgatggaag catcgattcc     2160
atttgggaaa gtgttcctta catccctatt gatcgttacc aaatggcgtg gcaaggagca     2220
agcggaactg ctaaagttct ttgggacgaa gggaatctgt atgtattagt acaagttaac     2280
gatgaccagt tagataagtc gagtacaaat ccttgggagc aggattcgat agaggtgttt     2340
gtggacgaaa ataatgcaaa aacatcgttt taccaagagg atgatggaca atatagagta     2400
aactttgaca acgaaacatc gtttaatcca ccaagcattg aaaatggatt tatgtccgaa     2460
actaatgtat ctgggactaa ttatgtggtg gagatgaaaa tccctttaag aagtatacaa     2520
ctaaaaaatg ggtctgaaat agggtttgat gttcaaatta atgatgggaa aaatggtgct     2580
cgtcagagtg tggctgcttg gaatgatacg actggaactg catatatgga tacatctgta     2640
ttcgggacac ttactctttt aaccacttta gataatgaaa atacaccagg cagcggcaca     2700
acaccaggta gtggcacaac accaggcagt ggcacaacac caggcagcag cacaacacca     2760
ggcagcggta caacaccagg tagcggcaca acaccaggca gtggcacaac accaggcagc     2820
ggcacaacac caggcagtgg cacaacacca ggcagtggca caacaccggg cagcggtaca     2880
acaccaggca gtggcacaac accaggcagt ggtacaacac cgggcagtgg cacaacacca     2940
gtgaagggtg aaaatggtac ggttgtttta cagccgaaag tagagacgaa agaaaaagac     3000
ggcaaagtag tagaaaaagt ggcaactatt tcaacaaatg aagttgaagc gattgtcaag     3060
gagctgtcga atgaaaataa acaagtcgtc gtctccctcg gctcgcttcc aaaaggtgta     3120
gccacaaaag tagatgtgcc agctacatta tttacacaag cggcaaataa acaagcagaa     3180
gcaacgattg tgagcgccag tgaacaagcg acgtacaaat tgccagtcaa agaagtgcag     3240
gcgtctcttg cgacgattgc ccggtcactc ggtgcaacga tagaacaagt tagcatctcg     3300
attgaaatga aagtgaacga tgcgccgtca ctacgtgtga aaccgttgtc tgatgcggta     3360
gagtttcatg tcgtggcgaa agcaaatgga aaggaacgcg tcatcgatcg gtttactcaa     3420
tatgtcgaac gcgaaatcgc gttaaagcaa tcggtcaacg ctagtcgtgc cattgcagtg     3480
cgcgtgaacg atgacggttc acttacccca gtaccgacaa cgtttgttgg caacaaagca     3540
gtcattaaat cgttgacgaa ctcgacgtat gttgttgtgg aaggaacaca tacatttagt     3600
gacatccaac cacattgggc gaaaggttat attgaaacac tcgcggcaaa acagcttgtc     3660
aaagggatga cggacacaac atatcgacca aatgatcgga tgacgcgcgc gcaatttgcg     3720
gtgttgctcg tacgggcgct aggattgccg agcgaaacgt atgacggtcg ctttgctgat     3780
gtgaagggaa cggagtggtt taacaagaac ggtgaattag cagcggcagt caagttcgga     3840
atcattcaag gaaaaacagc ttatatgttt gcgccgaatg agccaatcac tcgcgcacaa     3900
gcagctgtca tgatcgaacg ggcattgaaa ctttcgatcg ttggctatga tgaggcaaca     3960
agcgacaaaa cgaaaaaagt gacagatttc cgcgatgcaa aacaattgcc aacatgggca     4020
aaacaggcga ttgaagcagt ataccaagca ggcatcatgc aaggacgaga tagcggaaac     4080
tttgatccga caagccatgt gacgcgtgcc gaaatggcga aggtgttaat ggatatttta     4140
gagttgacaa aacttattta a                                               4161
```

<210> 284
<211> 1386
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(28)

<400> 284
Met Tyr Lys Ser Phe Val Lys Lys Val Ser Leu Val Leu Ser Thr Leu
1 5 10 15
Leu Leu Leu Val Ser Ala Phe Pro Val Ser Tyr Ala Gln Met Asn Ser
20 25 30
Ile Pro Val Tyr Glu Glu Thr Phe Glu Asn Gln Gly Asn Tyr Val Gln
35 40 45
Ser Gly Gly Ala Thr Leu Thr Leu Val Lys Asn Lys Val Phe Ala Gly
50 55 60
Asn Glu Asp Gly Thr Ala Leu Tyr Ile Ser Asn Arg Ser Asn Asn Trp
65 70 75 80
Asp Gly Ala Asp Phe Arg Phe Thr Asp Leu Gly Leu Gln Asp Gly Lys
85 90 95
Thr Tyr Thr Ile Asn Ile Ile Gly Tyr Val Asp Glu Asn Glu Val Val
100 105 110
Pro Ser Gly Ala Gln Val Tyr Leu Gln Thr Val Asp Lys Thr Tyr Gly
115 120 125
Trp Leu Ala Ser Ala Asp Leu Lys Asn Gly Glu Ser Phe Thr Ile Asn
130 135 140
Thr Thr Phe Thr Leu Asp Met Ser Lys Gly Asp Thr Arg Leu Arg Ile
145 150 155 160
Gln Ser Asn Asp Ser Gly Lys Lys Val Ser Phe Tyr Val Gly Tyr Phe
165 170 175
Ser Ile Ser Ile Ser Asp Val Glu Gly Glu Asp Gly Gly Ser Ser Ile
180 185 190
Ser Arg Pro Pro Ala Leu Pro Phe Glu Thr Ile Asp Phe Glu Asp Gln
195 200 205
Ser Leu Ser Gly Phe Glu Gly Arg Ala Gly Thr Glu Thr Leu Thr Val
210 215 220
Thr Asn Glu Ala Asn Arg Thr Pro Gly Gly Ser Tyr Ala Leu Lys Val
225 230 235 240
Glu Asn Arg Ser Gln Asn Trp His Gly Pro Ser Leu Arg Ile Glu Lys
245 250 255
Tyr Ile Asp Leu Gly Tyr Glu Tyr Thr Ile Ser Leu Trp Val Lys Leu
260 265 270
Ile Ser Pro Thr Ser Ala Gln Ile Gln Leu Ser Thr Gln Val Gly Ser
275 280 285
Gly Ser Gly Ala Ser Tyr Asn Asn Ile Leu Ser Lys Val Ile Ser Val
290 295 300
Asp Asp Gly Trp Val Leu Tyr Glu Gly Lys Tyr Arg Tyr Asn Ser Ser
305 310 315 320
Gly Gly Glu Tyr Leu Thr Ile Tyr Val Glu Ser Pro Asn Asn Ser Thr
325 330 335
Ala Ser Phe Tyr Ile Asp Asp Ile Arg Leu Ile Lys Ser Gly Asp Pro
340 345 350
Ile Ser Val Gln Lys Asp Leu Leu Pro Ile Lys Ser Val Tyr Glu Gly
355 360 365
Asp Phe Leu Val Gly Ser Ala Val Ser Ala Thr Asp Leu Glu Gly Glu
370 375 380
Arg Leu Glu Leu Leu Lys Leu His Tyr Asn Ser Ile Thr Ala Glu Asn
385 390 395 400
Ala Met Lys Pro Ser Tyr Leu Gln Pro Thr Lys Gly Asn Phe Thr Phe
405 410 415
Glu Ala Ala Asp Ser Ile Val Asn Lys Ala Leu Glu Glu Gly Met Lys
420 425 430
Val His Gly His Val Leu Val Trp His Gln Gln Thr Pro Glu Trp Met
435 440 445
Thr Thr Arg Glu Asp Gly Ser Pro Leu Gly Arg Glu Glu Ala Leu Glu
450 455 460
Asn Leu Lys Asn His Ile Glu Thr Val Met Lys His Phe Gly Asp Arg
465 470 475 480
Val Ile Ser Trp Asp Val Val Asn Glu Ala Ile Ile Asp Asn Pro Pro
485 490 495
Asn Pro Asp Asn Trp Glu Glu Ser Leu Arg Lys Ser Pro Trp Tyr Tyr
500 505 510
Ser Ile Gly Ser Asp Tyr Val Glu Gln Ala Phe Arg Ile Ala Arg Gln
515 520 525

Val Leu Asp Glu Asn Gly Trp Asp Ile Lys Leu Tyr Tyr Asn Asp Tyr
530 535 540
Asn Glu Asp Asn Gln Arg Lys Ala Gln Ala Ile Tyr His Met Val Lys
545 550 555 560
Glu Leu Asn Glu Lys Tyr Ala Gln Glu His Pro Gly Lys Arg Leu Ile
565 570 575
Asp Gly Ile Gly Met Gln Gly His Tyr Ser Ile Arg Thr Asn Pro Asp
580 585 590
Asn Val Lys Met Ser Leu Glu Arg Phe Ile Ser Leu Gly Val Glu Val
595 600 605
Ser Ile Thr Glu Leu Asp Ile Gln Ala Gly Thr Asp Asn His Leu Thr
610 615 620
Glu Glu Gln Ser Lys Ala Gln Ala Tyr Leu Tyr Ala Lys Leu Phe Lys
625 630 635 640
Ile Phe Lys Glu Asn Ala Ser His Ile Ser Arg Val Thr Leu Trp Gly
645 650 655
Leu Asn Asp Ala Ala Ser Trp Arg Ala Ser Thr Ser Pro Leu Leu Phe
660 665 670
Asp Arg Asn Leu Gln Ala Lys Pro Ser Tyr Tyr Ala Val Ile Asp Pro
675 680 685
Asp Thr Phe Ile Glu Glu Asn Pro Thr Val Thr Glu Glu Ser Arg Lys
690 695 700
Ala Ile Ala Leu Tyr Gly Ile Pro Val Ile Asp Gly Ser Ile Asp Ser
705 710 715 720
Ile Trp Glu Ser Val Pro Tyr Ile Pro Ile Asp Arg Tyr Gln Met Ala
725 730 735
Trp Gln Gly Ala Ser Gly Thr Ala Lys Val Leu Trp Asp Glu Gly Asn
740 745 750
Leu Tyr Val Leu Val Gln Val Asn Asp Asp Gln Leu Asp Lys Ser Ser
755 760 765
Thr Asn Pro Trp Glu Gln Asp Ser Ile Glu Val Phe Val Asp Glu Asn
770 775 780
Asn Ala Lys Thr Ser Phe Tyr Gln Glu Asp Asp Gly Gln Tyr Arg Val
785 790 795 800
Asn Phe Asp Asn Glu Thr Ser Phe Asn Pro Pro Ser Ile Glu Asn Gly
805 810 815
Phe Met Ser Glu Thr Asn Val Ser Gly Thr Asn Tyr Val Val Glu Met
820 825 830
Lys Ile Pro Leu Arg Ser Ile Gln Leu Lys Asn Gly Ser Glu Ile Gly
835 840 845
Phe Asp Val Gln Ile Asn Asp Gly Lys Asn Gly Ala Arg Gln Ser Val
850 855 860
Ala Ala Trp Asn Asp Thr Thr Gly Thr Ala Tyr Met Asp Thr Ser Val
865 870 875 880
Phe Gly Thr Leu Thr Leu Leu Thr Thr Leu Asp Asn Glu Asn Thr Pro
885 890 895
Gly Ser Gly Thr Thr Pro Gly Ser Gly Thr Thr Pro Gly Ser Gly Thr
900 905 910
Thr Pro Gly Ser Ser Thr Thr Pro Gly Ser Gly Thr Thr Pro Gly Ser
915 920 925
Gly Thr Thr Pro Gly Ser Gly Thr Thr Pro Gly Ser Gly Thr Thr Pro
930 935 940
Gly Ser Gly Thr Thr Pro Gly Ser Gly Thr Thr Pro Gly Ser Gly Thr
945 950 955 960
Thr Pro Gly Ser Gly Thr Thr Pro Gly Ser Gly Thr Thr Pro Gly Ser
965 970 975
Gly Thr Thr Pro Val Lys Gly Glu Asn Gly Thr Val Val Leu Gln Pro
980 985 990
Lys Val Glu Thr Lys Glu Lys Asp Gly Lys Val Val Glu Lys Val Ala
995 1000 1005
Thr Ile Ser Thr Asn Glu Val Glu Ala Ile Val Lys Glu Leu Ser Asn
1010 1015 1020
Glu Asn Lys Gln Val Val Val Ser Leu Gly Ser Leu Pro Lys Gly Val
1025 1030 1035 1040
Ala Thr Lys Val Asp Val Pro Ala Thr Leu Phe Thr Gln Ala Ala Asn
1045 1050 1055
Lys Gln Ala Glu Ala Thr Ile Val Ser Ala Ser Glu Gln Ala Thr Tyr
1060 1065 1070
Lys Leu Pro Val Lys Glu Val Gln Ala Ser Leu Ala Thr Ile Ala Arg

1075 1080 1085
Ser Leu Gly Ala Thr Ile Glu Gln Val Ser Ile Ser Ile Glu Met Lys
1090 1095 1100
Val Asn Asp Ala Pro Ser Leu Arg Val Lys Pro Leu Ser Asp Ala Val
1105 1110 1115 1120
Glu Phe His Val Val Ala Lys Ala Asn Gly Lys Glu Arg Val Ile Asp
1125 1130 1135
Arg Phe Thr Gln Tyr Val Glu Arg Glu Ile Ala Leu Lys Gln Ser Val
1140 1145 1150
Asn Ala Ser Arg Ala Ile Ala Val Arg Val Asn Asp Asp Gly Ser Leu
1155 1160 1165
Thr Pro Val Pro Thr Thr Phe Val Gly Asn Lys Ala Val Ile Lys Ser
1170 1175 1180
Leu Thr Asn Ser Thr Tyr Val Val Val Glu Gly Thr His Thr Phe Ser
1185 1190 1195 1200
Asp Ile Gln Pro His Trp Ala Lys Gly Tyr Ile Glu Thr Leu Ala Ala
1205 1210 1215
Lys Gln Leu Val Lys Gly Met Thr Asp Thr Thr Tyr Arg Pro Asn Asp
1220 1225 1230
Arg Met Thr Arg Ala Gln Phe Ala Val Leu Leu Val Arg Ala Leu Gly
1235 1240 1245
Leu Pro Ser Glu Thr Tyr Asp Gly Arg Phe Ala Asp Val Lys Gly Thr
1250 1255 1260
Glu Trp Phe Asn Lys Asn Gly Glu Leu Ala Ala Ala Val Lys Phe Gly
1265 1270 1275 1280
Ile Ile Gln Gly Lys Thr Ala Tyr Met Phe Ala Pro Asn Glu Pro Ile
1285 1290 1295
Thr Arg Ala Gln Ala Ala Val Met Ile Glu Arg Ala Leu Lys Leu Ser
1300 1305 1310
Ile Val Gly Tyr Asp Glu Ala Thr Ser Asp Lys Thr Lys Lys Val Thr
1315 1320 1325
Asp Phe Arg Asp Ala Lys Gln Leu Pro Thr Trp Ala Lys Gln Ala Ile
1330 1335 1340
Glu Ala Val Tyr Gln Ala Gly Ile Met Gln Gly Arg Asp Ser Gly Asn
1345 1350 1355 1360
Phe Asp Pro Thr Ser His Val Thr Arg Ala Glu Met Ala Lys Val Leu
1365 1370 1375
Met Asp Ile Leu Glu Leu Thr Lys Leu Ile
1380 1385

<210> 285
<211> 1569
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 285
gtgaaccgaa acacatctcc ggacttcaag cttggagcag gcgttacggt aagtgatttc 60
ctgaacaagg gcaggcaata tgaggtcgct gtggcgaatc ttgatgaaat gacggccgga 120
aatgccatga agcagtcttc tgtaatgagg cctgacggat ccatggattt cactcaggtc 180
agaagattca tcgaggaggc cgaacgtgtc ggaatgacag tgtacggcca tacattggca 240
tggcattcac agcagcagaa cgcctatctt aacggtctga tcaagggcaa gaagaccgag 300
gtcgagccag gccaggagtc agaggtcgtt cttctccaga cagatttcaa tgacggaaat 360
gtcacattca acggatgggg aaacaattct tcaaggactg tcgagaatgg tgcattaaag 420
cttacaaacc cttctgtagt aaacagttgg gaggcccagt tcgcatatga tttttcagag 480
gccttcgaga tggacaagac atataagctc aagttcagga tcaagggctc ggctgcagga 540
aagatcgcgg caggcttcca gatcactgac ggctaccttt cggcaggtga gttcggaacc 600
gtagagttca atacccagtg gaaggatgtc gagctctcat gcgtatgttc cgctgaaggc 660
ggtacacgct tgatcttcag tttcggagag tttgccggag atatctatat cgacgatttc 720
tgcttcagtg tggaaggagc tggatatatc tacgaagatc ttaccccggc agagaagaag 780
gagcgcctta ccgaggcaat ggaccgttgg atcaagggaa tgatggaggt taccgctacc 840
agggtttctg cgtgggatgc tgtcaatgag gcgatttccg gccgtgatac aaatggcgac 900
ggcttctatg aacttgagtc ggcacaatgg ggaagctcga acaacttcta ttggcaggat 960
tatctcggct caggagatta tgtgcgtatc gtgatcgcaa aggcccgcaa gtattatgag 1020
gaattcggcg gtacggctcc tttgagactc ttcatcaatg actacaacct cgaatctgac 1080
tgggatgaca acaagaagct caagagcctt atccattgga tcggtgtctg ggagtctgac 1140
ggagtgacaa agatcgacgg aatcggtacc cagatgcacg tttcgtatta cgagaatcct 1200

gatattcagg caagcaagga gaaacattat gtgcagatgc ttcagcttat ggcaaataca 1260
ggaaagctcg tgaagatctc cgagcttgat atgggctatg tagaccgcaa cggaaatact 1320
gtgggaacag cggacatgac cgaccagcag catagggcca tggcggatta ttatgacttc 1380
atcgtgcgca agtactttga gatcgtgcct cctgcacagc agtatggcat cacgcagtgg 1440
tgcatgacgg atgctcccgg agctatcggc acaggctgga gaggcggtga gcctgtgggc 1500
ctgtgggacc agaattacaa ccgcaagtat gcgtacgcag gatttgcaaa cggacttaga 1560
gcgaaataa 1569

<210> 286
<211> 522
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 286
Met Asn Arg Asn Thr Ser Pro Asp Phe Lys Leu Gly Ala Gly Val Thr
1 5 10 15
Val Ser Asp Phe Leu Asn Lys Gly Arg Gln Tyr Glu Val Ala Val Ala
20 25 30
Asn Leu Asp Glu Met Thr Ala Gly Asn Ala Met Lys Gln Ser Ser Val
35 40 45
Met Arg Pro Asp Gly Ser Met Asp Phe Thr Gln Val Arg Arg Phe Ile
50 55 60
Glu Glu Ala Glu Arg Val Gly Met Thr Val Tyr Gly His Thr Leu Ala
65 70 75 80
Trp His Ser Gln Gln Gln Asn Ala Tyr Leu Asn Gly Leu Ile Lys Gly
85 90 95
Lys Lys Thr Glu Val Glu Pro Gly Gln Glu Ser Glu Val Val Leu Leu
100 105 110
Gln Thr Asp Phe Asn Asp Gly Asn Val Thr Phe Asn Gly Trp Gly Asn
115 120 125
Asn Ser Ser Arg Thr Val Glu Asn Gly Ala Leu Lys Leu Thr Asn Pro
130 135 140
Ser Val Val Asn Ser Trp Glu Ala Gln Phe Ala Tyr Asp Phe Ser Glu
145 150 155 160
Ala Phe Glu Met Asp Lys Thr Tyr Lys Leu Lys Phe Arg Ile Lys Gly
165 170 175
Ser Ala Ala Gly Lys Ile Ala Ala Gly Phe Gln Ile Thr Asp Gly Tyr
180 185 190
Leu Ser Ala Gly Glu Phe Gly Thr Val Glu Phe Asn Thr Gln Trp Lys
195 200 205
Asp Val Glu Leu Ser Cys Val Cys Ser Ala Glu Gly Gly Thr Arg Leu
210 215 220
Ile Phe Ser Phe Gly Glu Phe Ala Gly Asp Ile Tyr Ile Asp Asp Phe
225 230 235 240
Cys Phe Ser Val Glu Gly Ala Gly Tyr Ile Tyr Glu Asp Leu Thr Pro
245 250 255
Ala Glu Lys Lys Glu Arg Leu Thr Glu Ala Met Asp Arg Trp Ile Lys
260 265 270
Gly Met Met Glu Val Thr Ala Thr Arg Val Ser Ala Trp Asp Ala Val
275 280 285
Asn Glu Ala Ile Ser Gly Arg Asp Thr Asn Gly Asp Gly Phe Tyr Glu
290 295 300
Leu Glu Ser Ala Gln Trp Gly Ser Ser Asn Asn Phe Tyr Trp Gln Asp
305 310 315 320
Tyr Leu Gly Ser Gly Asp Tyr Val Arg Ile Val Ile Ala Lys Ala Arg
325 330 335
Lys Tyr Tyr Glu Glu Phe Gly Gly Thr Ala Pro Leu Arg Leu Phe Ile
340 345 350
Asn Asp Tyr Asn Leu Glu Ser Asp Trp Asp Asp Asn Lys Lys Leu Lys
355 360 365
Ser Leu Ile His Trp Ile Gly Val Trp Glu Ser Asp Gly Val Thr Lys
370 375 380
Ile Asp Gly Ile Gly Thr Gln Met His Val Ser Tyr Tyr Glu Asn Pro
385 390 395 400
Asp Ile Gln Ala Ser Lys Glu Lys His Tyr Val Gln Met Leu Gln Leu
405 410 415

Met Ala Asn Thr Gly Lys Leu Val Lys Ile Ser Glu Leu Asp Met Gly
420 425 430
Tyr Val Asp Arg Asn Gly Asn Thr Val Gly Thr Ala Asp Met Thr Asp
435 440 445
Gln Gln His Arg Ala Met Ala Asp Tyr Tyr Asp Phe Ile Val Arg Lys
450 455 460
Tyr Phe Glu Ile Val Pro Pro Ala Gln Gln Tyr Gly Ile Thr Gln Trp
465 470 475 480
Cys Met Thr Asp Ala Pro Gly Ala Ile Gly Thr Gly Trp Arg Gly Gly
485 490 495
Glu Pro Val Gly Leu Trp Asp Gln Asn Tyr Asn Arg Lys Tyr Ala Tyr
500 505 510
Ala Gly Phe Ala Asn Gly Leu Arg Ala Lys
515 520

<210> 287
<211> 1695
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 287
atgactattc atctacaaaa aaatctgctc tttgcagcag tcttactgac agggcaagca 60
gcgcatgcgc tcacctccgg atctggcgag gccacgctgg atgttaataa cagctggggt 120
tcaggttatt gcgctaacgt caccattgcc aacaacggca gccaagccat tacttcctgg 180
acggttggcc tgaaccttaa cggcacgacg atcaataatc tttggaacgg taatttgagt 240
ggggttacgg ttaccccgt ggcctacaat gcgaatgtgg cgccgggtgc taataccagc 300
tttggtttct gtgctaatgg cagcgcaacc cccacgttgg cgacgtttga agttcaaggc 360
ggcggtggcg cagccagtag ttccagcagt tctgctattt caagcagctc cagcagttcg 420
gttgccggcg gcagcaacag cgtcaccgta cgcatgagcg gcgtaaccgg agacgaaagc 480
gtgagcctgg aaatcggtgg tcagaccatc gagacctgga ccctgagcgt cggtatgctc 540
gactacaccg tacagaccaa cgctaccggt gagttgcgtg ttgcgtttac caatgatgaa 600
ggtgaccgcg atgtcgaagt ggattacatc atggtcaacg gcgtgaccta tcaggccgaa 660
gatcaggaag ataacaccgg cgcgtgggac ggagagtgtg gtgcgggttc cttctcgcag 720
atgctgcact gcaacggttc tatcggcttt ggcaatccat tcgatggcag caactcgtcg 780
tccagctcca gcaacacttc gagctcgagc agcagctcta accctaaccc tggcaatccg 840
aatttccccg atttcttcgt aggtaacatc accaccagcg gctcagttcg ctctgacttc 900
atgcagtatt gggatcaaat tacgccggaa aacgaaggta aatggggctc cgtagaggga 960
actcgcgacc agtacaactg ggtccgctg gatgcaattt acaatttcgc ccgtgcgaac 1020
ggtattcctg taaaagcgca cactctggtg tggggcagtc agcaaccggg ttggattggc 1080
ggcttgagtg ccgctgagca gcgcgcggaa attgaagagt ggattcgcga ttactgcgca 1140
cgctacccgg atacggcgat gatcgatgtg gtgaatgaag ctctgccttc gcacgctccg 1200
gcaaactatg cggccaatgc atttggaagc gattggatca ctgaatcctt ccgtttggca 1260
cgtcagtact gtccggatgc cgtgctgatc tacaacgact ataacttcat gacctgggac 1320
accgatgcca tcattcagat gattcgccca gccgtgaact ccggttatgt cgatgcactg 1380
ggtcttcaag cgcacagcct gtattcccca caagtctgga ccgctcagca aatccagagc 1440
aaattggatc agatttccga gttgggcttg ccgctgtaca tctccgagta cgacatcgaa 1500
gcaacgaatg atcagactca gttacagtac atgcagatgc acttcccgat cttctacaac 1560
catcccaacg tggccggtat taccctttgg ggttatgttg tgggtgctac ctggcgtgat 1620
ggcactggcc tgatccaaag caatggtcag cagcgcccgg ccatgcagtg gttgatggag 1680
tatctaaacc gctaa 1695

<210> 288
<211> 564
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(23)

<400> 288
Met Thr Ile His Leu Gln Lys Asn Leu Leu Phe Ala Ala Val Leu Leu
1 5 10 15
Thr Gly Gln Ala Ala His Ala Leu Thr Ser Gly Ser Gly Glu Ala Thr

20 25 30
Leu Asp Val Asn Asn Ser Trp Gly Ser Gly Tyr Cys Ala Asn Val Thr
35 40 45
Ile Ala Asn Asn Gly Ser Gln Ala Ile Thr Ser Trp Thr Val Gly Leu
50 55 60
Asn Leu Asn Gly Thr Thr Ile Asn Asn Leu Trp Asn Gly Asn Leu Ser
65 70 75 80
Gly Val Thr Val Thr Pro Val Ala Tyr Asn Ala Asn Val Ala Pro Gly
85 90 95
Ala Asn Thr Ser Phe Gly Phe Cys Ala Asn Gly Ser Ala Thr Pro Thr
100 105 110
Leu Ala Thr Phe Glu Val Gln Gly Gly Gly Gly Ala Ala Ser Ser Ser
115 120 125
Ser Ser Ser Ala Ile Ser Ser Ser Ser Ser Ser Ser Val Ala Gly Gly
130 135 140
Ser Asn Ser Val Thr Val Arg Met Ser Gly Val Thr Gly Asp Glu Ser
145 150 155 160
Val Ser Leu Glu Ile Gly Gly Gln Thr Ile Glu Thr Trp Thr Leu Ser
165 170 175
Val Gly Met Leu Asp Tyr Thr Val Gln Thr Asn Ala Thr Gly Glu Leu
180 185 190
Arg Val Ala Phe Thr Asn Asp Glu Gly Asp Arg Asp Val Glu Val Asp
195 200 205
Tyr Ile Met Val Asn Gly Val Thr Tyr Gln Ala Glu Asp Gln Glu Asp
210 215 220
Asn Thr Gly Ala Trp Asp Gly Glu Cys Gly Ala Gly Ser Phe Ser Gln
225 230 235 240
Met Leu His Cys Asn Gly Ser Ile Gly Phe Gly Asn Pro Phe Asp Gly
245 250 255
Ser Asn Ser Ser Ser Ser Ser Ser Asn Thr Ser Ser Ser Ser Ser Ser
260 265 270
Ser Asn Pro Asn Pro Gly Asn Pro Asn Phe Pro Asp Phe Phe Val Gly
275 280 285
Asn Ile Thr Thr Ser Gly Ser Val Arg Ser Asp Phe Met Gln Tyr Trp
290 295 300
Asp Gln Ile Thr Pro Glu Asn Glu Gly Lys Trp Gly Ser Val Glu Gly
305 310 315 320
Thr Arg Asp Gln Tyr Asn Trp Gly Pro Leu Asp Ala Ile Tyr Asn Phe
325 330 335
Ala Arg Ala Asn Gly Ile Pro Val Lys Ala His Thr Leu Val Trp Gly
340 345 350
Ser Gln Gln Pro Gly Trp Ile Gly Gly Leu Ser Ala Ala Glu Gln Arg
355 360 365
Ala Glu Ile Glu Glu Trp Ile Arg Asp Tyr Cys Ala Arg Tyr Pro Asp
370 375 380
Thr Ala Met Ile Asp Val Val Asn Glu Ala Leu Pro Ser His Ala Pro
385 390 395 400
Ala Asn Tyr Ala Ala Asn Ala Phe Gly Ser Asp Trp Ile Thr Glu Ser
405 410 415
Phe Arg Leu Ala Arg Gln Tyr Cys Pro Asp Ala Val Leu Ile Tyr Asn
420 425 430
Asp Tyr Asn Phe Met Thr Trp Asp Thr Asp Ala Ile Ile Gln Met Ile
435 440 445
Arg Pro Ala Val Asn Ser Gly Tyr Val Asp Ala Leu Gly Leu Gln Ala
450 455 460
His Ser Leu Tyr Ser Pro Gln Val Trp Thr Ala Gln Gln Ile Gln Ser
465 470 475 480
Lys Leu Asp Gln Ile Ser Glu Leu Gly Leu Pro Leu Tyr Ile Ser Glu
485 490 495
Tyr Asp Ile Glu Ala Thr Asn Asp Gln Thr Gln Leu Gln Tyr Met Gln
500 505 510
Met His Phe Pro Ile Phe Tyr Asn His Pro Asn Val Ala Gly Ile Thr
515 520 525
Leu Trp Gly Tyr Val Val Gly Ala Thr Trp Arg Asp Gly Thr Gly Leu
530 535 540
Ile Gln Ser Asn Gly Gln Gln Arg Pro Ala Met Gln Trp Leu Met Glu
545 550 555 560
Tyr Leu Asn Arg

<210> 289
<211> 2796
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 289
atgaagttca ctttgacacc gctgctgtgc gggttcgcct tattgttggg ttgcgcggtg 60
caggcaaccc cagccgcttc gttaaagcag gcctatcagc cgtttttcca tatcggcacc 120
gcagtcagtc tggcgcaatt acaaccatcc aaagaacatg aacgcgcttt aattgcgcag 180
cactttaaca gtctgaccgc cgaaaacctg atgaaatggg aggaaattca acccacggaa 240
ggcaactttg attttaaagc ggccgatcag ttggttgcgt ttgccgaaca acatcaaatg 300
tggatgatcg gccataccat tctgtggcat gaacaaaccc cagactgggt gtttcagggg 360
ctggatggca aacccgccag caagcagctg ctactggccc gcttgaccaa acatatccaa 420
acggtcgttg gccgttacca gggccgggtc aatggctggg atgtggtgaa tgaagcgctc 480
aatgaagatg gcagcctgcg cgataccccg tggcggcgca ttttgggtga tgattacatt 540
gccaccactt ttgcgttggt gcatcaggtc gaccctaaag ccaaactcta ttacaacgat 600
tacaacctgt ttaaaccgga aaaacgcgcc ggggtgctgc ggattatcca acaactgcag 660
caaaaaaatg tgcctattca tgccattggt gaacaagcgc attacggcct tgattcgcct 720
gcattcaaag acgttgaaga ttcgatcaac gcttttgctg ccaccggcct ggacgtgatg 780
ctaaccgaac tggagatttc agtattgccg tatccatccg gcatgacgca gggtgccgat 840
atcagtcagc atcaggaatt gcaggaacaa ctaaacccct atcgcgatgg tttgcccaaa 900
gccgtcgaac aagcctggca acaacggtat ctcgatttgt tttcgctgtt attacgccag 960
cagcaaaaac tgcatcgcgt gaccttctgg ggcttagatg atggccaaag ctggcgtaat 1020
aatttcccga tgcgcggtcg caccgattac ccactgctgt ttgatcgcaa gctgcaagcc 1080
aaaccgctgt taagcgcact gacggcatta gccgcagacc agactaaagc caagcccaaa 1140
atgaatcagc tgggctttgc gccgacttcg accaaactgt tgattgtgcc gggtcggcaa 1200
tcagtgcctt ttcatgtttt ggataccgag accggccaaa cggtgctgca aggccaaagt 1260
tcggcggcca ggttttggcc tgaatcgggg gaatgggtca gtgctgccga tttttctgcg 1320
gtgataactc ccggcaccta tcagatcaac atctcaggaa cgccgccaca aactgtcaag 1380
atccaggccg aaccctatgc cgcgctgcat gatgcggcaa tcaaagccta ttattttaac 1440
cgcgcctcgc tcacactgga gccaaagttt gccggacctt gggcacgcgc agcgggggcat 1500
ccggatacca aagtacgggt gcatgcttct gctgcatcgg ccagcaggcc agaaggttat 1560
gagctcagcg ctgccaaagg ctggtatgac gccggtgact acaacaaata cgtggtgaat 1620
tccggcatta ccagttacac cctgttgcag gcctggcagg attttcctga gttttatcaa 1680
agccggacct ggaatattcc ggagtccggc aacgcggtac cggacattct cgacgaaacc 1740
ttatggaatc tgcagtggtt cagcgccatg caagacccaa acgacggggg cgtctatcac 1800
aagctgactg aactgaattt ttcggcaacc caaatgccgg accaagtgac agcagagcgt 1860
tatgtggtgc aaaaaaccac cgccgcggca ctgaatttcg ctgcggtgtt ggccaaagcc 1920
agtacggttt ttgccaaatt tgacgcccag ttgcccggcc tgtcgcaaca ataccgtcag 1980
caagcactgc tcgcctggca atgggcgcaa aaaaatccgc agcaaatcta tcaacaaccc 2040
aaagatgtcc acactggcgc ttatggtgac aaacaactgg ctgatgaatg ggcctgggct 2100
ggcgccgagc tgtatttatt gaccggcgag caaagttatc tgcagccact gttggcgctg 2160
gacacgccaa tcagtgcagc atcctgggcc agtgtcagcg ctttggggta tttttctttg 2220
gcttcggcga aacagcttga gcccgcacta cggcaacagg tacaacagaa aatccaacaa 2280
gccgccgcgc aaatcctgca ggaacatcaa acatccgcct atcaggtggc gatgaccaaa 2340
aacgattttg tctggggcag taatgcggtg gcaatgaata aagcgatgtt gttataccag 2400
gcgtggaaaa tagcgccaaa accggagctg ctacaggcga tgcaaggtct ggttgattac 2460
gttttggggc gcaacccgtt gcagcagtct tatgtcacag ggtttggcga gcaaagcccg 2520
cagcagatcc accaccgacc ttcggccgcc gatgccatca aagcgccggt accaggttgg 2580
ttagtcggtg gtgcacagcc gggtaagcag gataaatgca cttatgccgg cgctttaccc 2640
gctgtcggcg ctttacccgc tgccagcacc ttaccagcca ccacttatct tgatgactgg 2700
tgcagttacg ccaccaacga agtggcgatt aactggaatg cacctttggt gtatgtgctg 2760
gcatggcacc tttcgcaaaa caccaagaca ccataa 2796

<210> 290
<211> 931
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(22)

<400> 290
Met Lys Phe Thr Leu Thr Pro Leu Leu Cys Gly Phe Ala Leu Leu Leu
1 5 10 15
Gly Cys Ala Val Gln Ala Thr Pro Ala Ala Ser Leu Lys Gln Ala Tyr
20 25 30
Gln Pro Phe Phe His Ile Gly Thr Ala Val Ser Leu Ala Gln Leu Gln
35 40 45
Pro Ser Lys Glu His Glu Arg Ala Leu Ile Ala Gln His Phe Asn Ser
50 55 60
Leu Thr Ala Glu Asn Leu Met Lys Trp Glu Glu Ile Gln Pro Thr Glu
65 70 75 80
Gly Asn Phe Asp Phe Lys Ala Ala Asp Gln Leu Val Ala Phe Ala Glu
85 90 95
Gln His Gln Met Trp Met Ile Gly His Thr Ile Leu Trp His Glu Gln
100 105 110
Thr Pro Asp Trp Val Phe Gln Gly Leu Asp Gly Lys Pro Ala Ser Lys
115 120 125
Gln Leu Leu Leu Ala Arg Leu Thr Lys His Ile Gln Thr Val Val Gly
130 135 140
Arg Tyr Gln Gly Arg Val Asn Gly Trp Asp Val Val Asn Glu Ala Leu
145 150 155 160
Asn Glu Asp Gly Ser Leu Arg Asp Thr Pro Trp Arg Arg Ile Leu Gly
165 170 175
Asp Asp Tyr Ile Ala Thr Thr Phe Ala Leu Val His Gln Val Asp Pro
180 185 190
Lys Ala Lys Leu Tyr Tyr Asn Asp Tyr Asn Leu Phe Lys Pro Glu Lys
195 200 205
Arg Ala Gly Val Leu Arg Ile Ile Gln Gln Leu Gln Gln Lys Asn Val
210 215 220
Pro Ile His Ala Ile Gly Glu Gln Ala His Tyr Gly Leu Asp Ser Pro
225 230 235 240
Ala Phe Lys Asp Val Glu Asp Ser Ile Asn Ala Phe Ala Ala Thr Gly
245 250 255
Leu Asp Val Met Leu Thr Glu Leu Glu Ile Ser Val Leu Pro Tyr Pro
260 265 270
Ser Gly Met Thr Gln Gly Ala Asp Ile Ser Gln His Gln Glu Leu Gln
275 280 285
Glu Gln Leu Asn Pro Tyr Arg Asp Gly Leu Pro Lys Ala Val Glu Gln
290 295 300
Ala Trp Gln Gln Arg Tyr Leu Asp Leu Phe Ser Leu Leu Leu Arg Gln
305 310 315 320
Gln Gln Lys Leu His Arg Val Thr Phe Trp Gly Leu Asp Asp Gly Gln
325 330 335
Ser Trp Arg Asn Asn Phe Pro Met Arg Gly Arg Thr Asp Tyr Pro Leu
340 345 350
Leu Phe Asp Arg Lys Leu Gln Ala Lys Pro Leu Leu Ser Ala Leu Thr
355 360 365
Ala Leu Ala Ala Asp Gln Thr Lys Ala Lys Pro Lys Met Asn Gln Leu
370 375 380
Gly Phe Ala Pro Thr Ser Thr Lys Leu Leu Ile Val Pro Gly Arg Gln
385 390 395 400
Ser Val Pro Phe His Val Leu Asp Thr Glu Thr Gly Gln Thr Val Leu
405 410 415
Gln Gly Gln Ser Ser Ala Ala Arg Phe Trp Pro Glu Ser Gly Glu Trp
420 425 430
Val Ser Ala Ala Asp Phe Ser Ala Val Ile Thr Pro Gly Thr Tyr Gln
435 440 445
Ile Asn Ile Ser Gly Thr Pro Pro Gln Thr Val Lys Ile Gln Ala Glu
450 455 460
Pro Tyr Ala Ala Leu His Asp Ala Ala Ile Lys Ala Tyr Tyr Phe Asn
465 470 475 480
Arg Ala Ser Leu Thr Leu Glu Pro Lys Phe Ala Gly Pro Trp Ala Arg
485 490 495
Ala Ala Gly His Pro Asp Thr Lys Val Arg Val His Ala Ser Ala Ala
500 505 510
Ser Ala Ser Arg Pro Glu Gly Tyr Glu Leu Ser Ala Ala Lys Gly Trp
515 520 525
Tyr Asp Ala Gly Asp Tyr Asn Lys Tyr Val Val Asn Ser Gly Ile Thr
530 535 540

Ser Tyr Thr Leu Leu Gln Ala Trp Gln Asp Phe Pro Glu Phe Tyr Gln
545 550 555 560
Ser Arg Thr Trp Asn Ile Pro Glu Ser Gly Asn Ala Val Pro Asp Ile
565 570 575
Leu Asp Glu Thr Leu Trp Asn Leu Gln Trp Phe Ser Ala Met Gln Asp
580 585 590
Pro Asn Asp Gly Gly Val Tyr His Lys Leu Thr Glu Leu Asn Phe Ser
595 600 605
Ala Thr Gln Met Pro Asp Gln Val Thr Ala Glu Arg Tyr Val Val Gln
610 615 620
Lys Thr Thr Ala Ala Ala Leu Asn Phe Ala Ala Val Leu Ala Lys Ala
625 630 635 640
Ser Thr Val Phe Ala Lys Phe Asp Ala Gln Leu Pro Gly Leu Ser Gln
645 650 655
Gln Tyr Arg Gln Gln Ala Leu Leu Ala Trp Gln Trp Ala Gln Lys Asn
660 665 670
Pro Gln Gln Ile Tyr Gln Gln Pro Lys Asp Val His Thr Gly Ala Tyr
675 680 685
Gly Asp Lys Gln Leu Ala Asp Glu Trp Ala Trp Ala Gly Ala Glu Leu
690 695 700
Tyr Leu Leu Thr Gly Glu Gln Ser Tyr Leu Gln Pro Leu Leu Ala Leu
705 710 715 720
Asp Thr Pro Ile Ser Ala Ala Ser Trp Ala Ser Val Ser Ala Leu Gly
725 730 735
Tyr Phe Ser Leu Ala Ser Ala Lys Gln Leu Glu Pro Ala Leu Arg Gln
740 745 750
Gln Val Gln Gln Lys Ile Gln Gln Ala Ala Ala Gln Ile Leu Gln Glu
755 760 765
His Gln Thr Ser Ala Tyr Gln Val Ala Met Thr Lys Asn Asp Phe Val
770 775 780
Trp Gly Ser Asn Ala Val Ala Met Asn Lys Ala Met Leu Leu Tyr Gln
785 790 795 800
Ala Trp Lys Ile Ala Pro Lys Pro Glu Leu Leu Gln Ala Met Gln Gly
805 810 815
Leu Val Asp Tyr Val Leu Gly Arg Asn Pro Leu Gln Gln Ser Tyr Val
820 825 830
Thr Gly Phe Gly Glu Gln Ser Pro Gln Gln Ile His His Arg Pro Ser
835 840 845
Ala Ala Asp Ala Ile Lys Ala Pro Val Pro Gly Trp Leu Val Gly Gly
850 855 860
Ala Gln Pro Gly Lys Gln Asp Lys Cys Thr Tyr Ala Gly Ala Leu Pro
865 870 875 880
Ala Val Gly Ala Leu Pro Ala Ala Ser Thr Leu Pro Ala Thr Thr Tyr
885 890 895
Leu Asp Asp Trp Cys Ser Tyr Ala Thr Asn Glu Val Ala Ile Asn Trp
900 905 910
Asn Ala Pro Leu Val Tyr Val Leu Ala Trp His Leu Ser Gln Asn Thr
915 920 925
Lys Thr Pro
930

<210> 291
<211> 1230
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 291
atggtcaaag aaagaagttt tcttcatcat tcattcaata ggggcgaaaa tggacaggac 60
agtctgatgt ggaaaaaaga ggcggatgat cgaatctcag agcatagaca aagagatctt 120
gtgatcaacg taacaaacgg tgaaaaaaag ccaatagcag gtatagaggt tgaaataaag 180
caaatcagac atgaattcgc ctttggttca gcgatgaatg atcaagtgtt atttaatcaa 240
caatatgctg atttttcgt gaagtatttt aattgggctg tttttgaaaa tgaggcaaaa 300
tggtatgcga atgagccaca aagagggaga atcacctacg aaaaagcaga tgcgatgctg 360
aattttgcag atcgacatca gcttccagtg agagggcacg ctttgttttg ggaggtagag 420
gatgcgaatc caagctggct aaggtcactg ccaaatcatg aagtatatga agccatgaaa 480
aaccggcttg agcatgcggg caatcacttt aagggaaggt tccgtcattg ggatgtaaac 540

aatgaaatga tgcatggttc attttttaaa gatcgctttg ggaaaaatat ttggaagtgg 600
atgtatgaag aaacgaaaaa aattgaccct caagcactat tgtttgtgaa tgattataat 660
gtgatctcat atggtgaaca ccatgcctat aaagcgcata tcaatgaact gcgtcagtta 720
ggcgcaccta ttgaggcgat tggggttcaa ggccattttg aagaacgggt cgatccagtc 780
attgtcaaag agagactcga tgtgcttgct gagctaggtc ttccaatatg ggtcacagag 840
tacgattcgg ttcaccctga ccctaatcga agagcggata acctggaagc tttatatcgc 900
gtcgcattta gtcatccagc cgtaaaagga gtgctgatgt ggggattttg ggcaggtgcc 960
cattggagag gggaaaatgc agccatcgtg aattatgatt ggtctttaaa tgaagcagga 1020
agacgttatg aaaagcttct aaatgagtgg acgacccaaa gaattgaaaa aacagatgct 1080
aatggccatg tgagatgtcc agcatttcac ggaacatatg aggttcgaat cggtaaagaa 1140
agtaaaatgt tgaaacagca gacgattgaa cttgattcaa atgaacaaac accgtttcaa 1200
ctagacgtga tcctgcctca agaaggatag 1230

<210> 292
<211> 409
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 292
Met Val Lys Glu Arg Ser Phe Leu His His Ser Phe Asn Arg Gly Glu
1   5   10   15
Asn Gly Gln Asp Ser Leu Met Trp Lys Lys Glu Ala Asp Asp Arg Ile
            20   25   30
Ser Glu His Arg Gln Arg Asp Leu Val Ile Asn Val Thr Asn Gly Glu
        35   40   45
Lys Lys Pro Ile Ala Gly Ile Glu Val Glu Ile Lys Gln Ile Arg His
    50   55   60
Glu Phe Ala Phe Gly Ser Ala Met Asn Asp Gln Val Leu Phe Asn Gln
65   70   75   80
Gln Tyr Ala Asp Phe Phe Val Lys Tyr Phe Asn Trp Ala Val Phe Glu
                85   90   95
Asn Glu Ala Lys Trp Tyr Ala Asn Glu Pro Gln Arg Gly Arg Ile Thr
            100   105   110
Tyr Glu Lys Ala Asp Ala Met Leu Asn Phe Ala Asp Arg His Gln Leu
        115   120   125
Pro Val Arg Gly His Ala Leu Phe Trp Glu Val Glu Asp Ala Asn Pro
    130   135   140
Ser Trp Leu Arg Ser Leu Pro Asn His Glu Val Tyr Glu Ala Met Lys
145   150   155   160
Asn Arg Leu Glu His Ala Gly Asn His Phe Lys Gly Arg Phe Arg His
                165   170   175
Trp Asp Val Asn Asn Glu Met Met His Gly Ser Phe Phe Lys Asp Arg
            180   185   190
Phe Gly Lys Asn Ile Trp Lys Trp Met Tyr Glu Glu Thr Lys Lys Ile
        195   200   205
Asp Pro Gln Ala Leu Leu Phe Val Asn Asp Tyr Asn Val Ile Ser Tyr
    210   215   220
Gly Glu His His Ala Tyr Lys Ala His Ile Asn Glu Leu Arg Gln Leu
225   230   235   240
Gly Ala Pro Ile Glu Ala Ile Gly Val Gln Gly His Phe Glu Glu Arg
                245   250   255
Val Asp Pro Val Ile Val Lys Glu Arg Leu Asp Val Leu Ala Glu Leu
            260   265   270
Gly Leu Pro Ile Trp Val Thr Glu Tyr Asp Ser Val His Pro Asp Pro
        275   280   285
Asn Arg Arg Ala Asp Asn Leu Glu Ala Leu Tyr Arg Val Ala Phe Ser
    290   295   300
His Pro Ala Val Lys Gly Val Leu Met Trp Gly Phe Trp Ala Gly Ala
305   310   315   320
His Trp Arg Gly Glu Asn Ala Ala Ile Val Asn Tyr Asp Trp Ser Leu
                325   330   335
Asn Glu Ala Gly Arg Arg Tyr Glu Lys Leu Leu Asn Glu Trp Thr Thr
            340   345   350
Gln Arg Ile Glu Lys Thr Asp Ala Asn Gly His Val Arg Cys Pro Ala
        355   360   365
Phe His Gly Thr Tyr Glu Val Arg Ile Gly Lys Glu Ser Lys Met Leu

```
    370                 375                 380
Lys Gln Gln Thr Ile Glu Leu Asp Ser Asn Glu Gln Thr Pro Phe Gln
385                 390                 395                 400
Leu Asp Val Ile Leu Pro Gln Glu Gly
                405
```

<210> 293
<211> 1002
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 293

```
atgaagatga acagctccct cccctccctc cgcgatgtat tcgcgaatga tttccgcatc      60
ggggcggcgg tcaatcctgt gacgatcgag atgcaaaaac agttgttgat cgatcatgtc     120
aacagtatta cggcagagaa ccatatgaag tttgagcatc ttcagccgga agaagggaaa     180
tttacctttc aggaagcgga tcggattgtg gattttgctt gttcgcaccg aatggcggtt     240
cgagggcaca cacttgtatg gcacaaccag actccggatt gggtgtttca agatggtcaa     300
ggccatttcg tcagtcggga tgtgttgctt gagcggatga aatgtcacat ttcaactgtt     360
gtacggcgat acaagggaaa aatatattgt tgggatgtca tcaacgaagc ggtagccgac     420
gaaggagacg aattgttgag gccgtcgaag tggcgacaaa tcatcgggga cgattttatg     480
gaacaagcat ttctctacgc ttatgaagct gacccagatg cactgctttt ttacaatgac     540
tataatgaat gttttccgga aaagagagaa aaaatttttg cacttgtcaa atcgctgcgt     600
gataaaggca ttccgattca tggcatcggg atgcaagcgc attggagttt gactcgcccg     660
tcgcttgatg aaattcgtgc ggccattgaa cgatatgcgt cccttggtgt tgttcttcat     720
attacggaac tcgatgtatc catgtttgaa tttcacgatc gtcgaaccga tttggcagct     780
ccaacgtcag aaatgatcga acggcaggca gagcggtatg ggcaaatttt tgctttgttt     840
aaggagtatc gcgatgttat tcaaagtgtc acattttggg gaattgctga tgaccataca     900
tggctcgata actttccagt gcacgggaga aaaaactggc cgcttttgtt cgatgaacag     960
cataaaccga aaccagcttt ttggcgggca gtgagtgtct ga                       1002
```

<210> 294
<211> 333
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 294

```
Met Lys Met Asn Ser Ser Leu Pro Ser Leu Arg Asp Val Phe Ala Asn
1               5                   10                  15
Asp Phe Arg Ile Gly Ala Ala Val Asn Pro Val Thr Ile Glu Met Gln
            20                  25                  30
Lys Gln Leu Leu Ile Asp His Val Asn Ser Ile Thr Ala Glu Asn His
        35                  40                  45
Met Lys Phe Glu His Leu Gln Pro Glu Glu Gly Lys Phe Thr Phe Gln
    50                  55                  60
Glu Ala Asp Arg Ile Val Asp Phe Ala Cys Ser His Arg Met Ala Val
65                  70                  75                  80
Arg Gly His Thr Leu Val Trp His Asn Gln Thr Pro Asp Trp Val Phe
                85                  90                  95
Gln Asp Gly Gln Gly His Phe Val Ser Arg Asp Val Leu Leu Glu Arg
            100                 105                 110
Met Lys Cys His Ile Ser Thr Val Val Arg Arg Tyr Lys Gly Lys Ile
        115                 120                 125
Tyr Cys Trp Asp Val Ile Asn Glu Ala Val Ala Asp Glu Gly Asp Glu
    130                 135                 140
Leu Leu Arg Pro Ser Lys Trp Arg Gln Ile Ile Gly Asp Asp Phe Met
145                 150                 155                 160
Glu Gln Ala Phe Leu Tyr Ala Tyr Glu Ala Asp Pro Asp Ala Leu Leu
                165                 170                 175
Phe Tyr Asn Asp Tyr Asn Glu Cys Phe Pro Glu Lys Arg Glu Lys Ile
            180                 185                 190
Phe Ala Leu Val Lys Ser Leu Arg Asp Lys Gly Ile Pro Ile His Gly
        195                 200                 205
Ile Gly Met Gln Ala His Trp Ser Leu Thr Arg Pro Ser Leu Asp Glu
```

```
    210                 215                 220
Ile Arg Ala Ala Ile Glu Arg Tyr Ala Ser Leu Gly Val Val Leu His
225                 230                 235                 240
Ile Thr Glu Leu Asp Val Ser Met Phe Glu Phe His Asp Arg Arg Thr
                245                 250                 255
Asp Leu Ala Ala Pro Thr Ser Glu Met Ile Glu Arg Gln Ala Glu Arg
            260                 265                 270
Tyr Gly Gln Ile Phe Ala Leu Phe Lys Glu Tyr Arg Asp Val Ile Gln
        275                 280                 285
Ser Val Thr Phe Trp Gly Ile Ala Asp Asp His Thr Trp Leu Asp Asn
    290                 295                 300
Phe Pro Val His Gly Arg Lys Asn Trp Pro Leu Leu Phe Asp Glu Gln
305                 310                 315                 320
His Lys Pro Lys Pro Ala Phe Trp Arg Ala Val Ser Val
                325                 330
```

<210> 295
<211> 1134
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 295
```
atgagatccg tccgcatcgt cacctttgct ctcgccgccg cgctggccgt cccgctggtg      60
acgtcgacgg ccacggccaa gccgtccgcc gaccacgagg ccgcgcccca ctccaacgcc     120
aagttcgacc gcctgcgctg ggccgccccc gaagggttct tcataggctc cgcggcggcc     180
ggcggcggcc accacctcga acaggactac ccggacccct tcaccttcga caagaagtac     240
cggaagatcc tgggccagca gttcaactcg gtctccgccg agaaccagat gaagtgggag     300
ttcatccacc ccgagcgcga ccagtaccgc ttcgaggagg ccgacgccat cgtcgagttc     360
gcccagcgga accgccaggc cgtgcgcggg cacaccctcc tgtggcacag ccagaacccc     420
gaatggctgg aggagggcga cttcaccaag gaggaactgc gcgccatcct caaggaccac     480
atcgacacgg tcgtcggccg ctacgccggc aagatccagc agtgggacgt ggccaacgag     540
atcttcaacg accaggccga gctgcgcacc gacgagaaca tctggatacg tgagctcggc     600
ccggagatcg tcgcggacgc cttccgctgg gcccacgagg ccgaccccga ggccaagctg     660
ttcctcaacg actacaacgt cgagggcatc aacgccaaga gcgacgccta ctacgagctc     720
gcccaggaga tgctggagca gggcgtgccg ctccacggat tcggcgccca gggccacctg     780
agcacccgct acggcttccc gggcgacctg cagcagaacc tgcagcggtt cgccgacctc     840
ggtctggaga ccgccatcac cgagatcgac gtccgcatgg acctcccggc gagcggcaag     900
cccaccaagg agcagctgcg gcagcaggcc gactactacc agcaggcact gtcggcctgc     960
ctggccgtga acgactgcaa ctccttcacc atctggggct tcaccgacaa gtactcgtgg    1020
gtgccggtct tcttcgaggg tgagggcagc gccacggtca tgacggagaa gttcgtccgc    1080
aagccggcct tcttcgccct gcagtccacc ctgaaggagg cgcgcaagcg ctga          1134
```

<210> 296
<211> 377
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(26)

<400> 296
```
Met Arg Ser Val Arg Ile Val Thr Phe Ala Leu Ala Ala Ala Leu Ala
1               5                   10                  15
Val Pro Leu Val Thr Ser Thr Ala Thr Ala Lys Pro Ser Ala Asp His
            20                  25                  30
Glu Ala Ala Pro His Ser Asn Ala Lys Phe Asp Arg Leu Arg Trp Ala
        35                  40                  45
Ala Pro Glu Gly Phe Phe Ile Gly Ser Ala Ala Ala Gly Gly Gly His
    50                  55                  60
His Leu Glu Gln Asp Tyr Pro Asp Pro Phe Thr Phe Asp Lys Lys Tyr
65                  70                  75                  80
Arg Lys Ile Leu Gly Gln Gln Phe Asn Ser Val Ser Ala Glu Asn Gln
                85                  90                  95
```

Met Lys Trp Glu Phe Ile His Pro Glu Arg Asp Gln Tyr Arg Phe Glu
100 105 110
Glu Ala Asp Ala Ile Val Glu Phe Ala Gln Arg Asn Arg Gln Ala Val
115 120 125
Arg Gly His Thr Leu Leu Trp His Ser Gln Asn Pro Glu Trp Leu Glu
130 135 140
Glu Gly Asp Phe Thr Lys Glu Glu Leu Arg Ala Ile Leu Lys Asp His
145 150 155 160
Ile Asp Thr Val Val Gly Arg Tyr Ala Gly Lys Ile Gln Gln Trp Asp
165 170 175
Val Ala Asn Glu Ile Phe Asn Asp Gln Ala Glu Leu Arg Thr Asp Glu
180 185 190
Asn Ile Trp Ile Arg Glu Leu Gly Pro Glu Ile Val Ala Asp Ala Phe
195 200 205
Arg Trp Ala His Glu Ala Asp Pro Glu Ala Lys Leu Phe Leu Asn Asp
210 215 220
Tyr Asn Val Glu Gly Ile Asn Ala Lys Ser Asp Ala Tyr Tyr Glu Leu
225 230 235 240
Ala Gln Glu Met Leu Glu Gln Gly Val Pro Leu His Gly Phe Gly Ala
245 250 255
Gln Gly His Leu Ser Thr Arg Tyr Gly Phe Pro Gly Asp Leu Gln Gln
260 265 270
Asn Leu Gln Arg Phe Ala Asp Leu Gly Leu Glu Thr Ala Ile Thr Glu
275 280 285
Ile Asp Val Arg Met Asp Leu Pro Ala Ser Gly Lys Pro Thr Lys Glu
290 295 300
Gln Leu Arg Gln Gln Ala Asp Tyr Tyr Gln Gln Ala Leu Ser Ala Cys
305 310 315 320
Leu Ala Val Asn Asp Cys Asn Ser Phe Thr Ile Trp Gly Phe Thr Asp
325 330 335
Lys Tyr Ser Trp Val Pro Val Phe Phe Glu Gly Glu Gly Ser Ala Thr
340 345 350
Val Met Thr Glu Lys Phe Val Arg Lys Pro Ala Phe Phe Ala Leu Gln
355 360 365
Ser Thr Leu Lys Glu Ala Arg Lys Arg
370 375

<210> 297
<211> 1842
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 297
ttgaggtcag gcgcgttctg tttcatcata gtcgttttaa tcctgaacct tatatgcagg 60
gagttgtatg agtgtaaaaa agttgttacc gcagcactgg tatgcttggc tttcgggtca 120
tcgctgactt gggggcaatg caccacattt accaccagta ccattcggaa ttgcgatggt 180
atagattacg agctctggag ccagaataac tctggcacga ccaatatgca aatcacggga 240
gggaactcga atccaaacgg tggaaccttt gaggcgacat ggagtggcac gatcaatgtt 300
ctattccgcg cgggtaaaaa atggggcaca tccagcacca gtacccccaa aaccatcggc 360
aatatctctc ttgaattcgc agcgacatgg agttcggtcg ataatgtgaa aatgcttggc 420
atctatggct gggcgtatta tccctcggga agcgaaccaa caaaaacgga aagcggtcaa 480
agcacgaact tttccaatca gattgagtat tacatcattc aagaccgcgg tagctataac 540
ccggcatccg gcggcaccaa cgccaaaaag tacggtgaag ggacgatcga cggaatcgcg 600
tatgattttt atgtcgccga ccgtatcggc caggccatgc tgacaggaac gggaaatttc 660
aaacagtact tcagcgtgcc gaagagcaca agcagtcaca ggcaaagcgg cacggtttcc 720
gtctccaaac attttgaggc ctgggaaaaa gcgggcatga agatgatgga ttgtcggtta 780
tacgaagtcg cgatgaaagt ggaatcgtat accggttccg cgaatggcaa cggctcggcg 840
aaagtgacca aaaatctcct cacgatcggc ggaagcagca gcaacgagtt tagtctcgta 900
acgaatgttt ctcctgccag cgcgggaacg gtgtccaaga gcccggacaa cgcatcctat 960
gccccgaacg cctccgttca gctcacggcg accccgaata ccggttggaa gtttgtgggc 1020
tgggaagggg acgcctcggg ttccacgagc ccaaccagcg ttaccatgag caaagacctc 1080
acggttacag cgaagtttga gctggtatcg gaagaaggca gcacaaacct gatccaggat 1140
ggcaacttcc cgagcggcag cgtaatctct acagatgacg gggcttcatg gaaactcgga 1200
caaggggaaa actggggaaa ttccgcagcc acaacgagcg tcagcaatgg aatcgcgaca 1260
gtcaatgtga caactgtcgg agcggaagct tatcaaccgc agcttgtaca gtacggtttg 1320
ggactcgaca tggacatgag ttacaaactt accttcaagg caagagccga tgcggcaagg 1380

aagattgaag ttgcgttcca gcaggcggtg gatccttggg ctggttatgc ttcccaggaa 1440
ttcgacctga ccacgaccga tcaggatttc gagttcgtat tcacgatgac caacgccagc 1500
gacccggcat cacagttcgc gttcaatctt ggccaggcga caggcgatgt ctatatcagt 1560
gatgttaaac tggtatacac gacaggcacc acacccatat cccgcaccat agtccgcggc 1620
aatacggcat tcgtctcggt aagtggcaga accctgaata tttcggcagt cgacgcgtcc 1680
acacttcaga tcaaggtagt agatataaac ggaaaggtaa gagcgaattt caacacggct 1740
ggtgcagcaa gtgtttcctt gtccaatatt cctgcgggcc agtacttcgt tggtatcaca 1800
ggcacaggca taaaacaaat ctcaccgatc gttttggaat aa 1842

<210> 298
<211> 613
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 298
Met Arg Ser Gly Ala Phe Cys Phe Ile Ile Val Val Leu Ile Leu Asn
1 5 10 15
Leu Ile Cys Arg Glu Leu Tyr Glu Cys Lys Lys Val Val Thr Ala Ala
20 25 30
Leu Val Cys Leu Ala Phe Gly Ser Ser Leu Thr Trp Gly Gln Cys Thr
35 40 45
Thr Phe Thr Thr Ser Thr Ile Arg Asn Cys Asp Gly Ile Asp Tyr Glu
50 55 60
Leu Trp Ser Gln Asn Asn Ser Gly Thr Thr Asn Met Gln Ile Thr Gly
65 70 75 80
Gly Asn Ser Asn Pro Asn Gly Gly Thr Phe Glu Ala Thr Trp Ser Gly
85 90 95
Thr Ile Asn Val Leu Phe Arg Ala Gly Lys Lys Trp Gly Thr Ser Ser
100 105 110
Thr Ser Thr Pro Lys Thr Ile Gly Asn Ile Ser Leu Glu Phe Ala Ala
115 120 125
Thr Trp Ser Ser Val Asp Asn Val Lys Met Leu Gly Ile Tyr Gly Trp
130 135 140
Ala Tyr Tyr Pro Ser Gly Ser Glu Pro Thr Lys Thr Glu Ser Gly Gln
145 150 155 160
Ser Thr Asn Phe Ser Asn Gln Ile Glu Tyr Tyr Ile Ile Gln Asp Arg
165 170 175
Gly Ser Tyr Asn Pro Ala Ser Gly Gly Thr Asn Ala Lys Lys Tyr Gly
180 185 190
Glu Gly Thr Ile Asp Gly Ile Ala Tyr Asp Phe Tyr Val Ala Asp Arg
195 200 205
Ile Gly Gln Ala Met Leu Thr Gly Thr Gly Asn Phe Lys Gln Tyr Phe
210 215 220
Ser Val Pro Lys Ser Thr Ser Ser His Arg Gln Ser Gly Thr Val Ser
225 230 235 240
Val Ser Lys His Phe Glu Ala Trp Glu Lys Ala Gly Met Lys Met Met
245 250 255
Asp Cys Arg Leu Tyr Glu Val Ala Met Lys Val Glu Ser Tyr Thr Gly
260 265 270
Ser Ala Asn Gly Asn Gly Ser Ala Lys Val Thr Lys Asn Leu Leu Thr
275 280 285
Ile Gly Gly Ser Ser Ser Asn Glu Phe Ser Leu Val Thr Asn Val Ser
290 295 300
Pro Ala Ser Ala Gly Thr Val Ser Lys Ser Pro Asp Asn Ala Ser Tyr
305 310 315 320
Ala Pro Asn Ala Ser Val Gln Leu Thr Ala Thr Pro Asn Thr Gly Trp
325 330 335
Lys Phe Val Gly Trp Glu Gly Asp Ala Ser Gly Ser Thr Ser Pro Thr
340 345 350
Ser Val Thr Met Ser Lys Asp Leu Thr Val Thr Ala Lys Phe Glu Leu
355 360 365
Val Ser Glu Glu Gly Ser Thr Asn Leu Ile Gln Asp Gly Asn Phe Pro
370 375 380
Ser Gly Ser Val Ile Ser Thr Asp Asp Gly Ala Ser Trp Lys Leu Gly
385 390 395 400
Gln Gly Glu Asn Trp Gly Asn Ser Ala Ala Thr Thr Ser Val Ser Asn

```
                405                     410                     415
Gly Ile Ala Thr Val Asn Val Thr Thr Val Gly Ala Glu Ala Tyr Gln
            420                     425                     430
Pro Gln Leu Val Gln Tyr Gly Leu Gly Leu Asp Met Asp Met Ser Tyr
        435                     440                     445
Lys Leu Thr Phe Lys Ala Arg Ala Asp Ala Ala Arg Lys Ile Glu Val
    450                     455                     460
Ala Phe Gln Gln Ala Val Asp Pro Trp Ala Gly Tyr Ala Ser Gln Glu
465                     470                     475                     480
Phe Asp Leu Thr Thr Thr Asp Gln Asp Phe Glu Phe Val Phe Thr Met
                485                     490                     495
Thr Asn Ala Ser Asp Pro Ala Ser Gln Phe Ala Phe Asn Leu Gly Gln
            500                     505                     510
Ala Thr Gly Asp Val Tyr Ile Ser Asp Val Lys Leu Val Tyr Thr Thr
        515                     520                     525
Gly Thr Thr Pro Ile Ser Arg Thr Ile Val Arg Gly Asn Thr Ala Phe
    530                     535                     540
Val Ser Val Ser Gly Arg Thr Leu Asn Ile Ser Ala Val Asp Ala Ser
545                     550                     555                     560
Thr Leu Gln Ile Lys Val Val Asp Ile Asn Gly Lys Val Arg Ala Asn
                565                     570                     575
Phe Asn Thr Ala Gly Ala Ala Ser Val Ser Leu Ser Asn Ile Pro Ala
            580                     585                     590
Gly Gln Tyr Phe Val Gly Ile Thr Gly Thr Gly Ile Lys Gln Ile Ser
        595                     600                     605
Pro Ile Val Leu Glu
    610
```

<210> 299
<211> 1047
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 299
```
atgtttttga gtctcaaaag agtggcggcg cttgtttgcg tcgccggtct cggcatctct      60
gcggcccaag cacagacctg cctgacctcg agtcaaaccg gcactaacaa cggcttctac     120
tattcgttct ggaaagacaa tcccggcacc gtgaatttct gtctgcagtc cggcggccgc     180
tacacctcca actggagcgg catcaacaac tgggtcggcg gaaagggatg gcagacgggt     240
tcccgcagag tggtgaacta ctcgggcagc ttcaattcgc ctggcaatgg gtacctgact     300
ctctatgggt ggaccaccaa tccgctcatc gagtactaca ttgtcgacaa ctggggcacg     360
tatcgtccgc cgggtgggca ggggttcatg ggcacggtga ccagcgatgg cgcgacgtat     420
gacgtctatc gcacgcagcg cgtcaatcag ccctgcatca ccggcagcag ttgcacgttc     480
tatcaatact ggagcgtgcg gcagtcgaag cggaccggtg gcacgatcac caccggcaac     540
cacttcgatg cctgggccag ctacggaatg aatctgggcg ctcacaacta ccagatcatg     600
gcgaccgagg gctatcaaag cagcggcagc tctgacatca cggtgagtga gggaagcagc     660
agcagtagca gcggtggtgg cagcagcacg agcagcagtg gcggcggcgg caccaagagc     720
ttcacggtcc gggcgcgcgg aaccgcgggt ggtgagtcca tcacgctgcg tgtgaacaat     780
cagaacgtgc agacctggac gctgggcacc agcatgacga actacacggc atcgacgtcg     840
ttgagcggtg gcatcaccgt ggcttacacg aacgacagtg gcaatcgcga cgtgcaggtg     900
gattacatca tcgtgaacgg ctcgacgcgt cagtcagaag cgcagagcta caacaccggg     960
ctctatgcca acggtagttg tggtggcggc tccaatagcg aatggatgca ttgcaacggc    1020
gccattggct acgggaatac gccgtag                                        1047
```

<210> 300
<211> 348
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(24)

<400> 300
```
Met Phe Leu Ser Leu Lys Arg Val Ala Ala Leu Val Cys Val Ala Gly
```

1 5 10 15
Leu Gly Ile Ser Ala Ala Gln Ala Gln Thr Cys Leu Thr Ser Ser Gln
20 25 30
Thr Gly Thr Asn Asn Gly Phe Tyr Tyr Ser Phe Trp Lys Asp Asn Pro
35 40 45
Gly Thr Val Asn Phe Cys Leu Gln Ser Gly Gly Arg Tyr Thr Ser Asn
50 55 60
Trp Ser Gly Ile Asn Asn Trp Val Gly Gly Lys Gly Trp Gln Thr Gly
65 70 75 80
Ser Arg Arg Val Val Asn Tyr Ser Gly Ser Phe Asn Ser Pro Gly Asn
85 90 95
Gly Tyr Leu Thr Leu Tyr Gly Trp Thr Thr Asn Pro Leu Ile Glu Tyr
100 105 110
Tyr Ile Val Asp Asn Trp Gly Thr Tyr Arg Pro Pro Gly Gly Gln Gly
115 120 125
Phe Met Gly Thr Val Thr Ser Asp Gly Ala Thr Tyr Asp Val Tyr Arg
130 135 140
Thr Gln Arg Val Asn Gln Pro Cys Ile Thr Gly Ser Ser Cys Thr Phe
145 150 155 160
Tyr Gln Tyr Trp Ser Val Arg Gln Ser Lys Arg Thr Gly Gly Thr Ile
165 170 175
Thr Thr Gly Asn His Phe Asp Ala Trp Ala Ser Tyr Gly Met Asn Leu
180 185 190
Gly Ala His Asn Tyr Gln Ile Met Ala Thr Glu Gly Tyr Gln Ser Ser
195 200 205
Gly Ser Ser Asp Ile Thr Val Ser Glu Gly Ser Ser Ser Ser Ser Ser
210 215 220
Gly Gly Gly Ser Ser Thr Ser Ser Ser Gly Gly Gly Gly Thr Lys Ser
225 230 235 240
Phe Thr Val Arg Ala Arg Gly Thr Ala Gly Gly Glu Ser Ile Thr Leu
245 250 255
Arg Val Asn Asn Gln Asn Val Gln Thr Trp Thr Leu Gly Thr Ser Met
260 265 270
Thr Asn Tyr Thr Ala Ser Thr Ser Leu Ser Gly Gly Ile Thr Val Ala
275 280 285
Tyr Thr Asn Asp Ser Gly Asn Arg Asp Val Gln Val Asp Tyr Ile Ile
290 295 300
Val Asn Gly Ser Thr Arg Gln Ser Glu Ala Gln Ser Tyr Asn Thr Gly
305 310 315 320
Leu Tyr Ala Asn Gly Ser Cys Gly Gly Gly Ser Asn Ser Glu Trp Met
325 330 335
His Cys Asn Gly Ala Ile Gly Tyr Gly Asn Thr Pro
340 345

<210> 301
<211> 642
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 301
atgtttaagt ttacaaagaa attcttagtt gggttaacgg cagctttgat gagtatgagc 60
ttgttttcgg caaacgcctc tgcagctaac acagactact ggcaaaattg gactgatggg 120
ggcggaacag taaacgctgt caatgggtct ggcgggaatt acagtgtgaa ttggtctaat 180
accggaaatt tcgttgttgg taaaggttgg actacaggtt cgccatttag gacgataaac 240
tataatgccg gagtttgggc gccgaacggc aatgcatatt tgactttata tggttggacg 300
cgatcccctc tcatagaata ttatgtagtg gattcatggg gtacttatag acctactgga 360
acgtataaag gtacggttta cagtgatggg ggtacatatg acgtgtacac aactacacgt 420
tatgatgcac cttccattga tggcgataaa actactttta cgcagtactg gagtgttcgc 480
cagtcgaaga gaccaactgg aagcaacgct acaatcactt tcagcaatca cgttaacgca 540
tggaagagat atgggatgaa tctgggtagt aattggtctt accaagtctt agcgacagag 600
ggatatcgaa gtagtggaag ttctaacgta acagtgtggt aa 642

<210> 302
<211> 213
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(28)

<400> 302
Met Phe Lys Phe Thr Lys Lys Phe Leu Val Gly Leu Thr Ala Ala Leu
1 5 10 15
Met Ser Met Ser Leu Phe Ser Ala Asn Ala Ser Ala Ala Asn Thr Asp
20 25 30
Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr Val Asn Ala Val Asn
35 40 45
Gly Ser Gly Gly Asn Tyr Ser Val Asn Trp Ser Asn Thr Gly Asn Phe
50 55 60
Val Val Gly Lys Gly Trp Thr Thr Gly Ser Pro Phe Arg Thr Ile Asn
65 70 75 80
Tyr Asn Ala Gly Val Trp Ala Pro Asn Gly Asn Ala Tyr Leu Thr Leu
85 90 95
Tyr Gly Trp Thr Arg Ser Pro Leu Ile Glu Tyr Tyr Val Val Asp Ser
100 105 110
Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys Gly Thr Val Tyr Ser
115 120 125
Asp Gly Gly Thr Tyr Asp Val Tyr Thr Thr Thr Arg Tyr Asp Ala Pro
130 135 140
Ser Ile Asp Gly Asp Lys Thr Thr Phe Thr Gln Tyr Trp Ser Val Arg
145 150 155 160
Gln Ser Lys Arg Pro Thr Gly Ser Asn Ala Thr Ile Thr Phe Ser Asn
165 170 175
His Val Asn Ala Trp Lys Arg Tyr Gly Met Asn Leu Gly Ser Asn Trp
180 185 190
Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Arg Ser Ser Gly Ser Ser
195 200 205
Asn Val Thr Val Trp
210

<210> 303
<211> 1404
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 303
ttgactataa aggcctggcc cgggacggct gccagctata ataccaatag aggttttatc 60
atgtcctacg ctcagtttaa gggggccgct accctagcga cgtccttcct gctcgcagtc 120
accttgacag cctgtggagg cagcaaatcc aaacccgttc tgccagaccc atcgaacagc 180
agctcgtcat caagcagcag ctcgtcatca agcagcagct cctcaagttc ctccagtagc 240
agttcgagct cttctagtgc tccctccagc caaacgttct tcattgagcc ggatttccag 300
cttcacaccc tggcggactt cccgattgga gtggcagtct cggcagccaa tgagccatac 360
agcatcttca accaaaccga tggtactgat cggcaggatg tgatcctgga gcatttcaac 420
gaaatgaccg ctggcaacat catgaaaatg agctacgtgt acgcaggtca acgtgcaaat 480
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ttcatgcaga attatgatgg cgactttgct gagatgttgg ccaatcacgc gcggagtgtt 660
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<211> 467
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(74)

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35 40 45
Lys Ser Lys Pro Val Leu Pro Asp Pro Ser Asn Ser Ser Ser Ser Ser
50 55 60
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
65 70 75 80
Ser Ser Ser Ser Ser Ser Ala Pro Ser Ser Gln Thr Phe Phe Ile Glu
85 90 95
Pro Asp Phe Gln Leu His Thr Leu Ala Asp Phe Pro Ile Gly Val Ala
100 105 110
Val Ser Ala Ala Asn Glu Pro Tyr Ser Ile Phe Asn Gln Thr Asp Gly
115 120 125
Thr Asp Arg Gln Asp Val Ile Leu Glu His Phe Asn Glu Met Thr Ala
130 135 140
Gly Asn Ile Met Lys Met Ser Tyr Val Tyr Ala Gly Gln Arg Ala Asn
145 150 155 160
Gln Gln Pro Asp Gln Phe Asp Phe Ser Arg Ala Asp Glu Leu Val Gly
165 170 175
Phe Ala His Ala Asn Ser Val Lys Ile His Gly His Ala Leu Val Trp
180 185 190
His Ala Asp Tyr Gln Val Pro Gly Phe Met Gln Asn Tyr Asp Gly Asp
195 200 205
Phe Ala Glu Met Leu Ala Asn His Ala Arg Ser Val Val Glu His Phe
210 215 220
Asp Glu Glu Phe Pro Gly Thr Val Val Ser Trp Asp Val Val Asn Glu
225 230 235 240
Ala Ile Thr Asp Asn Phe Gly Thr Asp Thr Asn Gly Trp Arg Arg Ser
245 250 255
Leu Phe Tyr Asn Ala Leu Pro Pro Ala Thr Glu Asp Asp Ile Pro Glu
260 265 270
Tyr Ile Arg Val Ala Phe Gln Ala Ala Arg Asp Ala Asn Pro Asp Ile
275 280 285
Asp Leu Tyr Tyr Asn Asp Tyr Asp Asn Thr Ala Asn Thr Asn Arg Leu
290 295 300
Asn Lys Thr Leu Gln Ile Ala Asp Ala Leu Ala Glu Asp Glu Leu Ile
305 310 315 320
Asp Gly Val Gly Phe Gln Met His Val Tyr Met Thr Tyr Pro Ser Leu
325 330 335
Ser His Phe Gln Asn Ala Phe Gln Glu Val Val Asp Arg Gly Leu Lys
340 345 350
Val Lys Ile Thr Glu Leu Asp Val Ser Val Val Asn Pro Tyr Gly Gln
355 360 365
Ser Thr Pro Pro Pro Gln Pro Val Tyr Asp Glu Ala Leu Ala Gly Ala
370 375 380
Gln Lys Lys Arg Phe Cys Asp Ile Thr Arg Val Tyr Leu Glu Thr Val
385 390 395 400
Pro Ala Glu Leu Arg Gly Gly Leu Thr Val Trp Gly Leu Ala Asp Asn
405 410 415
Glu Ser Trp Leu Met Gln Gln Phe Arg Asn Ala Thr Gly Ala Asn Tyr
420 425 430
Thr Asp Val Trp Pro Leu Leu Phe Asn Ala Asp Leu Ser Ala Lys Pro

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Thr Leu Gln Gly Val Ala Asp Ala Leu Gln Gly Leu Pro Cys Thr Thr
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Asp Leu Asp
465
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<210> 305
<211> 3705
<212> DNA
<213> Bacteria

<400> 305

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tctaatgggg actttgagac aggcacaatt gatggctgga ttaagcaagg taatcctaca     180
ttagaagtaa cgactgaaca agcaattggg caatacagta tgaaagttac gggtagaaca     240
cagacatatg aaggacctgc atatagcttt ttaggaaaaa tgcagaaagg tgaatcatat     300
aatgtatcgc ttaaagttag acttgtttct ggacaaaatt cttctaatcc ttttattacc     360
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gatttttggg tgaaatttgt taatggcaat gatacagaac aaataaaggc tactgttaaa     840
gcgacttcta acaaagacaa ttatatacaa gttaatgatt ttgtaaatgt aaataaaggc     900
gaatggacag aaataaaagg cagttttact ttacctgtga cagattacag cggtgtcagc     960
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gattatgaaa tagcacataa tatgaagatg agaggtcata cattgctttg gcataatcag    1320
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gaccaaggca gtggcaatat aaatgcgata acagtttgga atgattatac aaacagtcaa    2520
gatactaata cagcatattt tggagattta gtattatcaa aacctgcaca gattgcaaca    2580
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tccagtgtga atccttatga acaggattct gtggaagttt ttgtagatca gaataatgat    2820
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gactggtatg caaacgcgat agaagcagca tacaaaacag gaataatcga aggtgacgga    3420
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<211> 1234
<212> PRT
<213> Bacteria

<220>
<221> SIGNAL
<222> (1)...(32)

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Asp Asp Thr Asn Thr Asn Leu Val Ser Asn Gly Asp Phe Glu Thr Gly
35 40 45
Thr Ile Asp Gly Trp Ile Lys Gln Gly Asn Pro Thr Leu Glu Val Thr
50 55 60
Thr Glu Gln Ala Ile Gly Gln Tyr Ser Met Lys Val Thr Gly Arg Thr
65 70 75 80
Gln Thr Tyr Glu Gly Pro Ala Tyr Ser Phe Leu Gly Lys Met Gln Lys
85 90 95
Gly Glu Ser Tyr Asn Val Ser Leu Lys Val Arg Leu Val Ser Gly Gln
100 105 110
Asn Ser Ser Asn Pro Phe Ile Thr Val Thr Met Phe Arg Glu Asp Asp
115 120 125
Asn Gly Lys His Tyr Asp Thr Ile Val Trp Gln Lys Gln Val Ser Glu
130 135 140
Asp Ser Trp Thr Thr Val Ser Gly Thr Tyr Thr Leu Asp Tyr Thr Gly
145 150 155 160
Thr Leu Lys Thr Leu Tyr Met Tyr Val Glu Ser Pro Asp Pro Thr Leu
165 170 175
Glu Tyr Tyr Ile Asp Asp Val Val Val Thr Pro Gln Asn Pro Ile Gln
180 185 190
Val Gly Asn Val Ile Thr Asn Gly Thr Phe Glu Asn Gly Asn Thr Ser
195 200 205
Gly Trp Val Gly Thr Gly Ser Ser Val Val Lys Ala Val Tyr Gly Val
210 215 220
Ala His Ser Gly Gly Tyr Ser Leu Leu Thr Thr Gly Arg Thr Ala Asn
225 230 235 240
Trp Asn Gly Pro Ser Tyr Asp Leu Thr Gly Lys Ile Val Pro Gly Gln
245 250 255
Gln Tyr Asn Val Asp Phe Trp Val Lys Phe Val Asn Gly Asn Asp Thr
260 265 270
Glu Gln Ile Lys Ala Thr Val Lys Ala Thr Ser Asn Lys Asp Asn Tyr
275 280 285
Ile Gln Val Asn Asp Phe Val Asn Val Asn Lys Gly Glu Trp Thr Glu
290 295 300
Ile Lys Gly Ser Phe Thr Leu Pro Val Thr Asp Tyr Ser Gly Val Ser
305 310 315 320
Ile Tyr Val Glu Ser Gln Asn Pro Thr Leu Glu Phe Tyr Ile Asp Asp
325 330 335
Phe Ser Val Ile Gly Glu Ile Ser Asn Asn Gln Ile Thr Ile Gln Asn
340 345 350
Asp Ile Pro Asp Leu Tyr Ser Val Phe Lys Asp Tyr Phe Pro Ile Gly
355 360 365
Val Ala Val Asp Ser Ser Arg Leu Asn Asp Ala Asp Pro His Ala Gln
370 375 380
Leu Thr Ala Lys His Phe Asn Met Leu Val Ala Glu Asn Ala Met Lys
385 390 395 400
Pro Glu Ser Leu Gln Pro Thr Glu Gly Asn Phe Thr Phe Asp Asn Ala
405 410 415
Asp Lys Ile Val Asp Tyr Glu Ile Ala His Asn Met Lys Met Arg Gly

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            420                                     425                                     430
His Thr Leu Leu Trp His Asn Gln Val Pro Asp Trp Phe Phe Gln Asp
        435                                     440                                     445
Pro Ser Asp Pro Ser Lys Pro Ala Ser Arg Asp Leu Leu Leu Gln Arg
    450                                     455                                     460
Leu Arg Thr His Ile Thr Thr Val Leu Asp His Phe Lys Thr Lys Tyr
465                                     470                                     475                                     480
Gly Ser Gln Asn Pro Ile Ile Gly Trp Asp Val Val Asn Glu Val Leu
                        485                                     490                                     495
Asp Asp Asn Gly Asn Leu Arg Asn Ser Lys Trp Leu Gln Ile Ile Gly
            500                                     505                                     510
Pro Asp Tyr Ile Glu Lys Ala Phe Glu Tyr Ala His Glu Ala Asp Pro
        515                                     520                                     525
Ser Met Lys Leu Phe Ile Asn Asp Tyr Asn Ile Glu Asn Asn Gly Val
    530                                     535                                     540
Lys Thr Gln Ala Met Tyr Asp Leu Val Lys Lys Leu Lys Ser Glu Gly
545                                     550                                     555                                     560
Val Pro Ile Asn Gly Ile Gly Met Gln Met His Ile Ser Ile Asn Ser
                        565                                     570                                     575
Asn Ile Asp Asn Ile Lys Ala Ser Ile Glu Lys Leu Ala Ser Leu Gly
            580                                     585                                     590
Val Glu Ile Gln Val Thr Glu Leu Asp Met Asn Met Asn Gly Asn Val
        595                                     600                                     605
Ser Asn Asp Ala Leu Leu Lys Gln Ala Arg Leu Tyr Lys Gln Leu Phe
    610                                     615                                     620
Asp Leu Phe Lys Ala Glu Lys Gln Tyr Ile Thr Ala Val Val Phe Trp
625                                     630                                     635                                     640
Gly Val Ser Asp Asp Val Ser Trp Leu Ser Lys Pro Asn Ala Pro Leu
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Leu Phe Asp Ser Lys Leu Gln Ala Lys Pro Ala Tyr Trp Ala Ile Val
            660                                     665                                     670
Asp Gln Gly Lys Ala Ile Pro Asp Ile Gln Ser Ala Lys Ala Leu Glu
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Gly Ser Pro Thr Ile Gly Ala Asn Val Asp Ser Ser Trp Lys Leu Val
    690                                     695                                     700
Lys Pro Leu Tyr Ala Asn Thr Tyr Val Lys Gly Thr Ile Gly Ala Thr
705                                     710                                     715                                     720
Ala Ala Val Lys Ser Met Trp Asp Thr Lys Asn Leu Tyr Leu Leu Val
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Gln Val Ser Asp Asn Thr Pro Ser Asn Asn Asp Gly Ile Glu Ile Phe
            740                                     745                                     750
Val Asp Lys Asn Asp Asn Lys Ser Thr Thr Tyr Glu Ser Asp Asp Glu
        755                                     760                                     765
His Tyr Ile Val Lys Arg Asp Gly Thr Gly Ser Ser Asn Ile Thr Lys
    770                                     775                                     780
Tyr Val Met Ser Asn Ala Asp Gly Tyr Val Ala Gln Ile Ala Ile Pro
785                                     790                                     795                                     800
Ile Glu Asp Ile Ser Pro Val Leu Asn Asp Lys Ile Gly Phe Asp Ile
                        805                                     810                                     815
Arg Ile Asn Asp Asp Gln Gly Ser Gly Asn Ile Asn Ala Ile Thr Val
            820                                     825                                     830
Trp Asn Asp Tyr Thr Asn Ser Gln Asp Thr Asn Thr Ala Tyr Phe Gly
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Asp Leu Val Leu Ser Lys Pro Ala Gln Ile Ala Thr Ala Ile Tyr Gly
    850                                     855                                     860
Thr Pro Val Ile Asp Gly Lys Val Asp Gly Ile Trp Asn Asn Ala Glu
865                                     870                                     875                                     880
Ala Ile Ser Thr Asn Thr Trp Val Leu Gly Ser Asn Gly Ala Thr Ala
                        885                                     890                                     895
Thr Ala Lys Met Met Trp Asp Asp Lys Tyr Leu Tyr Ile Leu Ala Asp
            900                                     905                                     910
Val Thr Asp Asn Asn Leu Asn Lys Ser Ser Val Asn Pro Tyr Glu Gln
        915                                     920                                     925
Asp Ser Val Glu Val Phe Val Asp Gln Asn Asn Asp Lys Thr Thr Tyr
    930                                     935                                     940
Tyr Glu Asn Asp Asp Gly Gln Phe Arg Val Asn Tyr Asp Asn Glu Gln
945                                     950                                     955                                     960
Ser Phe Gly Gly Ser Thr Asn Ser Asn Gly Phe Lys Ser Ala Thr Ser
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980 985 990
Ile Thr Pro Ser Asn Gly Thr Ile Ile Gly Phe Asp Leu Gln Val Asn
995 1000 1005
Asp Ala Asp Glu Asn Gly Lys Arg Thr Gly Ile Val Thr Trp Cys Asp
1010 1015 1020
Pro Ser Gly Asn Ser Trp Gln Asp Thr Ser Gly Phe Gly Asn Leu Met
1025 1030 1035 1040
Leu Thr Gly Lys Pro Ser Gly Val Leu Lys Lys Val Val Ala Phe Asn
1045 1050 1055
Asp Ile Lys Asp Asn Trp Ala Lys Asp Val Ile Glu Val Leu Ala Ser
1060 1065 1070
Arg His Ile Val Glu Gly Met Thr Asp Thr Gln Tyr Glu Pro Asn Lys
1075 1080 1085
Thr Val Thr Arg Ala Glu Phe Thr Ala Met Ile Leu Arg Leu Leu Asn
1090 1095 1100
Ile Lys Glu Glu Ala Tyr Ser Gly Glu Phe Ser Asp Val Lys Ser Gly
1105 1110 1115 1120
Asp Trp Tyr Ala Asn Ala Ile Glu Ala Ala Tyr Lys Thr Gly Ile Ile
1125 1130 1135
Glu Gly Asp Gly Lys Asn Ala Arg Pro Asn Asp Ser Ile Thr Arg Glu
1140 1145 1150
Glu Met Thr Ala Ile Ala Met Arg Ala Tyr Glu Met Leu Thr Gln Tyr
1155 1160 1165
Glu Glu Glu Asn Ile Gly Ala Thr Thr Phe Ser Asp Asp Lys Ser Ile
1170 1175 1180
Ser Asp Trp Ala Arg Asn Val Val Ala Asn Ala Ala Lys Leu Gly Ile
1185 1190 1195 1200
Val Asn Gly Glu Pro Asn Asn Val Phe Ala Pro Lys Gly Asn Ala Thr
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Lys Leu

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<211> 3729
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

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caagaagtcg aagtgcaaat tgagcgcggc ccgaatgcgc gcccaattgc gccgcaaccg 2940
attaatctcg gccccgacga taaacccgca tttccccggg tgcccgccgg tttcgatgtc 3000
cgccgcaacg atattccgca tggcgaaatc aaactcgtgg aatatccatc cgctacagtg 3060
ggcacaaatc gtaagatgca ggtttacacg ccgcccggtt acaatccgca agaaaagtat 3120
gcggtgcttt atctgttgca cggaatcggc ggcgacgagt gggaatggaa aaatggcggc 3180
acgccggaag tgattctcga taatctttac gccgcgaaaa aactccagcc gatgattgtg 3240
gtcatgccca atggccgcgc gcaaaaagat gaccgtccaa tcggcaatgt gttcgcatca 3300
gcgcctgctt ttgaaacctt cgagaaagat ttactcaacg acgtaattcc gtttatcgaa 3360
aagaattatc cagtcaaaac cggcgccgaa aatcgcgcgc ttgcgggcct ttcgatgggc 3420
ggtgggcaat cgctgaactt tggtctgggc aatctcgaca cctttgcgtg ggtcggcggc 3480
ttttcttcgg cgcccaacac gcgcactggc gcaaggctat tagccaatcc cgacgatgcc 3540
aaaaagaagc tgaaattgtt atgggtttcg tgtggcgata aagacggctt gtttttcatc 3600
agccagcgca cgcatcgcta tctcgccgaa aacaatgtgc cacacgtctg gcatgtgcag 3660
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ttccgctaa 3729

<210> 308
<211> 1242
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 308
Met Lys Ser Ala Ile Gly Asp Ala Ala Phe Met Ala Ala Met Glu Arg
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Asn Ser Asp Ile Val Thr Met Gln Cys Tyr Ala Pro Ile Phe Val Asn
20 25 30
Val Asn Pro Gly Gly Arg Gln Trp Arg Pro Asn Leu Met Gly Tyr Asp
35 40 45
Ala Leu Ser Ala Phe Gly Ser Pro Ser Tyr Tyr Ala Ile Lys Met Phe
50 55 60
Ser Asn Asn Leu Gly Asp Thr Ile Leu Lys Pro Ser Leu Ser Gly Ala
65 70 75 80
Arg Leu Pro Val Ser Val Thr Gln Glu Gln Lys Ser Gly Thr Ile Phe
85 90 95
Ile Lys Leu Val Asn Pro Gln Thr Thr Pro Gln Ser Val Lys Ile Asp
100 105 110
Leu Lys Gly Val Arg Ser Val Glu Phe Ser Gly Thr Ala Thr Val Leu
115 120 125
Ala Ala Asp Ser Gly Ala Leu Asn Ser Ile Asp Ala Pro Thr Lys Val
130 135 140
Val Pro Val Thr Arg Arg Ile Thr Gly Ile Ser Pro Ser Phe Ala Gln
145 150 155 160
Thr Leu Glu Pro Tyr Ser Ile Thr Val Leu Gln Ile Lys Ala Thr Ala

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                165                     170                     175
Leu Pro Thr Ala Thr Ala Asn Ala Val Ala Pro Pro Thr Phe Thr Thr
            180                     185                     190
Glu Pro Lys Val Asn Thr Thr Thr Pro Val Thr Ile Pro Val Ala Thr
        195                     200                     205
Ser Gln Pro Gln Pro Val Ser Gln Pro Ser Pro Asp Ala Asn Ala Ile
    210                     215                     220
Ala Pro Leu Lys Asn Ala Phe Lys Gly Lys Phe Leu Ile Gly Thr Val
225                     230                     235                     240
Leu Ser Gly Pro Asp Leu Arg Gly Gln Gln Thr Arg Ser Val Gly Ile
                245                     250                     255
Ala Thr Thr His Phe Asp Ala Phe Thr Ala Glu Asn Glu Met Lys Pro
            260                     265                     270
Asp Ala Met Gln Pro Arg Glu Gly Gln Phe Asn Phe Ala Ala Gly Asp
        275                     280                     285
Arg Leu Val Glu Leu Ala Glu Lys Ser Gly Ala Thr Pro Ile Gly His
    290                     295                     300
Thr Leu Ile Trp His Ser Gln Thr Pro Arg Trp Phe Phe Glu Gly Pro
305                     310                     315                     320
Asp Gly Gln Pro Ala Asn Arg Glu Leu Ala Leu Ala Arg Met Arg Lys
                325                     330                     335
His Ile Ala Thr Val Val Gly His Tyr Lys Gly Arg Val Lys Gln Trp
            340                     345                     350
Asp Val Val Asn Glu Ala Ile Asn Asp Gly Pro Gly Val Leu Arg Gln
        355                     360                     365
Ser Pro Trp Leu Arg Ala Ile Gly Glu Asp Tyr Ile Ala Glu Ala Phe
    370                     375                     380
Arg Ala Ala His Ala Ala Asp Pro Asp Ala Ile Leu Ile Tyr Asn Asp
385                     390                     395                     400
Tyr Asn Ile Glu Met Gly Tyr Lys Arg Pro Lys Ala Ile Gln Leu Leu
                405                     410                     415
Lys Ser Leu Val Asp Gln Lys Val Pro Ile His Ala Val Gly Ile Gln
            420                     425                     430
Gly His Trp Arg Met Asp Thr Asn Leu Thr Glu Val Glu Gln Ala Ile
        435                     440                     445
Lys Glu Phe Ser Ala Leu Gly Leu Lys Val Met Ile Thr Glu Leu Asp
    450                     455                     460
Ile Gly Val Leu Pro Thr Arg Tyr Gln Gly Ala Asp Ile Ser Gln Val
465                     470                     475                     480
Gln Asn Met Thr Pro Glu Gln Arg Ala Ala Val Asn Pro Tyr Thr Asn
                485                     490                     495
Gly Leu Pro Asp Asp Val Ala Gln Lys His Ala Asp Lys Tyr Arg Gln
            500                     505                     510
Ala Phe Asp Ile Phe Leu Arg Tyr Lys Asp Val Ile Glu Arg Val Thr
        515                     520                     525
Phe Trp Gly Val Asp Asp Ala His Ser Trp Leu Asn Gly Phe Pro Ile
    530                     535                     540
Arg Gly Arg Thr Asp Tyr Pro Leu Leu Phe Asp Arg Gln Gly Lys Pro
545                     550                     555                     560
Lys Pro Ala Phe Phe Ala Val Gln Asn Leu Ala Leu Gly Val Thr Ala
                565                     570                     575
Ala Pro Gln Ser Asn Ala Ser Ser Ala Pro Arg Ala Val Ala Gln Ala
            580                     585                     590
Ala Pro Ala Thr Ser Asn Ile Arg Gly Gln Glu Phe Pro Arg Val Glu
        595                     600                     605
Ser Asp Leu Arg Val Thr Phe Arg Ile Lys Ala Pro Glu Ala Gln Lys
    610                     615                     620
Val Gln Phe Asp Leu Gly Lys Pro Tyr Asp Ala Thr Arg Asp Ala Glu
625                     630                     635                     640
Gly Asn Trp Thr Ala Thr Thr Glu Pro Gln Val Pro Gly Phe His Tyr
                645                     650                     655
Tyr Asn Leu Val Ile Asp Gly Val Arg Val Asn Asp Pro Ala Ser Glu
            660                     665                     670
Thr Phe Tyr Gly Ala Gly Arg Gln Met Ser Gly Ile Glu Ile Pro Asp
        675                     680                     685
Pro Asp Ser Ala Phe Tyr Ser Pro Gln Asn Val Pro His Gly Glu Val
    690                     695                     700
Arg Glu Arg Trp Tyr Phe Ser Asn Thr Thr Gln Ala Trp Arg Arg Ile
705                     710                     715                     720
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Phe Ile Tyr Thr Pro Pro Gly Tyr Asp Thr Asn Gln Val Glu Arg Phe
725 730 735
Pro Val Leu Tyr Leu Gln His Gly Gly Gly Glu Asp Glu Arg Gly Trp
740 745 750
Pro Gln Gln Gly Arg Met Ser Phe Ile Met Asp Asn Leu Ile Ala Thr
755 760 765
Arg Lys Ala Lys Pro Met Leu Val Val Met Glu Gln Gly Tyr Ala Arg
770 775 780
Lys Pro Asn Glu Pro Gln Val Pro Leu Arg Pro Pro Gly Gly Ser Ala
785 790 795 800
Gly Ala Met Pro Pro Asp Phe Asn Arg Met Phe Gly Thr Leu Gly Glu
805 810 815
Val Phe Thr Lys Asp Leu Ile Pro Phe Ile Asp Ala Asn Tyr Arg Thr
820 825 830
Lys Thr Asp Arg Glu Asn Arg Ala Met Ala Gly Leu Ser Met Gly Gly
835 840 845
Met Gln Ser Phe Leu Ile Gly Leu Ser Asn Thr Asp Leu Phe Ala His
850 855 860
Ile Gly Gly Phe Ser Gly Ala Gly Gly Gly Phe Gly Gly Gly Thr Phe
865 870 875 880
Asp Ala Lys Thr Ala His Gly Gly Val Met Ala Asp Ala Asp Ala Phe
885 890 895
Asn Lys Lys Val Arg Thr Leu Phe Leu Ser Ile Gly Thr Ala Glu Asn
900 905 910
Glu Arg Phe Gln Ser Ser Val Arg Gly Tyr Arg Asp Ala Leu Thr Lys
915 920 925
Ala Gly Ile Lys Thr Thr Phe Tyr Glu Ser Pro Gly Thr Ser His Glu
930 935 940
Trp Leu Thr Trp Arg Arg Ser Leu Lys Glu Phe Ala Pro Leu Leu Phe
945 950 955 960
Gln Glu Val Glu Val Gln Ile Glu Arg Gly Pro Asn Ala Arg Pro Ile
965 970 975
Ala Pro Gln Pro Ile Asn Leu Gly Pro Asp Asp Lys Pro Ala Phe Pro
980 985 990
Pro Val Pro Ala Gly Phe Asp Val Arg Arg Asn Asp Ile Pro His Gly
995 1000 1005
Glu Ile Lys Leu Val Glu Tyr Pro Ser Ala Thr Val Gly Thr Asn Arg
1010 1015 1020
Lys Met Gln Val Tyr Thr Pro Pro Gly Tyr Asn Pro Gln Glu Lys Tyr
1025 1030 1035 1040
Ala Val Leu Tyr Leu Leu His Gly Ile Gly Gly Asp Glu Trp Glu Trp
1045 1050 1055
Lys Asn Gly Gly Thr Pro Glu Val Ile Leu Asp Asn Leu Tyr Ala Ala
1060 1065 1070
Lys Lys Leu Gln Pro Met Ile Val Val Met Pro Asn Gly Arg Ala Gln
1075 1080 1085
Lys Asp Asp Arg Pro Ile Gly Asn Val Phe Ala Ser Ala Pro Ala Phe
1090 1095 1100
Glu Thr Phe Glu Lys Asp Leu Leu Asn Asp Val Ile Pro Phe Ile Glu
1105 1110 1115 1120
Lys Asn Tyr Pro Val Lys Thr Gly Ala Glu Asn Arg Ala Leu Ala Gly
1125 1130 1135
Leu Ser Met Gly Gly Gly Gln Ser Leu Asn Phe Gly Leu Gly Asn Leu
1140 1145 1150
Asp Thr Phe Ala Trp Val Gly Gly Phe Ser Ser Ala Pro Asn Thr Arg
1155 1160 1165
Thr Gly Ala Arg Leu Leu Ala Asn Pro Asp Asp Ala Lys Lys Lys Leu
1170 1175 1180
Lys Leu Leu Trp Val Ser Cys Gly Asp Lys Asp Gly Leu Phe Phe Ile
1185 1190 1195 1200
Ser Gln Arg Thr His Arg Tyr Leu Ala Glu Asn Asn Val Pro His Val
1205 1210 1215
Trp His Val Gln Pro Gly Gly His Asp Phe Arg Val Trp Lys Gln Asp
1220 1225 1230
Leu Tyr Asn Phe Ser Gln Leu Leu Phe Arg
1235 1240

<210> 309
<211> 1830

<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 309
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acagatgctt gtttgcaaaa tactcaatta aatgctaccg cccaaggagc acaaacctgg 120
actggcaaaa aaggagctac aactttaggc ggttcaggtg acgatgctta tggagttgaa 180
acttggacag aagctggtgg agacgctact aaatttacat ggtttggacc aaatcagggt 240
ggtggtttcg cttatagagc ggaatggaca aattccacag attacttagg tcgctttggt 300
tatttttggg gtattgacgg gaaaaaatgg gacaaattag gagacctttg cgttgattat 360
aactataaaa gatctgccaa tggcactgga ggttcatatt cttatatagg cgtttatgga 420
tggacaaacg ctggcggtgg tactgaagct gaatattata tagttgaaga ttggtttgga 480
gaaaatcaac agactgcaaa taatttaggc aatggttgcc aagagcacgg tgaaattaca 540
gtggacgaga aaagctataa agttgtcact tgcataagac cagcaggctc tggctgcgta 600
acttgcaacg gacaacaatt cgggcaagtc tttagcatac gccaaggcat gagaagcgaa 660
caacctaaaa catgcggaac aatctccatc aaaaagcact ttgaagaatg ggtaaaaatg 720
acaaccgaaa aaagcggaca atccccagct aaatatattt acgataaaac ttatgaatcc 780
aaatttttag cggaggcaca aggcggcact ggttggcttg aaaccacttt ccttaaattt 840
tctagaaacg gtgattgcgg cttcgatatt cctgatggtc atttcacccct tcaattagct 900
acctctccgt ctgagggcgg tactgtaagc agaaacccaa aggaatcttc ttatgcctcc 960
ggttcaactg taactctcac agccactccg gcagcaggtt ggaaatttgc cagttggagt 1020
ggtgatgcat gtcaaaccac aagcccattg acagtcacta tggacaaaaa caaggtaatc 1080
acagcgaaat ttaccccccgt tgtagatctc aataaaaacc ttgttacaaa tggtactttc 1140
acgaataaag agagttggac ttttaatact ggttccagtt atggcaactc cgaaggaact 1200
tttgatgtgt caaacagcga aggcagaata aatgtgacga aaattggctc caacccgtgg 1260
gaaccacagc tcgttcaaaa tggcatcacc cttgttgaag gaatgaatta caaaataact 1320
tttgaagctt ctgcctctgc tgctcgaaaa ataggcttgg ttatacaaat ggcaggcggc 1380
gattatacca cttattttga aaaagatata gacttgactg cctcaaatca acaattttcg 1440
tatgaattca aaatgaatgc accaagcgat gaaagcggtc gtattgggtt taatcttggg 1500
caaacgactg gaaacgtcac tctaagcaaa atcacccttc attatttaga agaagattca 1560
cacgaaccgt ccgacaatcc ctgcgaagac ccaagtccaa ttttgaaaaa acgcatccct 1620
gcaactcatt tctcccttca aacgcttagc gacaaagcct tgcgcataga agtgaacgct 1680
ccaaccattg tggacatttt tgacctgaga gggaataaag ttaagagttt gaatgtctcc 1740
ggctcgcaaa cggttaaatt atccctgcca agcggagtgt attttgccaa agcacgtgga 1800
atgaaaagcg tcagatttgt gttgaggtaa 1830

<210> 310
<211> 609
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(20)

<400> 310
Met Lys Lys Leu Thr Ile Ala Leu Ser Leu Ala Ile Thr Phe Ala Ala
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Pro Val Phe Ala Thr Asp Ala Cys Leu Gln Asn Thr Gln Leu Asn Ala
20 25 30
Thr Ala Gln Gly Ala Gln Thr Trp Thr Gly Lys Lys Gly Ala Thr Thr
35 40 45
Leu Gly Gly Ser Gly Asp Asp Ala Tyr Gly Val Glu Thr Trp Thr Glu
50 55 60
Ala Gly Gly Asp Ala Thr Lys Phe Thr Trp Phe Gly Pro Asn Gln Gly
65 70 75 80
Gly Gly Phe Ala Tyr Arg Ala Glu Trp Thr Asn Ser Thr Asp Tyr Leu
85 90 95
Gly Arg Phe Gly Tyr Phe Trp Gly Ile Asp Gly Lys Lys Trp Asp Lys
100 105 110
Leu Gly Asp Leu Cys Val Asp Tyr Asn Tyr Lys Arg Ser Ala Asn Gly
115 120 125
Thr Gly Gly Ser Tyr Ser Tyr Ile Gly Val Tyr Gly Trp Thr Asn Ala
130 135 140

Gly Gly Gly Thr Glu Ala Glu Tyr Tyr Ile Val Glu Asp Trp Phe Gly
145 150 155 160
Glu Asn Gln Gln Thr Ala Asn Asn Leu Gly Asn Gly Cys Gln Glu His
165 170 175
Gly Glu Ile Thr Val Asp Glu Lys Ser Tyr Lys Val Val Thr Cys Ile
180 185 190
Arg Pro Ala Gly Ser Gly Cys Val Thr Cys Asn Gly Gln Gln Phe Gly
195 200 205
Gln Val Phe Ser Ile Arg Gln Gly Met Arg Ser Glu Gln Pro Lys Thr
210 215 220
Cys Gly Thr Ile Ser Ile Lys Lys His Phe Glu Glu Trp Val Lys Met
225 230 235 240
Thr Thr Glu Lys Ser Gly Gln Ser Pro Ala Lys Tyr Ile Tyr Asp Lys
245 250 255
Thr Tyr Glu Ser Lys Phe Leu Ala Glu Ala Gln Gly Gly Thr Gly Trp
260 265 270
Leu Glu Thr Thr Phe Leu Lys Phe Ser Arg Asn Gly Asp Cys Gly Phe
275 280 285
Asp Ile Pro Asp Gly His Phe Thr Leu Gln Leu Ala Thr Ser Pro Ser
290 295 300
Glu Gly Gly Thr Val Ser Arg Asn Pro Lys Glu Ser Ser Tyr Ala Ser
305 310 315 320
Gly Ser Thr Val Thr Leu Thr Ala Thr Pro Ala Ala Gly Trp Lys Phe
325 330 335
Ala Ser Trp Ser Gly Asp Ala Cys Gln Thr Thr Ser Pro Leu Thr Val
340 345 350
Thr Met Asp Lys Asn Lys Val Ile Thr Ala Lys Phe Thr Pro Val Val
355 360 365
Asp Leu Asn Lys Asn Leu Val Thr Asn Gly Thr Phe Thr Asn Lys Glu
370 375 380
Ser Trp Thr Phe Asn Thr Gly Ser Ser Tyr Gly Asn Ser Glu Gly Thr
385 390 395 400
Phe Asp Val Ser Asn Ser Glu Gly Arg Ile Asn Val Thr Lys Ile Gly
405 410 415
Ser Asn Pro Trp Glu Pro Gln Leu Val Gln Asn Gly Ile Thr Leu Val
420 425 430
Glu Gly Met Asn Tyr Lys Ile Thr Phe Glu Ala Ser Ala Ser Ala Ala
435 440 445
Arg Lys Ile Gly Leu Val Ile Gln Met Ala Gly Gly Asp Tyr Thr Thr
450 455 460
Tyr Phe Glu Lys Asp Ile Asp Leu Thr Ala Ser Asn Gln Gln Phe Ser
465 470 475 480
Tyr Glu Phe Lys Met Asn Ala Pro Ser Asp Glu Ser Gly Arg Ile Gly
485 490 495
Phe Asn Leu Gly Gln Thr Thr Gly Asn Val Thr Leu Ser Lys Ile Thr
500 505 510
Leu His Tyr Leu Glu Glu Asp Ser His Glu Pro Ser Asp Asn Pro Cys
515 520 525
Glu Asp Pro Ser Pro Ile Leu Lys Lys Arg Ile Pro Ala Thr His Phe
530 535 540
Ser Leu Gln Thr Leu Ser Asp Lys Ala Leu Arg Ile Glu Val Asn Ala
545 550 555 560
Pro Thr Ile Val Asp Ile Phe Asp Leu Arg Gly Asn Lys Val Lys Ser
565 570 575
Leu Asn Val Ser Gly Ser Gln Thr Val Lys Leu Ser Leu Pro Ser Gly
580 585 590
Val Tyr Phe Ala Lys Ala Arg Gly Met Lys Ser Val Arg Phe Val Leu
595 600 605
Arg

<210> 311
<211> 3972
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 311
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attttaaaat ttgattttga aagcggtaat caaggctgga cggggagagg tctttcaaca 180
actgttgcaa ccgtttacaa tgttgcttat gaaggtgatt attcattaaa agtttctggc 240
agaaatgctt catgggatgg agctgttatt gatttaacag acaagctttc ggcaaatgtg 300
agttatacag tttctctgtt tgttcgtcac agtgaccaaa aacctcaaag attttcagta 360
tatgcatatg taaaagattc agcaagtgaa aaatatattc cagttgtaga taaagttgca 420
gttcctaatt attggaagca actggttggt aaattcacaa tcaacacttc aaatccagtc 480
caaaagattc agctgcttgt ctgtgttcct acaaataaat cattggaatt ttttatcgat 540
agcgtattaa ttgcaagtag tgcaggagca acatctggag ttgtaaaatc cacaaatttt 600
gaaagcggta caacagaagg ctggcaagca aggggaacag gttctgttgc tcagattagt 660
gttgtttcta cagtagctca ttcaggtagt aaaagtttgt atgtgacagg gcgagttcaa 720
acgtggcaag gtgcacaaat agatttgaca agtttgttag agaagggtaa agaatatcag 780
ttttctgtgt gggtatatca ggatagtgga agcgaccaaa agctgacact gaccatggaa 840
aggaaaaatg cagatggaag tacaaattat gatacaataa aatggcagca aacagtttca 900
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ggtacaacag aagactggca agcaagaggg acaggagtga ccgtttctgt tgttaacaca 1140
gtggcacata ctgggagcaa gagtttgtat gtgacaggga gaagtcaaaa ttggcatggt 1200
gcagaaattg atctgacaaa tgtgctagag aagggcaagg aatatcaatt ttctgtgtgg 1260
gtatatcagg atagtggaag cgatcagaag ctgacattga ccatgcaaag gaaaaatgca 1320
gataacacaa cagattatga ttctataaaa tatcagcaga cagtagcaac aaatacatgg 1380
gtagagctaa caggttcata tacagtgccg acaacagcca cccagttaat tttatatgtt 1440
gaagctgcag atactaccct aagcttttat attgatgatt ttactgctgt tgataaaaac 1500
ccagaggtaa taccaacagt atcgagagta ccagaatggg aaattccttc actctttgag 1560
cagtatacga attatttcag cattggtgtg gcaataccat ataaagtact tacaaatcca 1620
accgaaaagg caatggtact caaacatttc aacagtataa cagctgagaa tgaaatgaaa 1680
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acaccaaatt ggttcttcca gcatagtgat ggtactccgc ttgatccaag caatcctgct 1860
gacaaacaac ttctacgcga tagattaaga acgcatatcc aaacacttgt tggaagatac 1920
gcagggaaaa tttatgcatg ggatgttgta aacgaggcaa ttgacgagaa ccagccagat 1980
ggatacagaa gaagtgaatg gtacagaata ttggggccaa ctgatacaac agatggcatt 2040
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ttttataacg actataatac agaaaatcca aagaaaagac agtttatata caatcttgtt 2160
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gattcaccta cagttaaaga gatagaggat acaattaaac tgtttagtac aatccctggc 2280
ttagacattc acattacaga gcttgacatt agcgtttata caagcagcag ccagagatat 2340
gatactcttc cacaggatat aatgataaaa caggctttga agttcaaaga gctttttgag 2400
atgctaaaaa gatatagcta tgttgtcaca aacgttactt tctggggact caaagatgac 2460
tattcatggc tttcaacaag cagatctaac tggccactac tgtttgacaa caactaccag 2520
gcaaaatttg catactgggc aattgttgaa ccgtcagtat tgccacttgc tataaacaaa 2580
ggatatgcaa acaatgcatc agcaaggata gatggagttt tagacagaga atacaaaggt 2640
gcgattccaa ttaagattac aaatgaaagt ggacaagaag ttgcaactgt tcgagctcta 2700
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gatgactatt gggtttcaat tacgagaact ggtacaaaag cacaatcagc tcaaggctat 2880
gtaaaggatt atgctgtcgt gcagcaagca aatggatatg tggttgagtt gaagctttta 2940
attaataaca cgttaactgt taactcttct ataggttttg atatagcaat ctttgacaat 3000
ggagttcaat acagctggaa tgacaagaca aactcacagt ttatagaaac tgataactat 3060
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gtcacggtta caggcacagt atacgactca gcttatgcaa aggctaagat gatgtgggat 3240
gaaaatagta tctatgtcta tgcaattgtt tatgacttgc ttttgaacaa ggctaataca 3300
aatccatggg agcaggattc aattgagata tttgtggatg aaaataatca caaaacgcct 3360
tactatgaaa atgatgatgt tcagtacaga gtgaactatg agaatactca aacatttggc 3420
acgaacggtg ctcctcagaa cttcattaca gcaacaaaga taattccaaa cggatatata 3480
gtggaagctc aagtttacat gaggacgaca aagctttctg aaggaatggt tataggcttt 3540
gacattcaag tgaatgatgc agaccataca ggtaaaagag tcggtgttct aacctggaat 3600
gataaggttg ggaacaatta tagagacaca acaaggttta gatgcttaga gcttgtagca 3660
gcacctgtaa gccagccacc aatacaagct ccatcaccat cacaaccaac aacaataacg 3720
tatatactaa caccgacacc aacacagcca tcaacccaaa cacagcagca acctgctcag 3780
caaccatcac agcagcaaca gcaaccgcaa cagcagcagc ctgcacagac acaacaacct 3840
cagacacagc ctgcacaaaa gcctcagaat gttgtttcga taaagataga ccagacaaaa 3900
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ggtgcaaact ga 3972

<210> 312
<211> 1323
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(33)

<400> 312
Met Arg Lys Arg Val Ile Ala Leu Phe Val Thr Leu Ile Phe Val Met
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20 25 30
Ala Gln Thr Gln Asn Thr Pro Thr Ile Leu Lys Phe Asp Phe Glu Ser
35 40 45
Gly Asn Gln Gly Trp Thr Gly Arg Gly Leu Ser Thr Thr Val Ala Thr
50 55 60
Val Tyr Asn Val Ala Tyr Glu Gly Asp Tyr Ser Leu Lys Val Ser Gly
65 70 75 80
Arg Asn Ala Ser Trp Asp Gly Ala Val Ile Asp Leu Thr Asp Lys Leu
85 90 95
Ser Ala Asn Val Ser Tyr Thr Val Ser Leu Phe Val Arg His Ser Asp
100 105 110
Gln Lys Pro Gln Arg Phe Ser Val Tyr Ala Tyr Val Lys Asp Ser Ala
115 120 125
Ser Glu Lys Tyr Ile Pro Val Val Asp Lys Val Ala Val Pro Asn Tyr
130 135 140
Trp Lys Gln Leu Val Gly Lys Phe Thr Ile Asn Thr Ser Asn Pro Val
145 150 155 160
Gln Lys Ile Gln Leu Leu Val Cys Val Pro Thr Asn Lys Ser Leu Glu
165 170 175
Phe Phe Ile Asp Ser Val Leu Ile Ala Ser Ser Ala Gly Ala Thr Ser
180 185 190
Gly Val Val Lys Ser Thr Asn Phe Glu Ser Gly Thr Thr Glu Gly Trp
195 200 205
Gln Ala Arg Gly Thr Gly Ser Val Ala Gln Ile Ser Val Val Ser Thr
210 215 220
Val Ala His Ser Gly Ser Lys Ser Leu Tyr Val Thr Gly Arg Val Gln
225 230 235 240
Thr Trp Gln Gly Ala Gln Ile Asp Leu Thr Ser Leu Leu Glu Lys Gly
245 250 255
Lys Glu Tyr Gln Phe Ser Val Trp Val Tyr Gln Asp Ser Gly Ser Asp
260 265 270
Gln Lys Leu Thr Leu Thr Met Glu Arg Lys Asn Ala Asp Gly Ser Thr
275 280 285
Asn Tyr Asp Thr Ile Lys Trp Gln Gln Thr Val Ser Ser Asn Thr Trp
290 295 300
Val Glu Leu Thr Gly Ser Tyr Thr Val Pro Ala Thr Ala Thr Gln Leu
305 310 315 320
Ile Phe Tyr Ile Glu Ser Pro Asn Ala Thr Leu Ser Phe Tyr Ile Asp
325 330 335
Asp Phe Thr Ala Val Asp Lys Asn Ala Pro Val Val Ala Pro Gly Ile
340 345 350
Ile Lys Ser Ala Thr Phe Glu Ser Gly Thr Thr Glu Asp Trp Gln Ala
355 360 365
Arg Gly Thr Gly Val Thr Val Ser Val Val Asn Thr Val Ala His Thr
370 375 380
Gly Ser Lys Ser Leu Tyr Val Thr Gly Arg Ser Gln Asn Trp His Gly
385 390 395 400
Ala Glu Ile Asp Leu Thr Asn Val Leu Glu Lys Gly Lys Glu Tyr Gln
405 410 415
Phe Ser Val Trp Val Tyr Gln Asp Ser Gly Ser Asp Gln Lys Leu Thr
420 425 430
Leu Thr Met Gln Arg Lys Asn Ala Asp Asn Thr Thr Asp Tyr Asp Ser
435 440 445
Ile Lys Tyr Gln Gln Thr Val Ala Thr Asn Thr Trp Val Glu Leu Thr

450 455 460
Gly Ser Tyr Thr Val Pro Thr Thr Ala Thr Gln Leu Ile Leu Tyr Val
465 470 475 480
Glu Ala Ala Asp Thr Thr Leu Ser Phe Tyr Ile Asp Asp Phe Thr Ala
485 490 495
Val Asp Lys Asn Pro Glu Val Ile Pro Thr Val Ser Arg Val Pro Glu
500 505 510
Trp Glu Ile Pro Ser Leu Phe Glu Gln Tyr Thr Asn Tyr Phe Ser Ile
515 520 525
Gly Val Ala Ile Pro Tyr Lys Val Leu Thr Asn Pro Thr Glu Lys Ala
530 535 540
Met Val Leu Lys His Phe Asn Ser Ile Thr Ala Glu Asn Glu Met Lys
545 550 555 560
Pro Asp Ala Ile Gln Lys Thr Glu Gly Asn Phe Thr Phe Asn Val Ala
565 570 575
Asp Gln Tyr Val Asp Phe Ala Gln Gln Asn Arg Ile Gly Ile Arg Gly
580 585 590
His Thr Leu Val Trp His Gln Gln Thr Pro Asn Trp Phe Phe Gln His
595 600 605
Ser Asp Gly Thr Pro Leu Asp Pro Ser Asn Pro Ala Asp Lys Gln Leu
610 615 620
Leu Arg Asp Arg Leu Arg Thr His Ile Gln Thr Leu Val Gly Arg Tyr
625 630 635 640
Ala Gly Lys Ile Tyr Ala Trp Asp Val Val Asn Glu Ala Ile Asp Glu
645 650 655
Asn Gln Pro Asp Gly Tyr Arg Arg Ser Glu Trp Tyr Arg Ile Leu Gly
660 665 670
Pro Thr Asp Thr Thr Asp Gly Ile Pro Glu Tyr Ile Leu Leu Ala Phe
675 680 685
Gln Tyr Ala Arg Glu Ala Asp Pro Asn Thr Lys Leu Phe Tyr Asn Asp
690 695 700
Tyr Asn Thr Glu Asn Pro Lys Lys Arg Gln Phe Ile Tyr Asn Leu Val
705 710 715 720
Lys Lys Leu Lys Glu Arg Gly Leu Ile Asp Gly Val Gly Leu Gln Cys
725 730 735
His Ile Asn Val Asp Ser Pro Thr Val Lys Glu Ile Glu Asp Thr Ile
740 745 750
Lys Leu Phe Ser Thr Ile Pro Gly Leu Asp Ile His Ile Thr Glu Leu
755 760 765
Asp Ile Ser Val Tyr Thr Ser Ser Ser Gln Arg Tyr Asp Thr Leu Pro
770 775 780
Gln Asp Ile Met Ile Lys Gln Ala Leu Lys Phe Lys Glu Leu Phe Glu
785 790 795 800
Met Leu Lys Arg Tyr Ser Tyr Val Val Thr Asn Val Thr Phe Trp Gly
805 810 815
Leu Lys Asp Asp Tyr Ser Trp Leu Ser Thr Ser Arg Ser Asn Trp Pro
820 825 830
Leu Leu Phe Asp Asn Asn Tyr Gln Ala Lys Phe Ala Tyr Trp Ala Ile
835 840 845
Val Glu Pro Ser Val Leu Pro Leu Ala Ile Asn Lys Gly Tyr Ala Asn
850 855 860
Asn Ala Ser Ala Arg Ile Asp Gly Val Leu Asp Arg Glu Tyr Lys Gly
865 870 875 880
Ala Ile Pro Ile Lys Ile Thr Asn Glu Ser Gly Gln Glu Val Ala Thr
885 890 895
Val Arg Ala Leu Trp Asn Ser Ser Glu Leu Ser Leu Tyr Ile Ser Val
900 905 910
Asn Asp Thr Thr Ile Asp Ala Ala Asn Asp Lys Val Val Val Phe Val
915 920 925
Asp Gln Asp Asn Gly Lys Met Pro Glu Ile Lys Pro Asp Asp Tyr Trp
930 935 940
Val Ser Ile Thr Arg Thr Gly Thr Lys Ala Gln Ser Ala Gln Gly Tyr
945 950 955 960
Val Lys Asp Tyr Ala Val Val Gln Gln Ala Asn Gly Tyr Val Val Glu
965 970 975
Leu Lys Leu Leu Ile Asn Asn Thr Leu Thr Val Asn Ser Ser Ile Gly
980 985 990
Phe Asp Ile Ala Ile Phe Asp Asn Gly Val Gln Tyr Ser Trp Asn Asp
995 1000 1005

Lys Thr Asn Ser Gln Phe Ile Glu Thr Asp Asn Tyr Gly Ile Leu Thr
1010 1015 1020
Met Ala Asp Ser Val Lys Phe Ala Ser Ala Pro Lys Gly Thr Ala Ile
1025 1030 1035 1040
Ile Asp Ala Glu Leu Asp Asp Thr Trp Lys Asn Ala Gln Glu Ile Thr
1045 1050 1055
Thr Asp Thr Lys Val Thr Val Thr Gly Thr Val Tyr Asp Ser Ala Tyr
1060 1065 1070
Ala Lys Ala Lys Met Met Trp Asp Glu Asn Ser Ile Tyr Val Tyr Ala
1075 1080 1085
Ile Val Tyr Asp Leu Leu Leu Asn Lys Ala Asn Thr Asn Pro Trp Glu
1090 1095 1100
Gln Asp Ser Ile Glu Ile Phe Val Asp Glu Asn Asn His Lys Thr Pro
1105 1110 1115 1120
Tyr Tyr Glu Asn Asp Asp Val Gln Tyr Arg Val Asn Tyr Glu Asn Thr
1125 1130 1135
Gln Thr Phe Gly Thr Asn Gly Ala Pro Gln Asn Phe Ile Thr Ala Thr
1140 1145 1150
Lys Ile Ile Pro Asn Gly Tyr Ile Val Glu Ala Gln Val Tyr Met Arg
1155 1160 1165
Thr Thr Lys Leu Ser Glu Gly Met Val Ile Gly Phe Asp Ile Gln Val
1170 1175 1180
Asn Asp Ala Asp His Thr Gly Lys Arg Val Gly Val Leu Thr Trp Asn
1185 1190 1195 1200
Asp Lys Val Gly Asn Asn Tyr Arg Asp Thr Thr Arg Phe Arg Cys Leu
1205 1210 1215
Glu Leu Val Ala Ala Pro Val Ser Gln Pro Pro Ile Gln Ala Pro Ser
1220 1225 1230
Pro Ser Gln Pro Thr Thr Ile Thr Tyr Ile Leu Thr Pro Thr Pro Thr
1235 1240 1245
Gln Pro Ser Thr Gln Thr Gln Gln Gln Pro Ala Gln Gln Pro Ser Gln
1250 1255 1260
Gln Gln Gln Gln Pro Gln Gln Gln Gln Pro Ala Gln Thr Gln Gln Pro
1265 1270 1275 1280
Gln Thr Gln Pro Ala Gln Lys Pro Gln Asn Val Val Ser Ile Lys Ile
1285 1290 1295
Asp Gln Thr Lys Ala Glu Thr Phe Thr Val Gly Ala Asp Thr Lys Val
1300 1305 1310
Val Val Pro Gln Gly Ser Val Thr Gly Ala Asn
1315 1320

<210> 313
<211> 1392
<212> DNA
<213> Bacteria

<400> 313
gtgaaacgtc tatccgcgct gaccgccgtc gtattgttag cgctaacaac tcacgtcgcc 60
gccgctgacc ccgcgccacc cgccaccggc cccgccatcg acttccgggc cgaactccag 120
cccatcgacg gattcggctt ctccatggcc ttccagcggg ccgacctgct gcacggcgcg 180
cgcggcctca gccccgccaa gcggcgcgag gtgctcgacc tgctgctcga caaggagagg 240
ggcgcgggcc tgtcgatcct gcgcctgggc atcgggtcgt cgaccgaccg ggtctacgac 300
cacatgccga cgatcctgcc gaccgatccc ggcgggccgg acgccccgcc gaagtacgtc 360
tgggacggct gggacggcgg ccaggtctgg ctcgccaagg aggccaaggc gtacggcgtc 420
aagcggttct tcgccgacgc ctggagcgcg ccggccttca tgaagaccaa cggcagcgag 480
aacgacggcg gcgagctccg gcccgaatgg cgccaggcct acgcgaacta cctcgtcaag 540
tacgcgaagt tctaccaacg ggaaggcatc ccgatcaccg acctggggtt caccaacgaa 600
cccgactggg cggcgaccta cgcctcgatg cgtttcaccc cgcagcaggc cgtcgacttc 660
ctcaaggtgc tcgggccgac cgtccgcgcg tccggactga agaccggcgt cgtctgctgc 720
gacgcggcgg gctgggaccg gcaggtcgcc tacaccgagg ccatcgaggc ggaccccgag 780
gccgccaagg ccgtgcggac cgtcaccggc caccgctaca gcggtccgac cacggtcccg 840
cagcccaccg acaagcgggt ctggatgtcg gagtggtcac cggacggcac cacctggaac 900
gagaactggg acgacggcag cggctacgac ggcctcaccg tcgccgccga catccagaac 960
accctcaccg tcggcaacgc caacgcctac gtctactgga ccggcgcgtc cctcggcgcc 1020
acccggggac tcatccagct cgccaacccc ggcgactcct accgggtgtc caagcggtac 1080
tgggcgctgg ccgccttcag ccgcttcatc cgccccgacg ccgtccgcgt accggtcacg 1140
aacgccgacc cggccctgag cgtcacggcc ttccgcaaca ccgacggcag ccgcgtgatc 1200
gagatcctca acacggcgac caccgagaag tccgcccagt tcgccctccg cggcggccac 1260
gaccggcacc ccgagggcta cgtcaccgac gagacccgct cgatcacccc ggcccacgtc 1320

gcctccgcgc gcggtacgac cctcaaggcc acgctcgccc cgcgcgcgct gaccacgatc 1380
gtcctcgact ga 1392

<210> 314
<211> 463
<212> PRT
<213> Bacteria

<220>
<221> SIGNAL
<222> (1)...(22)

<400> 314
Met Lys Arg Leu Ser Ala Leu Thr Ala Val Val Leu Leu Ala Leu Thr
1 5 10 15
Thr His Val Ala Ala Ala Asp Pro Ala Pro Pro Ala Thr Gly Pro Ala
20 25 30
Ile Asp Phe Arg Ala Glu Leu Gln Pro Ile Asp Gly Phe Gly Phe Ser
35 40 45
Met Ala Phe Gln Arg Ala Asp Leu Leu His Gly Ala Arg Gly Leu Ser
50 55 60
Pro Ala Lys Arg Arg Glu Val Leu Asp Leu Leu Leu Asp Lys Glu Arg
65 70 75 80
Gly Ala Gly Leu Ser Ile Leu Arg Leu Gly Ile Gly Ser Ser Thr Asp
85 90 95
Arg Val Tyr Asp His Met Pro Thr Ile Leu Pro Thr Asp Pro Gly Gly
100 105 110
Pro Asp Ala Pro Pro Lys Tyr Val Trp Asp Gly Trp Asp Gly Gly Gln
115 120 125
Val Trp Leu Ala Lys Glu Ala Lys Ala Tyr Gly Val Lys Arg Phe Phe
130 135 140
Ala Asp Ala Trp Ser Ala Pro Ala Phe Met Lys Thr Asn Gly Ser Glu
145 150 155 160
Asn Asp Gly Gly Glu Leu Arg Pro Glu Trp Arg Gln Ala Tyr Ala Asn
165 170 175
Tyr Leu Val Lys Tyr Ala Lys Phe Tyr Gln Arg Glu Gly Ile Pro Ile
180 185 190
Thr Asp Leu Gly Phe Thr Asn Glu Pro Asp Trp Ala Ala Thr Tyr Ala
195 200 205
Ser Met Arg Phe Thr Pro Gln Gln Ala Val Asp Phe Leu Lys Val Leu
210 215 220
Gly Pro Thr Val Arg Ala Ser Gly Leu Lys Thr Gly Val Val Cys Cys
225 230 235 240
Asp Ala Ala Gly Trp Asp Arg Gln Val Ala Tyr Thr Glu Ala Ile Glu
245 250 255
Ala Asp Pro Glu Ala Ala Lys Ala Val Arg Thr Val Thr Gly His Arg
260 265 270
Tyr Ser Gly Pro Thr Thr Val Pro Gln Pro Thr Asp Lys Arg Val Trp
275 280 285
Met Ser Glu Trp Ser Pro Asp Gly Thr Thr Trp Asn Glu Asn Trp Asp
290 295 300
Asp Gly Ser Gly Tyr Asp Gly Leu Thr Val Ala Ala Asp Ile Gln Asn
305 310 315 320
Thr Leu Thr Val Gly Asn Ala Asn Ala Tyr Val Tyr Trp Thr Gly Ala
325 330 335
Ser Leu Gly Ala Thr Arg Gly Leu Ile Gln Leu Ala Asn Pro Gly Asp
340 345 350
Ser Tyr Arg Val Ser Lys Arg Tyr Trp Ala Leu Ala Ala Phe Ser Arg
355 360 365
Phe Ile Arg Pro Asp Ala Val Arg Val Pro Val Thr Asn Ala Asp Pro
370 375 380
Ala Leu Ser Val Thr Ala Phe Arg Asn Thr Asp Gly Ser Arg Val Ile
385 390 395 400
Glu Ile Leu Asn Thr Ala Thr Thr Glu Lys Ser Ala Gln Phe Ala Leu
405 410 415
Arg Gly Gly His Asp Arg His Pro Glu Gly Tyr Val Thr Asp Glu Thr
420 425 430
Arg Ser Ile Thr Pro Ala His Val Ala Ser Ala Arg Gly Thr Thr Leu
435 440 445

Lys Ala Thr Leu Ala Pro Arg Ala Leu Thr Thr Ile Val Leu Asp
450 455 460

<210> 315
<211> 1224
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 315
atgcggaacg tcgtgcgtaa accattgaca atcggactcg ctttaacact attattgccc 60
atgggaatga cggcaacatc agcgaagaat gcagattcct atgcgaaaaa acctcacatc 120
agcgcattga atgccccaca attggatcaa cgctacaaaa acgagttcac gattggtgcg 180
gcagtagaac cttatcaact acaaaatgaa aaagacgtac aaatgctaaa gcgccacttc 240
aacagcattg ttgccgagaa cgtaatgaaa ccgatcagca ttcaacctga ggaaggaaaa 300
ttcaattttg aacaagcgga tcgaattgtg aagttcgcta aggcaaatgg catggatatt 360
cgcttccata cactcgtttg gcacagccaa gtacctcaat ggttctttct tgacaaggaa 420
ggcaagccaa tggttaatga aacagatcca gtgaaacgtg aacaaaataa acaactgctg 480
ttaaaacgac ttgaaactca tattaaaacg atcgtcgagc ggtacaaaga tgacattaag 540
tactgggacg ttgtaaatga ggttgtgggg gacgacggaa aactgcgcaa ctctccatgg 600
tatcaaatcg ccggcatcga ttatattaaa gtggcattcc aaacagcgag aaaatatggc 660
ggcaacaaga ttaaacttta tatcaatgat tacaataccg aagtggaacc aaagcgaagc 720
gctctttata acttggtgaa gcaattaaaa gaagagggcg ttcctattga cggcatcggc 780
catcaatccc acattcaaat cggctggcct tctgaagcag aaatcgagaa aacgattaac 840
atgttcgccg ctctcggctt agacaaccaa atcactgagc ttgatgtgag catgtacggt 900
tggccgccgc gcgcttaccc gacgtatgac gccattccaa aacaaaagtt tttggatcag 960
gcagcgcgct atgatcgttt gttcaaactg tatgaaaagt tgagcgataa aattagcaac 1020
gtcaccttct ggggcatcgc cgacaatcat acgtggctcg acagccgtgc ggatgtgtac 1080
tatgacgcca acgggaatgt tgtggttgac ccgaacgctc cgtacgcaaa agtggaaaaa 1140
gggaaaggaa aagatgcgcc gttcgttttt ggaccggatt acaaagtcaa acccgcatat 1200
tgggctatta tcgaccacaa atag 1224

<210> 316
<211> 407
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(28)

<400> 316
Met Arg Asn Val Val Arg Lys Pro Leu Thr Ile Gly Leu Ala Leu Thr
1 5 10 15
Leu Leu Leu Pro Met Gly Met Thr Ala Thr Ser Ala Lys Asn Ala Asp
20 25 30
Ser Tyr Ala Lys Lys Pro His Ile Ser Ala Leu Asn Ala Pro Gln Leu
35 40 45
Asp Gln Arg Tyr Lys Asn Glu Phe Thr Ile Gly Ala Ala Val Glu Pro
50 55 60
Tyr Gln Leu Gln Asn Glu Lys Asp Val Gln Met Leu Lys Arg His Phe
65 70 75 80
Asn Ser Ile Val Ala Glu Asn Val Met Lys Pro Ile Ser Ile Gln Pro
85 90 95
Glu Glu Gly Lys Phe Asn Phe Glu Gln Ala Asp Arg Ile Val Lys Phe
100 105 110
Ala Lys Ala Asn Gly Met Asp Ile Arg Phe His Thr Leu Val Trp His
115 120 125
Ser Gln Val Pro Gln Trp Phe Phe Leu Asp Lys Glu Gly Lys Pro Met
130 135 140
Val Asn Glu Thr Asp Pro Val Lys Arg Glu Gln Asn Lys Gln Leu Leu
145 150 155 160
Leu Lys Arg Leu Glu Thr His Ile Lys Thr Ile Val Glu Arg Tyr Lys
165 170 175
Asp Asp Ile Lys Tyr Trp Asp Val Val Asn Glu Val Val Gly Asp Asp

180 185 190
Gly Lys Leu Arg Asn Ser Pro Trp Tyr Gln Ile Ala Gly Ile Asp Tyr
195 200 205
Ile Lys Val Ala Phe Gln Thr Ala Arg Lys Tyr Gly Gly Asn Lys Ile
210 215 220
Lys Leu Tyr Ile Asn Asp Tyr Asn Thr Glu Val Glu Pro Lys Arg Ser
225 230 235 240
Ala Leu Tyr Asn Leu Val Lys Gln Leu Lys Glu Glu Gly Val Pro Ile
245 250 255
Asp Gly Ile Gly His Gln Ser His Ile Gln Ile Gly Trp Pro Ser Glu
260 265 270
Ala Glu Ile Glu Lys Thr Ile Asn Met Phe Ala Ala Leu Gly Leu Asp
275 280 285
Asn Gln Ile Thr Glu Leu Asp Val Ser Met Tyr Gly Trp Pro Pro Arg
290 295 300
Ala Tyr Pro Thr Tyr Asp Ala Ile Pro Lys Gln Lys Phe Leu Asp Gln
305 310 315 320
Ala Ala Arg Tyr Asp Arg Leu Phe Lys Leu Tyr Glu Lys Leu Ser Asp
325 330 335
Lys Ile Ser Asn Val Thr Phe Trp Gly Ile Ala Asp Asn His Thr Trp
340 345 350
Leu Asp Ser Arg Ala Asp Val Tyr Tyr Asp Ala Asn Gly Asn Val Val
355 360 365
Val Asp Pro Asn Ala Pro Tyr Ala Lys Val Glu Lys Gly Lys Gly Lys
370 375 380
Asp Ala Pro Phe Val Phe Gly Pro Asp Tyr Lys Val Lys Pro Ala Tyr
385 390 395 400
Trp Ala Ile Ile Asp His Lys
405

<210> 317
<211> 1695
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 317
gtggctggaa gctcgctcac gagcaacggc ctctcggcca ttctctcgct ccagtcggac 60
tggggcagcg gttactgcgc gacggtagaa cttcagaacg tcggcggaac tccgatcacg 120
gcgtgggagg tccaggtgga gctcgctggg acgaccgtga acagcagcca cagcgcggcg 180
ttctcctcga caggcacccg cctggtcgcc aagcccttgt cctggaacgc gacgctggca 240
cccgccgcca agacgacctt cggcttctgc gcggccgctc cgagcgcagc ggcgcgcccg 300
tccgtggtgc aagtgacagc gaacggctcc gccaccggaa cgggcggaac gagcggcggc 360
ggcacgggcg gctcgaccgc tacgggcggc tcgaccgcta cgggcggctc cggtgggtcg 420
accgcgggag tgtgcgcggc aacctacgag gccgagagca tgctccacag caccggcaac 480
gccatcagcg gcggctggaa catctattcg aacggcaaca tcaccgccac gcactccttc 540
gcagccggct cgaatcgact caccgtgcac gccaagggcg accaggccaa cggggcgccc 600
atcatgcgcg tcagcgtggg caacaccgtc gtcggcgagg tgccagtgcc ggtgaccgtg 660
tggacaccgt actgcttcga ctacgccgcg gcgagcgcag gcgcgcagac cgtcaagatc 720
gagttcacga acgactacaa tggcggcacc ggcgccgacc gcaatctgca cgtggacaag 780
gtcgcggtgc agtgcggcgc gagctgcaac agcgggagcg gagggggcac cggcggctcg 840
agcggaagcg gcggcacctc ggccaccggc ggctccgcca gcggtggcgc ggcagggacg 900
acctgcacga acgttcgtcc cactggaacc gactgggacg cggcgacctg cgacatgtgg 960
gcctcgcaaa ctagcgagtg cagcgcggcc tggatgatcg acaaccatta ctgcgaccag 1020
agctgcgggc gctgctcggg cgggagcggg accggtggca cgaacacggg aggcaccggc 1080
ggtggagtga ccccgagtac ctgcacggag cccaattctc agcagtgctc cacctacaag 1140
gtcgggactc actgcggcct cacctacgag atctggaccg acggctccgc gggctgcatg 1200
acgaacacct cctacgggtt cctcgccaat tggagccagg ggaacgcaaa ctacctggct 1260
cgcaagggcg ttcggcccgg ctcgtcgcga ccggtcgtga cgtacagcgc gaactaccag 1320
ccgaacggga attcctacct ggggatctac ggttggacgc agaacccgct cgtcgagtac 1380
tacatcatcg atagctgggg gagctggcgt ccaccgggga cccaggcgat gggcaccgtc 1440
caggtggacg gcgggaccta cgatatctac cggagcgagc gggtgaacaa gccctcgatc 1500
gagggcaaca agaccttctg gcagtactgg agcgtccgca cccagaagcg caccagtggg 1560
accatcaccg tggctccgca cttcgccgcg tgggcggcat ccggactgca gatgggctcc 1620
ttctacgagg tctccctggt ggtggagggc tacaacagct ccggcagcgc cgacgtaacg 1680
gtgtcgttcc ggtag 1695

<210> 318
<211> 564
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 318
Met Ala Gly Ser Ser Leu Thr Ser Asn Gly Leu Ser Ala Ile Leu Ser
1 5 10 15
Leu Gln Ser Asp Trp Gly Ser Gly Tyr Cys Ala Thr Val Glu Leu Gln
20 25 30
Asn Val Gly Gly Thr Pro Ile Thr Ala Trp Glu Val Gln Val Glu Leu
35 40 45
Ala Gly Thr Thr Val Asn Ser Ser His Ser Ala Ala Phe Ser Ser Thr
50 55 60
Gly Thr Arg Leu Val Ala Lys Pro Leu Ser Trp Asn Ala Thr Leu Ala
65 70 75 80
Pro Ala Ala Lys Thr Thr Phe Gly Phe Cys Ala Ala Ala Pro Ser Ala
85 90 95
Ala Ala Arg Pro Ser Val Val Gln Val Thr Ala Asn Gly Ser Ala Thr
100 105 110
Gly Thr Gly Gly Thr Ser Gly Gly Gly Thr Gly Gly Ser Thr Ala Thr
115 120 125
Gly Gly Ser Thr Ala Thr Gly Gly Ser Gly Gly Ser Thr Ala Gly Val
130 135 140
Cys Ala Ala Thr Tyr Glu Ala Glu Ser Met Leu His Ser Thr Gly Asn
145 150 155 160
Ala Ile Ser Gly Gly Trp Asn Ile Tyr Ser Asn Gly Asn Ile Thr Ala
165 170 175
Thr His Ser Phe Ala Ala Gly Ser Asn Arg Leu Thr Val His Ala Lys
180 185 190
Gly Asp Gln Ala Asn Gly Ala Pro Ile Met Arg Val Ser Val Gly Asn
195 200 205
Thr Val Val Gly Glu Val Pro Val Pro Val Thr Val Trp Thr Pro Tyr
210 215 220
Cys Phe Asp Tyr Ala Ala Ala Ser Ala Gly Ala Gln Thr Val Lys Ile
225 230 235 240
Glu Phe Thr Asn Asp Tyr Asn Gly Gly Thr Gly Ala Asp Arg Asn Leu
245 250 255
His Val Asp Lys Val Ala Val Gln Cys Gly Ala Ser Cys Asn Ser Gly
260 265 270
Ser Gly Gly Gly Thr Gly Gly Ser Ser Gly Ser Gly Gly Thr Ser Ala
275 280 285
Thr Gly Gly Ser Ala Ser Gly Gly Ala Ala Gly Thr Thr Cys Thr Asn
290 295 300
Val Arg Pro Thr Gly Thr Asp Trp Asp Ala Ala Thr Cys Asp Met Trp
305 310 315 320
Ala Ser Gln Thr Ser Glu Cys Ser Ala Ala Trp Met Ile Asp Asn His
325 330 335
Tyr Cys Asp Gln Ser Cys Gly Arg Cys Ser Gly Gly Ser Gly Thr Gly
340 345 350
Gly Thr Asn Thr Gly Gly Thr Gly Gly Gly Val Thr Pro Ser Thr Cys
355 360 365
Thr Glu Pro Asn Ser Gln Gln Cys Ser Thr Tyr Lys Val Gly Thr His
370 375 380
Cys Gly Leu Thr Tyr Glu Ile Trp Thr Asp Gly Ser Ala Gly Cys Met
385 390 395 400
Thr Asn Thr Ser Tyr Gly Phe Leu Ala Asn Trp Ser Gln Gly Asn Ala
405 410 415
Asn Tyr Leu Ala Arg Lys Gly Val Arg Pro Gly Ser Ser Arg Pro Val
420 425 430
Val Thr Tyr Ser Ala Asn Tyr Gln Pro Asn Gly Asn Ser Tyr Leu Gly
435 440 445
Ile Tyr Gly Trp Thr Gln Asn Pro Leu Val Glu Tyr Tyr Ile Ile Asp
450 455 460
Ser Trp Gly Ser Trp Arg Pro Pro Gly Thr Gln Ala Met Gly Thr Val
465 470 475 480

```
Gln Val Asp Gly Gly Thr Tyr Asp Ile Tyr Arg Ser Glu Arg Val Asn
                485                 490                 495
Lys Pro Ser Ile Glu Gly Asn Lys Thr Phe Trp Gln Tyr Trp Ser Val
            500                 505                 510
Arg Thr Gln Lys Arg Thr Ser Gly Thr Ile Thr Val Ala Pro His Phe
        515                 520                 525
Ala Ala Trp Ala Ala Ser Gly Leu Gln Met Gly Ser Phe Tyr Glu Val
    530                 535                 540
Ser Leu Val Val Glu Gly Tyr Asn Ser Ser Gly Ser Ala Asp Val Thr
545                 550                 555                 560
Val Ser Phe Arg
```

<210> 319
<211> 1095
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 319

```
atgaaggtga cccgaacagc tgtcgcgggc attgtcgccg cagcggtcct catcacgatc      60
ggcacgtcga ccgcgtcggc tgaggatgaa ccaaccagcg agaacacgtc gacggatcag     120
ccgttgcgcg tcctggcagc caaagccggg atcgcgttcg gcacggccgt cgacatgaac     180
gcgtacaaca acgacgcgac ctaccgtgag ctcgtcggcc aggagttctc gagcgtcacg     240
gccgagaacg tcatgaagtg gcagctcctc gagccgcagc gaggggtcta caactggggt     300
ccggccgatc agctcgtgcg cgtagccaac gagaacggcc agaaggtgcg cgggcacacg     360
ctcatctggc acaaccagct gcccacctgg cttaccagcg gagtcgcctc cggtgagatc     420
acaccggacg agctccggca gctcctgagg aaccacatct tcacggtgat gcgccacttc     480
aagggcgaga tccaccagtg ggatgtcgcc aacgaggtca tcgacgacag cggcaacctg     540
cgcaacacga tctggctgca gaacctgggt ccgagctaca tcgcggacgc gttccggtgg     600
gctcgcaagg ccgacccgga cgccgccctc tatctgaacg actacaacgt cgagggcccg     660
aacgccaagg ccgatgcgta ctacgccctg gtcaagcagc tcctcgccga cgacgtgccg     720
gtggacggct tcggaataca ggggcacctc ggtgtgcagt tcggcttctg gcccgcgagt     780
gcggtggccg acaacatggg gcgcttcgag gcactcggcc tgcagacggc ggtcaccgag     840
gcggatgtcc ggatgatcat gccgcccgac gaggacaagc tggccgcaca ggcacgtggc     900
tacagcacgt tggtccaggg ctgcctgatg gccaagcgtt gcaggtcgtt caccgtctgg     960
ggcttcaccg acaagtactc ctgggttccg ggcaccttcc ccggccaggg cgcggcgaac    1020
ctcctggccg aggacttcca gcccaagccg gcttactacg ccgtccagga tgacctcgcg    1080
cgcgccggac ggtag                                                     1095
```

<210> 320
<211> 364
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(27)

<400> 320

```
Met Lys Val Thr Arg Thr Ala Val Ala Gly Ile Val Ala Ala Ala Val
1               5                   10                  15
Leu Ile Thr Ile Gly Thr Ser Thr Ala Ser Ala Glu Asp Glu Pro Thr
            20                  25                  30
Ser Glu Asn Thr Ser Thr Asp Gln Pro Leu Arg Val Leu Ala Ala Lys
        35                  40                  45
Ala Gly Ile Ala Phe Gly Thr Ala Val Asp Met Asn Ala Tyr Asn Asn
    50                  55                  60
Asp Ala Thr Tyr Arg Glu Leu Val Gly Gln Glu Phe Ser Ser Val Thr
65                  70                  75                  80
Ala Glu Asn Val Met Lys Trp Gln Leu Leu Glu Pro Gln Arg Gly Val
                85                  90                  95
Tyr Asn Trp Gly Pro Ala Asp Gln Leu Val Arg Val Ala Asn Glu Asn
            100                 105                 110
Gly Gln Lys Val Arg Gly His Thr Leu Ile Trp His Asn Gln Leu Pro
```

```
        115                 120                 125
Thr Trp Leu Thr Ser Gly Val Ala Ser Gly Glu Ile Thr Pro Asp Glu
    130                 135                 140
Leu Arg Gln Leu Leu Arg Asn His Ile Phe Thr Val Met Arg His Phe
145                 150                 155                 160
Lys Gly Glu Ile His Gln Trp Asp Val Ala Asn Glu Val Ile Asp Asp
                165                 170                 175
Ser Gly Asn Leu Arg Asn Thr Ile Trp Leu Gln Asn Leu Gly Pro Ser
            180                 185                 190
Tyr Ile Ala Asp Ala Phe Arg Trp Ala Arg Lys Ala Asp Pro Asp Ala
        195                 200                 205
Ala Leu Tyr Leu Asn Asp Tyr Asn Val Glu Gly Pro Asn Ala Lys Ala
    210                 215                 220
Asp Ala Tyr Tyr Ala Leu Val Lys Gln Leu Leu Ala Asp Asp Val Pro
225                 230                 235                 240
Val Asp Gly Phe Gly Ile Gln Gly His Leu Gly Val Gln Phe Gly Phe
                245                 250                 255
Trp Pro Ala Ser Ala Val Ala Asp Asn Met Gly Arg Phe Glu Ala Leu
            260                 265                 270
Gly Leu Gln Thr Ala Val Thr Glu Ala Asp Val Arg Met Ile Met Pro
        275                 280                 285
Pro Asp Glu Asp Lys Leu Ala Ala Gln Ala Arg Gly Tyr Ser Thr Leu
    290                 295                 300
Val Gln Gly Cys Leu Met Ala Lys Arg Cys Arg Ser Phe Thr Val Trp
305                 310                 315                 320
Gly Phe Thr Asp Lys Tyr Ser Trp Val Pro Gly Thr Phe Pro Gly Gln
                325                 330                 335
Gly Ala Ala Asn Leu Leu Ala Glu Asp Phe Gln Pro Lys Pro Ala Tyr
            340                 345                 350
Tyr Ala Val Gln Asp Asp Leu Ala Arg Ala Gly Arg
        355                 360
```

<210> 321
<211> 1608
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 321
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gtggactggt gggacgtgga tattttttcc gcgaaggaaa tcacccaccc gcaactggca      60
accttcctgg atgcctcacg agaccatcgc aagccggtca tgatcggcga gatgacccca     120
cgccacgtcg gcgtgatcga ggggcagaaa tgctgggatg aatggtttgg cccgatgatt     180
gatctgctca aacgtcgccc cgaaatcaag gccacggcct atatcaactg ggaatggcgc     240
gagtggtccg accgcctcgg cttccgctgg cacaactggg gcgacgcccg catcgagggc     300
aacgcccttg ttcgtgatcg ctgggtgcag gaactctccc accccatcta tctccacgcg     360
gcgcgcgacg gatcttgtcc gctgccgcca atcaccgccc tcccatccgc gaccccgtcg     420
ctccagaccg tgttccagga ccatttcctg atgggtgctg ccttgaatgt gaggcagttc     480
accgaaaacg acgcaaccaa gaccgctctc atcaagaagc aattcaacac catcacgccc     540
gagaatgttc tcaagtgggg gccggttcat cctgagccca accggttcaa cttcgaatcc     600
accgatcgtt acgtggactt tggtgtgaag aaccggatgt tcatcgtcgg ccacaccctc     660
gtctggcacc accagacacc cgcctgggtg tttcaagatt cccaaggcca gccgctcgac     720
cgggatggac tgctcaatcg cttgagcaac cacatccaca cggtggttgg acgctacaag     780
ggccgcatcc acgggtggga tatggtgaac gaggccttga acgatgacgg caccctccgc     840
cctagccaat ggcttaaaat catcggcccc gactacattg ccaaagcgtt tgcccttgcc     900
cacgccgccg accctgccgc tgaactgtat tacaacgatt acagtctcga tcatcccgcc     960
aagtgtgctg gtgcgatcgc gctggtgaag cagctccaga cgaatggcat atccattgcc    1020
gggattggca cgcagaccca cgtcggactc aacggacctt ccccccagtc ggtggatgat    1080
tcattgacgg cctttggcca gctcggcgtg aaggtcatgg ttaccgaact cgacgttgat    1140
gtgctgcccg ccgccagcca aaatcaaaac gcggatctca accagcccgc cttgtccaat    1200
cccgccctca atcccgccct caatccctat cccgatgggc tgccgcaagc cgtccaggac    1260
aaactggccg ctcgctatgc ggaactcttc gccgtgttcg tcaagcacgc cgacaaaatc    1320
agccgcgtca cgttctggtg cgtcaccgac ggcgactcct ggctgaacaa ctggcccgtg    1380
cgtggccgcg tcaactatcc gctgctgttc gaccgtgcca gccagcccaa gcccgccttc    1440
gatgcggtca ttcgcgtcgc caaggacccg ccgacggttt cgcacaatct caccccgctc    1500
cacgatgcgg cgcgggtcct ggtcaatccg cacaagggct ggtaccacca ctacccggac    1560
aatcacatca acaagtatga gatcgcccgc gatgccgacc tgacggaa                1608
```

<210> 322
<211> 536
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 322
Met Asp Trp Trp Asp Val Asp Ile Phe Ser Ala Lys Glu Ile Thr His
1   5   10   15
Pro Gln Leu Ala Thr Phe Leu Asp Ala Ser Arg Asp His Arg Lys Pro
            20   25   30
Val Met Ile Gly Glu Met Thr Pro Arg His Val Gly Val Ile Glu Gly
        35   40   45
Gln Lys Cys Trp Asp Glu Trp Phe Gly Pro Met Ile Asp Leu Leu Lys
    50   55   60
Arg Arg Pro Glu Ile Lys Ala Thr Ala Tyr Ile Asn Trp Glu Trp Arg
65   70   75   80
Glu Trp Ser Asp Arg Leu Gly Phe Arg Trp His Asn Trp Gly Asp Ala
                85   90   95
Arg Ile Glu Gly Asn Ala Leu Val Arg Asp Arg Trp Val Gln Glu Leu
            100   105   110
Ser His Pro Ile Tyr Leu His Ala Ala Arg Asp Gly Ser Cys Pro Leu
        115   120   125
Pro Pro Ile Thr Ala Leu Pro Ser Ala Thr Pro Ser Leu Gln Thr Val
    130   135   140
Phe Gln Asp His Phe Leu Met Gly Ala Ala Leu Asn Val Arg Gln Phe
145   150   155   160
Thr Glu Asn Asp Ala Thr Lys Thr Ala Leu Ile Lys Lys Gln Phe Asn
                165   170   175
Thr Ile Thr Pro Glu Asn Val Leu Lys Trp Gly Pro Val His Pro Glu
            180   185   190
Pro Asn Arg Phe Asn Phe Glu Ser Thr Asp Arg Tyr Val Asp Phe Gly
        195   200   205
Val Lys Asn Arg Met Phe Ile Val Gly His Thr Leu Val Trp His His
    210   215   220
Gln Thr Pro Ala Trp Val Phe Gln Asp Ser Gln Gly Gln Pro Leu Asp
225   230   235   240
Arg Asp Gly Leu Leu Asn Arg Leu Ser Asn His Ile His Thr Val Val
                245   250   255
Gly Arg Tyr Lys Gly Arg Ile His Gly Trp Asp Met Val Asn Glu Ala
            260   265   270
Leu Asn Asp Asp Gly Thr Leu Arg Pro Ser Gln Trp Leu Lys Ile Ile
        275   280   285
Gly Pro Asp Tyr Ile Ala Lys Ala Phe Ala Leu Ala His Ala Ala Asp
    290   295   300
Pro Ala Ala Glu Leu Tyr Tyr Asn Asp Tyr Ser Leu Asp His Pro Ala
305   310   315   320
Lys Cys Ala Gly Ala Ile Ala Leu Val Lys Gln Leu Gln Thr Asn Gly
                325   330   335
Ile Ser Ile Ala Gly Ile Gly Thr Gln Thr His Val Gly Leu Asn Gly
            340   345   350
Pro Ser Pro Gln Ser Val Asp Asp Ser Leu Thr Ala Phe Gly Gln Leu
        355   360   365
Gly Val Lys Val Met Val Thr Glu Leu Asp Val Asp Val Leu Pro Ala
    370   375   380
Ala Ser Gln Asn Gln Asn Ala Asp Leu Asn Gln Pro Ala Leu Ser Asn
385   390   395   400
Pro Ala Leu Asn Pro Ala Leu Asn Pro Tyr Pro Asp Gly Leu Pro Gln
                405   410   415
Ala Val Gln Asp Lys Leu Ala Ala Arg Tyr Ala Glu Leu Phe Ala Val
            420   425   430
Phe Val Lys His Ala Asp Lys Ile Ser Arg Val Thr Phe Trp Cys Val
        435   440   445
Thr Asp Gly Asp Ser Trp Leu Asn Asn Trp Pro Val Arg Gly Arg Val
    450   455   460
Asn Tyr Pro Leu Leu Phe Asp Arg Ala Ser Gln Pro Lys Pro Ala Phe
465   470   475   480

Asp Ala Val Ile Arg Val Ala Lys Asp Pro Pro Thr Val Ser His Asn
485 490 495
Leu Thr Pro Leu His Asp Ala Ala Arg Val Leu Val Asn Pro His Lys
500 505 510
Gly Trp Tyr His His Tyr Pro Asp Asn His Ile Asn Lys Tyr Glu Ile
515 520 525
Ala Arg Asp Ala Asp Leu Thr Glu
530 535

<210> 323
<211> 2355
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 323
atgatgctca atgcccgttg tatccaactt atgaagttgt tgcttcgctc ttctctttat 60
cttaccgctg acaaattggc gcaatcattg aatgtatcca agcgaacgat ttattacgat 120
atacaaaaaa cgaatgaatg gttgcatcat gaagggctga agccgattca atatgcgcgc 180
gggctcggat ttcgcttgga tgatgaagtg aaacaagaaa taacaacaaa gtggaacaca 240
ttacaacctg cccgacatta cacatatcag tcatgggagc gaaaagcttg gattggttta 300
tggattttga ctcgcgttca tccactgtat ttgtctgatt ttttagagaa attacatgta 360
agcaggagca cgttgttaaa tgacataaag gaactgaaag aagattggca gtcatttcag 420
ttgcgattgt cattccatcg caaaaaaggg tatttttcat caggggaaga aatccaaaaa 480
aggaaattga tgattcgtta tattcatcaa atattagcgg cgatggatga ccagcatttc 540
gctgcagaat tgtcagctga gtgtcaatgg ccaatctttg attggatttg ccaattcgag 600
tctacttttt ctattcgcta taccggtgag gttattcaaa ctttacctat ttacctcgca 660
ttgttccaaa gacggtgggc tagaggcaaa tttgtgcaaa tggacgagca agaaaaagaa 720
gtgctaaggt caatgcggga ataccagatt gctgatcatc tcgttagacg aattgaaaac 780
gtttccgaaa tatctattcc cgatgacgag gtttgttatt tgacgaccca tttactcagt 840
tttcgagttg cagatgacaa gcaaatcgat cataacgatg acatcactac tttgaaacga 900
atcattcgac atatggtgga tgattttcaa acttatgcct gtgtacaatt caagcgtcgc 960
gaagagttgg aaaaaaattt attggttcat atgaagcctg cctattatcg actgaaatac 1020
ggttttcatc tgcaaaacga tctgaccgaa tcggtcaaag cgaactatca agatttattt 1080
accttaacga aaaaagtcgt ccatcattta gaaagtgtag ttggccagcc ggtcagcgac 1140
gatgaaattg cttatatcgc catgcatttt ggcggatggt tggacagaga gggggtgtcg 1200
gttccagtac ggaaaaaggt gttgatcgtc tgcgagagcg ggattggaac atcgcgaatg 1260
ttgcaaaaac aattggatca acgctacaaa aacgagttca cgattggtgc ggcagtagaa 1320
ccttatcaac tacaaaatga aaaagacgta caaatgctaa agcgccactt caacagcatt 1380
gttgccgaga acgtaatgaa accgatcagc attcaacctg aggaaggaaa attcaatttt 1440
gaacaagcgg atcgaattgt gaagttcgct aaggcaaatg gcatggatat tcgcttccat 1500
acactcgttt ggcacagcca agtacctcaa tggttctttc ttgacaagga aggcaagcca 1560
atggttaatg aaacagatcc agtgaaacgt gaacaaaata aacaactgct gttaaaacga 1620
cttgaaactc atattaaaac gatcgtcgag cggtacaaag atgacattaa gtactgggac 1680
gttgtaaatg aggttgtggg ggacgacgga aaactgcgca actctccatg gtatcaaatc 1740
gccggcatcg attatattaa agtggcattc caaacagcga gaaaatatgg cggcaacaag 1800
attaaacttt atatcaatga ttacaatacc gaagtggaac caaagcgaag cgctctttat 1860
aacttggtga agcaattaaa agaagagggc gttcctattg acggcatcgg ccatcaatcc 1920
cacattcaaa tcggctggcc ttctgaagca gaaatcgaga aaacgattaa catgttcgcc 1980
gctctcggct tagacaacca aatcactgag cttgatgtga gcatgtacgg ttggccgccg 2040
cgcgcttacc cgacgtatga cgccattcca aaacaaaagt ttttggatca ggcagcgcgc 2100
tatgatcgtt tgttcaaact gtatgaaaag ttgagcgata aaattagcaa cgtcaccttc 2160
tggggcatcg ccgacaatca tacgtggctc gacagccgtg cggatgtgta ctatgacgcc 2220
aacgggaatg ttgtggttga cccgaacgct ccgtacgcaa aagtggaaaa agggaaagga 2280
aaagatgcgc cgttcgtttt tggaccggat tacaaagtca aacccgcata ttgggctatt 2340
atcgaccaca aatag 2355

<210> 324
<211> 784
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 324
Met Met Leu Asn Ala Arg Cys Ile Gln Leu Met Lys Leu Leu Leu Arg

```
1               5                   10                  15
Ser Ser Leu Tyr Leu Thr Ala Asp Lys Leu Ala Gln Ser Leu Asn Val
            20                  25                  30
Ser Lys Arg Thr Ile Tyr Tyr Asp Ile Gln Lys Thr Asn Glu Trp Leu
        35                  40                  45
His His Glu Gly Leu Lys Pro Ile Gln Tyr Ala Arg Gly Leu Gly Phe
    50                  55                  60
Arg Leu Asp Asp Glu Val Lys Gln Glu Ile Thr Thr Lys Trp Asn Thr
65                  70                  75                  80
Leu Gln Pro Ala Arg His Tyr Thr Tyr Gln Ser Trp Glu Arg Lys Ala
                85                  90                  95
Trp Ile Gly Leu Trp Ile Leu Thr Arg Val His Pro Leu Tyr Leu Ser
            100                 105                 110
Asp Phe Leu Glu Lys Leu His Val Ser Arg Ser Thr Leu Leu Asn Asp
        115                 120                 125
Ile Lys Glu Leu Lys Glu Asp Trp Gln Ser Phe Gln Leu Arg Leu Ser
    130                 135                 140
Phe His Arg Lys Lys Gly Tyr Phe Ser Ser Gly Glu Glu Ile Gln Lys
145                 150                 155                 160
Arg Lys Leu Met Ile Arg Tyr Ile His Gln Ile Leu Ala Ala Met Asp
                165                 170                 175
Asp Gln His Phe Ala Ala Glu Leu Ser Ala Glu Cys Gln Trp Pro Ile
            180                 185                 190
Phe Asp Trp Ile Cys Gln Phe Glu Ser Thr Phe Ser Ile Arg Tyr Thr
        195                 200                 205
Gly Glu Val Ile Gln Thr Leu Pro Ile Tyr Leu Ala Leu Phe Gln Arg
    210                 215                 220
Arg Trp Ala Arg Gly Lys Phe Val Gln Met Asp Glu Gln Glu Lys Glu
225                 230                 235                 240
Val Leu Arg Ser Met Arg Glu Tyr Gln Ile Ala Asp His Leu Val Arg
                245                 250                 255
Arg Ile Glu Asn Val Ser Glu Ile Ser Ile Pro Asp Asp Glu Val Cys
            260                 265                 270
Tyr Leu Thr Thr His Leu Leu Ser Phe Arg Val Ala Asp Asp Lys Gln
        275                 280                 285
Ile Asp His Asn Asp Asp Ile Thr Thr Leu Lys Arg Ile Ile Arg His
    290                 295                 300
Met Val Asp Asp Phe Gln Thr Tyr Ala Cys Val Gln Phe Lys Arg Arg
305                 310                 315                 320
Glu Glu Leu Glu Lys Asn Leu Leu Val His Met Lys Pro Ala Tyr Tyr
                325                 330                 335
Arg Leu Lys Tyr Gly Phe His Leu Gln Asn Asp Leu Thr Glu Ser Val
            340                 345                 350
Lys Ala Asn Tyr Gln Asp Leu Phe Thr Leu Thr Lys Lys Val Val His
        355                 360                 365
His Leu Glu Ser Val Val Gly Gln Pro Val Ser Asp Asp Glu Ile Ala
    370                 375                 380
Tyr Ile Ala Met His Phe Gly Gly Trp Leu Asp Arg Glu Gly Val Ser
385                 390                 395                 400
Val Pro Val Arg Lys Lys Val Leu Ile Val Cys Glu Ser Gly Ile Gly
                405                 410                 415
Thr Ser Arg Met Leu Gln Lys Gln Leu Asp Gln Arg Tyr Lys Asn Glu
            420                 425                 430
Phe Thr Ile Gly Ala Ala Val Glu Pro Tyr Gln Leu Gln Asn Glu Lys
        435                 440                 445
Asp Val Gln Met Leu Lys Arg His Phe Asn Ser Ile Val Ala Glu Asn
    450                 455                 460
Val Met Lys Pro Ile Ser Ile Gln Pro Glu Glu Gly Lys Phe Asn Phe
465                 470                 475                 480
Glu Gln Ala Asp Arg Ile Val Lys Phe Ala Lys Ala Asn Gly Met Asp
                485                 490                 495
Ile Arg Phe His Thr Leu Val Trp His Ser Gln Val Pro Gln Trp Phe
            500                 505                 510
Phe Leu Asp Lys Glu Gly Lys Pro Met Val Asn Glu Thr Asp Pro Val
        515                 520                 525
Lys Arg Glu Gln Asn Lys Gln Leu Leu Leu Lys Arg Leu Glu Thr His
    530                 535                 540
Ile Lys Thr Ile Val Glu Arg Tyr Lys Asp Asp Ile Lys Tyr Trp Asp
545                 550                 555                 560
```

Val Val Asn Glu Val Val Gly Asp Asp Gly Lys Leu Arg Asn Ser Pro
565 570 575
Trp Tyr Gln Ile Ala Gly Ile Asp Tyr Ile Lys Val Ala Phe Gln Thr
580 585 590
Ala Arg Lys Tyr Gly Gly Asn Lys Ile Lys Leu Tyr Ile Asn Asp Tyr
595 600 605
Asn Thr Glu Val Glu Pro Lys Arg Ser Ala Leu Tyr Asn Leu Val Lys
610 615 620
Gln Leu Lys Glu Glu Gly Val Pro Ile Asp Gly Ile Gly His Gln Ser
625 630 635 640
His Ile Gln Ile Gly Trp Pro Ser Glu Ala Glu Ile Glu Lys Thr Ile
645 650 655
Asn Met Phe Ala Ala Leu Gly Leu Asp Asn Gln Ile Thr Glu Leu Asp
660 665 670
Val Ser Met Tyr Gly Trp Pro Pro Arg Ala Tyr Pro Thr Tyr Asp Ala
675 680 685
Ile Pro Lys Gln Lys Phe Leu Asp Gln Ala Ala Arg Tyr Asp Arg Leu
690 695 700
Phe Lys Leu Tyr Glu Lys Leu Ser Asp Lys Ile Ser Asn Val Thr Phe
705 710 715 720
Trp Gly Ile Ala Asp Asn His Thr Trp Leu Asp Ser Arg Ala Asp Val
725 730 735
Tyr Tyr Asp Ala Asn Gly Asn Val Val Val Asp Pro Asn Ala Pro Tyr
740 745 750
Ala Lys Val Glu Lys Gly Lys Gly Lys Asp Ala Pro Phe Val Phe Gly
755 760 765
Pro Asp Tyr Lys Val Lys Pro Ala Tyr Trp Ala Ile Ile Asp His Lys
770 775 780

<210> 325
<211> 1146
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 325
atgactattt cccgccggaa atttatgtgg ggcacagctg cactcctggc caccacccag 60
ctcaaaaccc gcgctctcgc cgctgccatg gccagcacag gcatcaagga cgccttcaag 120
ggcgacttcc atatcggcac cgccatcagc aacgctaccc tgcaaaacca ggatgccacc 180
atgctggatt tgatcaagcg cgaatttaat gcaattaccg ctgaaaattg catgaagtgg 240
gagcctattc gcccacagct ggatcagtgg aattgggagc tggccgaccg ctttgtggat 300
ttcggcgtta aaaacaagat gtatgtggta ggtcacacgc tgatttggca cagccaggcg 360
ccagcgcaca tttatctcga cgccgatggt aagcccaaca gtcgcgatgc ccagttgaaa 420
gtaatggagg agcacatacg taccctggcg ggccgctaca aaggaaagat agacgcctgg 480
gacgtggtta acgaagcagt ggaggatgat ggcagctggc gtcaaaccgg ctggtacaaa 540
aacatgggtg aagaatatat cgcccatgcc ttccgcttgg cagccgaggt agaccccaac 600
gccaagctac tctacaacga ctacaacgag gctgtacccg ccaagcgtga tgcgattatt 660
cgggtggtaa aaggcgtgca gaaggctggc gcacccattc acggtgtggg gatgcaaggg 720
cacatgagcc tgtcacatcc ggatttcgcg gagttcgaaa aatccataat cgaatacgcc 780
aagttggggg tgaaggtgca cgttaccgaa ctggatatcg acgtgttgcc actggcgtgg 840
aacctgagtg cggaaatttc caatcgcttt gaataccgcc cagagatgga tccttatcgc 900
gaaggtttgc ccgccaaagt cgaggaggag ctagcggctc gttacgaggc gctgtttaaa 960
atcctgctgc gtcatcgcga caaaattgag cgtgtgacca cttggggcac caacgactca 1020
gagacctggt taaatggctt ccccattccg ggcgcatga attacccaat gctgttcgat 1080
cgtaataacc agcccaagtt ggcctatcac cggctgctgg cactcaaaca aaagaaaagt 1140
cagtaa 1146

<210> 326
<211> 381
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(27)

<400> 326
Met Thr Ile Ser Arg Arg Lys Phe Met Trp Gly Thr Ala Ala Leu Leu
1   5   10   15
Ala Thr Thr Gln Leu Lys Thr Arg Ala Leu Ala Ala Ala Met Ala Ser
            20   25   30
Thr Gly Ile Lys Asp Ala Phe Lys Gly Asp Phe His Ile Gly Thr Ala
        35   40   45
Ile Ser Asn Ala Thr Leu Gln Asn Gln Asp Ala Thr Met Leu Asp Leu
    50   55   60
Ile Lys Arg Glu Phe Asn Ala Ile Thr Ala Glu Asn Cys Met Lys Trp
65   70   75   80
Glu Pro Ile Arg Pro Gln Leu Asp Gln Trp Asn Trp Glu Leu Ala Asp
                85   90   95
Arg Phe Val Asp Phe Gly Val Lys Asn Lys Met Tyr Val Val Gly His
            100   105   110
Thr Leu Ile Trp His Ser Gln Ala Pro Ala His Ile Tyr Leu Asp Ala
        115   120   125
Asp Gly Lys Pro Asn Ser Arg Asp Ala Gln Leu Lys Val Met Glu Glu
    130   135   140
His Ile Arg Thr Leu Ala Gly Arg Tyr Lys Gly Lys Ile Asp Ala Trp
145   150   155   160
Asp Val Val Asn Glu Ala Val Glu Asp Asp Gly Ser Trp Arg Gln Thr
                165   170   175
Gly Trp Tyr Lys Asn Met Gly Glu Glu Tyr Ile Ala His Ala Phe Arg
            180   185   190
Leu Ala Ala Glu Val Asp Pro Asn Ala Lys Leu Leu Tyr Asn Asp Tyr
        195   200   205
Asn Glu Ala Val Pro Ala Lys Arg Asp Ala Ile Ile Arg Val Val Lys
    210   215   220
Gly Val Gln Lys Ala Gly Ala Pro Ile His Gly Val Gly Met Gln Gly
225   230   235   240
His Met Ser Leu Ser His Pro Asp Phe Ala Glu Phe Glu Lys Ser Ile
                245   250   255
Ile Glu Tyr Ala Lys Leu Gly Val Lys Val His Val Thr Glu Leu Asp
            260   265   270
Ile Asp Val Leu Pro Leu Ala Trp Asn Leu Ser Ala Glu Ile Ser Asn
        275   280   285
Arg Phe Glu Tyr Arg Pro Glu Met Asp Pro Tyr Arg Glu Gly Leu Pro
    290   295   300
Ala Lys Val Glu Glu Glu Leu Ala Ala Arg Tyr Glu Ala Leu Phe Lys
305   310   315   320
Ile Leu Leu Arg His Arg Asp Lys Ile Glu Arg Val Thr Thr Trp Gly
                325   330   335
Thr Asn Asp Ser Glu Thr Trp Leu Asn Gly Phe Pro Ile Pro Gly Arg
            340   345   350
Met Asn Tyr Pro Met Leu Phe Asp Arg Asn Asn Gln Pro Lys Leu Ala
        355   360   365
Tyr His Arg Leu Leu Ala Leu Lys Gln Lys Lys Ser Gln
    370   375   380

<210> 327
<211> 1500
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 327
atgaaacgtt cagtctctat ctttatcgca tgtttagtaa tgacagtatt aacaattagc 60
ggtgtcgcgg caccagaagc atctgcagca ggggcgaaaa cgcctgtagc ccttaatggc 120
cagcttagca ttaaaggtac tcagctagtc aatcaaaacg gaaaatcggt gcagctgaag 180
gggatcagct cacacggttt gcagtggttc ggcgattatg tcaataaaga ctctttaaaa 240
tggctaagag acgattgggg aattaccgtc ttccgagcgg caatgtacac ggctgaaggc 300
ggttatatag agaatccgtc tgtgaaaaat aaagtcaaag aagctgttga agcggcaaaa 360
gagctcggga tatatgtcat cattgactgg catattttaa atgacggcaa tccaaatcaa 420
aataaagaga aggcgaagga attctttaag gaaatgtcga gcctttacgg aagcacacca 480
aacgttattt atgaaattgc taatgaaccg aacggtgatg taaattggaa gcgcgatatc 540

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aaaccgtatg cggaggaagt gatttccgtt atccgtaaaa atgacccgga taacatcatt    600
attaccggaa ctggcacttg gagtcaggat gtcaatgatg ctgctgatga tcagcttaag    660
gatgcaaacg tcatgtacgc gcttcatttt tatgcaggta cacacggcca gtatttaagg    720
gataaagccg attatgcgct cagcaaagga gcgccgattt ttgtaacgga atgggggacg    780
agtgacgctt ccggaaatgg cggggtcttc cttgaccagt cgagggaatg gctgaattat    840
ctcgacaaca agaaaatcag ctgggtaaac tggaaccttt ctgataagca ggaatcttcc    900
tcagctttaa agccgggggc atctaaaaca ggcggctggc cgttatcaga tttatccgct    960
tcagggacat ttgtaaggga aaagatccgt ggctcccaac attcgactga agacagatct   1020
gagacaccaa agcaagataa acccgtacag gaaaacagcc tatctgtgca atacagaaca   1080
ggggatggaa gtgtgaacag caaccaaatc cgtcctcaga tccatgtgaa aaacaacagc   1140
aagaccaccg ttaatttaaa aaatgtaact gtccgctact ggtataacac gaaaaacaaa   1200
ggccaaaact tcgactgtga ctacgcgaag atcggatgca gcaatgtgac gcacaagttt   1260
gtgacattac aaaaacctgt aaaaggtgca gatgcctatc tggaacttgg gtttaaaaac   1320
gggacactgt caccgggagc aaacactgga gaaatccaaa ttcgtcttca caatgaggat   1380
tggggcaatt attcacaaat cggggattat tctttttctc agtcaaatac gtttaaagat   1440
acaaaaaaaa tcacattata taataacgga aaactaattt ggggaactga acccaaatag   1500
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<210> 328
<211> 499
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(29)

<400> 328

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Met Lys Arg Ser Val Ser Ile Phe Ile Ala Cys Leu Val Met Thr Val
1               5                   10                  15
Leu Thr Ile Ser Gly Val Ala Ala Pro Glu Ala Ser Ala Ala Gly Ala
            20                  25                  30
Lys Thr Pro Val Ala Leu Asn Gly Gln Leu Ser Ile Lys Gly Thr Gln
        35                  40                  45
Leu Val Asn Gln Asn Gly Lys Ser Val Gln Leu Lys Gly Ile Ser Ser
    50                  55                  60
His Gly Leu Gln Trp Phe Gly Asp Tyr Val Asn Lys Asp Ser Leu Lys
65                  70                  75                  80
Trp Leu Arg Asp Asp Trp Gly Ile Thr Val Phe Arg Ala Ala Met Tyr
                85                  90                  95
Thr Ala Glu Gly Gly Tyr Ile Glu Asn Pro Ser Val Lys Asn Lys Val
            100                 105                 110
Lys Glu Ala Val Glu Ala Ala Lys Glu Leu Gly Ile Tyr Val Ile Ile
        115                 120                 125
Asp Trp His Ile Leu Asn Asp Gly Asn Pro Asn Gln Asn Lys Glu Lys
    130                 135                 140
Ala Lys Glu Phe Phe Lys Glu Met Ser Ser Leu Tyr Gly Ser Thr Pro
145                 150                 155                 160
Asn Val Ile Tyr Glu Ile Ala Asn Glu Pro Asn Gly Asp Val Asn Trp
                165                 170                 175
Lys Arg Asp Ile Lys Pro Tyr Ala Glu Glu Val Ile Ser Val Ile Arg
            180                 185                 190
Lys Asn Asp Pro Asp Asn Ile Ile Ile Thr Gly Thr Gly Thr Trp Ser
        195                 200                 205
Gln Asp Val Asn Asp Ala Ala Asp Asp Gln Leu Lys Asp Ala Asn Val
    210                 215                 220
Met Tyr Ala Leu His Phe Tyr Ala Gly Thr His Gly Gln Tyr Leu Arg
225                 230                 235                 240
Asp Lys Ala Asp Tyr Ala Leu Ser Lys Gly Ala Pro Ile Phe Val Thr
                245                 250                 255
Glu Trp Gly Thr Ser Asp Ala Ser Gly Asn Gly Gly Val Phe Leu Asp
            260                 265                 270
Gln Ser Arg Glu Trp Leu Asn Tyr Leu Asp Asn Lys Lys Ile Ser Trp
        275                 280                 285
Val Asn Trp Asn Leu Ser Asp Lys Gln Glu Ser Ser Ser Ala Leu Lys
    290                 295                 300
Pro Gly Ala Ser Lys Thr Gly Gly Trp Pro Leu Ser Asp Leu Ser Ala
305                 310                 315                 320
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Ser Gly Thr Phe Val Arg Glu Lys Ile Arg Gly Ser Gln His Ser Thr
325 330 335
Glu Asp Arg Ser Glu Thr Pro Lys Gln Asp Lys Pro Val Gln Glu Asn
340 345 350
Ser Leu Ser Val Gln Tyr Arg Thr Gly Asp Gly Ser Val Asn Ser Asn
355 360 365
Gln Ile Arg Pro Gln Ile His Val Lys Asn Asn Ser Lys Thr Thr Val
370 375 380
Asn Leu Lys Asn Val Thr Val Arg Tyr Trp Tyr Asn Thr Lys Asn Lys
385 390 395 400
Gly Gln Asn Phe Asp Cys Asp Tyr Ala Lys Ile Gly Cys Ser Asn Val
405 410 415
Thr His Lys Phe Val Thr Leu Gln Lys Pro Val Lys Gly Ala Asp Ala
420 425 430
Tyr Leu Glu Leu Gly Phe Lys Asn Gly Thr Leu Ser Pro Gly Ala Asn
435 440 445
Thr Gly Glu Ile Gln Ile Arg Leu His Asn Glu Asp Trp Gly Asn Tyr
450 455 460
Ser Gln Ile Gly Asp Tyr Ser Phe Ser Gln Ser Asn Thr Phe Lys Asp
465 470 475 480
Thr Lys Lys Ile Thr Leu Tyr Asn Asn Gly Lys Leu Ile Trp Gly Thr
485 490 495
Glu Pro Lys

<210> 329
<211> 2268
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 329
atgaggaacg ttcaggaaat aggaggcagt atgtacaaaa aggcttttct tgtactggca 60
ttgtttttgc tgttggcggc ggtggcgctc ccgtctgtgg gggctgcgcc gcaggggccg 120
cgcctgcgcg atgtggcggg cgacatttta gtgggttacg cctccagaaa cgatttctgg 180
aacatgtctg actcagccca atacacagaa gttgcccgca ctgagttcaa cttcatgacg 240
cccgaaaacg ccatgaagtg ggacgccatt catcccgcgc aaaactcata cagttttgcc 300
caggccgacc ggcacgtgca gtttgcccag gccaacaaca tggccgtgca tggacatgcc 360
ctcgtgtggc acagccaaaa tccaggctgg ctgaccaatg gcaactggtc ccgcagccaa 420
ttgatcaaca tcatgaacga ccacattgac acggtcgccg gccgttatgc aggtgaggtg 480
ctggtgtggg acgtggtcaa tcaggcgttt aatgaggatg gaacttatcg cagcaccatc 540
tggtacaacg ggatcggaca ggaatatatc gacctggcct ttacccgcgc ccgcgccgcc 600
gatcctcatg ccaaactcat ttacaacgat tacaacattg gctggttaaa cagtaagtcg 660
aatggcgtct acaacatggc cgccgatatg gtcaggcgcg gtgtgcccat cgacggcgtt 720
ggtttccaga tgcacctgga acggggcggc gtcagcggca gcagtctggc gagcaacatg 780
cagcgtttcg ccgatttggg attggaagtt tacatcaccg aattggacgt gcgcattccc 840
caaaacccaa cccagcagga tttgcaggct caggcggcag tttaccaaac ggtgacgaat 900
cgctgtttgg cgcagcctgc ctgcaaggcg ttgcaggtct ggggcatccc cgacaaatat 960
tcctgggtac cggacgtatt ccccggcacg ggcgcgcctc tgttgtttaa cgacaactat 1020
gaggccaaac ccgcctatta tgccgtccag gcagagttga tggccgcgaa tccgcagccc 1080
acaaacacac cgggaacgcc cgctcatacc ccttcggcca cgtctacgtc tgcggccact 1140
gctacgcccc cggcaacggc cacggcgacc gccaccaccc cctccggcgg cggcgtttgc 1200
gccgttgatt acgtcattgc caaccagtgg ggcaatggct ttcaggccaa cgtcaccatc 1260
accaatcaca gcgccgcgcc ggtgaacggc tataccctgg cctggaccca cgcgccgggg 1320
cagattgtca ccagcggctg gaacgtaacc atcgcccaaa gcggcagcgc cgtcagcgcc 1380
agcaacccgg ccggttattg gaacggtgtg atcggagcca acggcggcaa gatttctttt 1440
ggtttccagg gatctctggc gggcggcagc gcggtcgcgc ccacttattt tgccttgaac 1500
ggcgctgcct gtaacggggc cgtccttccg cctactgcca ccttcacgcc ttcaccgacg 1560
gctaccatgt gtccccaggc aacgcctgaa ctgcttgtcg tgcagccggt gacttcaccc 1620
actacccaac tgtctcaaac gctggtggtg cgtttaggca acggcgaatg ggtgcgcgct 1680
gccggaccgg caggcgttgt caccgtcact gcgccggacc cggatggtta tttccgcctg 1740
acgataccgc tggcagccaa taccagcaac gccattctgg tagaagggcg ggtgcgggtt 1800
atcacccatt caaatggctg cacctatggc ggttatacct tgagcagaac cgtaacgatt 1860
gtgcaagcca gcagcccagt caccttaacg ccgactgcca caccttcccc caccgccacg 1920
gcaacgccta cggtaaccgc cacgtcgccg tcaggcgcct gcaccgtcgc ctacgccatc 1980
accaacgact ggggcagcgg tttcaccgcc aacgttaccc tcaccaatac tggcggaagc 2040
gccctcaacg gctggaccct ggcctatgcc tttcccggca atcaaaccat cagcaacgcc 2100

tggaacggaa cggccgttca gtccggcagc agcgtcagcg tcaccaacgc cggttggaat 2160
ggcagcctgc cgcccaacgt ctccgccagc tttggcttcc aggcgagcta cagcggcaat 2220
aacagcgtcc ctgccagctt tacgctgaac ggcgcgcttt gccattga 2268

<210> 330
<211> 755
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(35)

<400> 330
Met Arg Asn Val Gln Glu Ile Gly Gly Ser Met Tyr Lys Lys Ala Phe
1 5 10 15
Leu Val Leu Ala Leu Phe Leu Leu Leu Ala Ala Val Ala Leu Pro Ser
20 25 30
Val Gly Ala Ala Pro Gln Gly Pro Arg Leu Arg Asp Val Ala Gly Asp
35 40 45
Ile Leu Val Gly Tyr Ala Ser Arg Asn Asp Phe Trp Asn Met Ser Asp
50 55 60
Ser Ala Gln Tyr Thr Glu Val Ala Arg Thr Glu Phe Asn Phe Met Thr
65 70 75 80
Pro Glu Asn Ala Met Lys Trp Asp Ala Ile His Pro Ala Gln Asn Ser
85 90 95
Tyr Ser Phe Ala Gln Ala Asp Arg His Val Gln Phe Ala Gln Ala Asn
100 105 110
Asn Met Ala Val His Gly His Ala Leu Val Trp His Ser Gln Asn Pro
115 120 125
Gly Trp Leu Thr Asn Gly Asn Trp Ser Arg Ser Gln Leu Ile Asn Ile
130 135 140
Met Asn Asp His Ile Asp Thr Val Ala Gly Arg Tyr Ala Gly Glu Val
145 150 155 160
Leu Val Trp Asp Val Val Asn Gln Ala Phe Asn Glu Asp Gly Thr Tyr
165 170 175
Arg Ser Thr Ile Trp Tyr Asn Gly Ile Gly Gln Glu Tyr Ile Asp Leu
180 185 190
Ala Phe Thr Arg Ala Arg Ala Ala Asp Pro His Ala Lys Leu Ile Tyr
195 200 205
Asn Asp Tyr Asn Ile Gly Trp Leu Asn Ser Lys Ser Asn Gly Val Tyr
210 215 220
Asn Met Ala Ala Asp Met Val Arg Arg Gly Val Pro Ile Asp Gly Val
225 230 235 240
Gly Phe Gln Met His Leu Glu Arg Gly Gly Val Ser Gly Ser Ser Leu
245 250 255
Ala Ser Asn Met Gln Arg Phe Ala Asp Leu Gly Leu Glu Val Tyr Ile
260 265 270
Thr Glu Leu Asp Val Arg Ile Pro Gln Asn Pro Thr Gln Gln Asp Leu
275 280 285
Gln Ala Gln Ala Ala Val Tyr Gln Thr Val Thr Asn Arg Cys Leu Ala
290 295 300
Gln Pro Ala Cys Lys Ala Leu Gln Val Trp Gly Ile Pro Asp Lys Tyr
305 310 315 320
Ser Trp Val Pro Asp Val Phe Pro Gly Thr Gly Ala Pro Leu Leu Phe
325 330 335
Asn Asp Asn Tyr Glu Ala Lys Pro Ala Tyr Tyr Ala Val Gln Ala Glu
340 345 350
Leu Met Ala Ala Asn Pro Gln Pro Thr Asn Thr Pro Gly Thr Pro Ala
355 360 365
His Thr Pro Ser Ala Thr Ser Thr Ser Ala Ala Thr Ala Thr Pro Pro
370 375 380
Ala Thr Ala Thr Ala Thr Ala Thr Thr Pro Ser Gly Gly Gly Val Cys
385 390 395 400
Ala Val Asp Tyr Val Ile Ala Asn Gln Trp Gly Asn Gly Phe Gln Ala
405 410 415
Asn Val Thr Ile Thr Asn His Ser Ala Ala Pro Val Asn Gly Tyr Thr

115 120 125
Gly Tyr Gln Trp Ile Gly Asn Thr Thr Ile Ser Thr Glu Ser Trp Thr
130 135 140
Thr Ile Arg Gly Thr Trp Leu Pro Arg Ala Asp Ala Asn Ala Ser Glu
145 150 155 160
Leu Tyr Val Tyr Pro Glu Val Thr Pro Val Ala Gly Phe Asp Tyr Leu
165 170 175
Leu Asp Asp Leu Leu Ile Glu Arg Ala Ala Pro Val Asp Gly Gly Ala
180 185 190
Pro Gly Thr Val Val Tyr Thr Ala Gly Phe Glu Thr Asp Leu Asp Gly
195 200 205
Trp Glu Ala Arg Ala Asp Gly Val Gly Val Gly Gln Leu Asp Arg Thr
210 215 220
Asp Ala Glu Ser Ala Glu Gly Asp Trp Ser Ala Ile Val Thr Asp Arg
225 230 235 240
Thr Ser His Gly His Gly Leu Arg Leu Asp Val Thr Asp Ile Met Asp
245 250 255
Ala Gly Val Thr Tyr Glu Ile Ser Ala Gln Val Lys Phe Ala Gly Thr
260 265 270
Gly Gly Pro Gly Asn Ile Trp Leu Ser Gln Glu Leu Val Val Asp Gly
275 280 285
Gly Ser Thr Tyr Gly Thr Val Leu Gln Val Pro Gly Val Thr Ser Thr
290 295 300
Ala Trp Thr Gln Ile Thr Thr Asn Tyr Val Thr Pro Thr Ala Asp Gln
305 310 315 320
Leu Phe Leu Tyr Phe Glu Thr Asn Trp Pro Asp Gly Ile Glu Asp Asp
325 330 335
Phe Leu Leu Asp Asp Val Arg Ile Arg Val Ala Pro Arg Ala Ile Ile
340 345 350
Gln Glu Asp Leu Thr Pro Leu Met Asp Thr Leu Asp Val Pro Met Gly
355 360 365
Val Ala Ile Asp Gln Arg Glu Thr Ser Gly Ser Leu Ala Asp Leu Leu
370 375 380
Leu Leu His Phe Asp Gln Val Thr Ala Glu Asn His Met Lys Pro Glu
385 390 395 400
Ala Trp Tyr Asp Ala Ala Gly Asn Phe Arg Ile His Pro Gln Ala Arg
405 410 415
Ala Ile Met Asp Phe Ala Ala Glu Asn Asp Leu Arg Val Phe Gly His
420 425 430
Val Leu Val Trp His Gly Gln Thr Pro Asp Phe Phe Phe Thr His Ala
435 440 445
Asp Gly Thr Pro Leu Thr Ser Ser Glu Ala Asp Gln Ala Ile Leu Arg
450 455 460
Asp Arg Met Arg Thr His Ile Phe Asn Val Ala Glu Ala Leu Ser Glu
465 470 475 480
Trp Gly Glu Tyr Gly Gly Asp Asn Pro Leu Val Ala Trp Asp Val Val
485 490 495
Asn Glu Val Val Ser Asp Ser Gly Glu His Ser Asp Gly Leu Arg Arg
500 505 510
Ser Arg Trp Tyr Asp Val Leu Gly Glu Glu Phe Ile Asp Leu Ala Phe
515 520 525
Ile Tyr Ala Asn Gln Ala Phe Asn Gly Glu Phe Ala Ala Asp Asp Ala
530 535 540
Asn His Pro Val Thr Leu Phe Ile Asn Asp Tyr Asn Thr Glu Gln Ser
545 550 555 560
Gly Lys Gln Asn Arg Tyr Ala Ala Leu Ile Asp Arg Leu Ile Glu Arg
565 570 575
Glu Val Pro Ile Asp Ala Val Gly His Gln Phe His Val Ser Leu Ala
580 585 590
Met Pro Ile Ala Asn Leu Arg Gly Ala Leu Glu Arg Phe Gln Asp Thr
595 600 605
Gly Leu Ile Gln Gly Val Thr Glu Leu Asp Val Thr Val Gly Asn Asn
610 615 620
Pro Thr Glu Ala Leu Leu Val Glu Gln Gly Tyr Tyr Tyr Arg Asp Ala
625 630 635 640
Phe Arg Leu Phe Arg Glu Phe Thr Glu Asp Leu Tyr Ser Val Thr Val
645 650 655
Trp Gly Leu Thr Asp Asp Arg Ser Trp Arg Ser Ala Gln Ala Pro Leu
660 665 670

Leu Phe Asp Ala Gly Leu Gln Ala Lys Pro Ala Tyr Tyr Gly Ala Ile
675 680 685
Asp Ala Asp Leu Asp Ala Arg Val Arg Ala Ala Tyr Val Phe Ala Glu
690 695 700
Asp Ile Ala Leu Asp Glu Ala Ala Leu Thr Ser Pro Thr Trp Asp Arg
705 710 715 720
Leu Pro Leu His Gln Ile Asp Gly Ala Gly Glu Phe Gln Leu Arg Trp
725 730 735
Ala Ala Asp His Leu Thr Val Phe Val His Val Thr Asp Gly Asp Glu
740 745 750
Val Glu Ile Val Leu Gly Asp Glu Thr Tyr Thr Val Ser Ser Asp Gly
755 760 765
Glu Gly Asp Leu Asp Ala Val Thr Ala Ala Gly Glu Asn Gly Ser Trp
770 775 780
Thr Ala Val Val Arg Val Pro Leu Thr Ala Glu Gln Gly Asp Thr Ala
785 790 795 800
Gln Phe Asp Leu Arg Ile Ile Asp Gly Ala Thr Thr Ser Gly Trp Asn
805 810 815
Val Glu Gly Val Leu Gly Thr Leu Thr Leu Val Glu Glu Leu Ser Phe
820 825 830
Val Glu Val Val Glu Ala Ala Asp Arg Pro Thr Ile Asp Gly Glu Ile
835 840 845
Asp Ala Val Trp Glu Asp Ala Asn Val Val Thr Thr Asp Val Arg Ile
850 855 860
Glu Gly Ala Ala Asp Gly Ala Lys Ala Glu Ile Arg Thr Leu Trp Asp
865 870 875 880
Asn Asn Thr Leu Phe Val Leu Ala Glu Ile Ala Asp Pro Val Ile Asp
885 890 895
Val Thr Ala Ser Ser Pro Trp Glu Gln Asp Ser Leu
900 905

<210> 361
<211> 5040
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 361
atggcaagaa gtaagcgagt attagcatgg attatgtcta gtgtgcttct gatatccatg 60
gcgatgccat ccttcgcatc aggtgattca agccaagtgc caagggttat atttgaaaca 120
ggttttgaaa cgggattaga tggcttcaaa ggacggggta gtgccacctt aactcgaacg 180
actgatgaaa cgcaagcagg cgactattcg gttcttgtga gcaatcggct tgagcactgg 240
aatggggcat cattgccact tacaggcttc gttctaccag gtaatacata tgaatttgtt 300
ggttacataa aagcaaaagc agatgtagca gacaattatg tcatgagtgg tgagtacaat 360
gaggggattt ctggaaatca atatccatgg atatctaatc gtttgttaac ggttcaagat 420
ggctttgttg agtttagagg tgaactaacc atactagagg atatgacgtc ctttaatcta 480
aactttgaac atcaaaatgc tgaagtggaa ttttatttag attctgttca ggttattcta 540
atcgaagaag gtcaagtcaa tgacttacca atgaatgtaa gaagagcgcc acttacactt 600
gctgaaactc ccttacatga gatttgggca gatcacttta ctattggcaa tatttatacg 660
ccaggttttc gcacagatat acgtggtgag gtattagccc atcattttaa tgtgatcaca 720
gctgaaaata ttatgaagcc agatcatttg caaagggaac aaggtatttt tactttagt 780
gcttccaacg atatgatgga atttgccaga gcaaataatc aagaagtcat tggacatact 840
ttggtgtggc attctcaatc cttcccatgg tttgaagctt taaatccaac acgtgatgaa 900
gctatagcca ttatgcatgc ccatattgaa actgttatgg gacattttaa tgaaaactac 960
ccaggtgtca ttacaggatg ggatgttttg aatgaagcca ttcaaccaag acagggtcaa 1020
gatcctgaaa attggcgctt gcatttaagg gataccaaat ggttacgtgc cattggtgat 1080
gattatattg ccatcgcttt taacaaagcc catgaaatgg atccagatgc tattctttat 1140
tataatgatt ataatgataa tgactatttt aaagcaacca ttataaaagc catggtgcag 1200
gagttgcgta atgaaggcgt gcccattcat cgtattggga tgcaaggtca ttataattta 1260
cagacaccat taaactctat tagaaccagc gttgagcgtt ttagtgaaat tactggtcat 1320
gaagatctac cacctattgg cattagtttc acagaaattg atgtaacggt accagggttt 1380
gaaagtgcag cccgtttacc tgaagaggta gaaattcgcc aagctcagtt ttatgctcaa 1440
ttaatgcaga ttttaagaga caacagcgat gtgattcatc gtgttacttt ctggggtatg 1500
tctgatcgtg aatcatggcg tgcagatcgt catcctaaca tgttagatcc tcagtatggt 1560
ccaaagcatg tctttcatgc tatagccaat ccagaggctt tccttacggc ctacccatta 1620
ccagagacgc cagatgctca aacagcctat gcatctcaag gtcaaccagt tgtggggcag 1680
tttaatttgg atgcgtatca aaattcagaa gtaataccag tggctaatca aatgacagcc 1740

ctgtcgatgc gcgtccggct cgtgggcgac ggcacggcga cgacgccggc ccggtggatc 360
ggccgcgacc ccggagccga gaacggctac cagtggatcg gtaacacgac gatctcgacc 420
gagagctgga cgaccatccg gggaacgtgg ctccctcggg cggacgcgaa cgcctcggag 480
ctctatgtct accccgaggt cacaccggtg gccggcttcg actacctcct cgatgacctg 540
ctcatcgagc gtgctgcccc tgtcgacggc ggcgccccgg gcaccgtcgt ctacaccgct 600
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ctcgaccgga ccgacgcgga gtcggccgag ggcgactggt ccgcgatcgt gaccgaccgc 720
acctcgcacg gccacggcct gcgcctggac gtcacggaca tcatggacgc gggcgtcacg 780
tacgagatca gcgcccaggt gaagttcgcc gggaccggtg gtccgggcaa catctggctg 840
agccaggagc tggtcgtgga cgggggtagc acctacggca ccgtcctcca ggtccctggc 900
gtcacctcga cagcctggac gcagatcacc acgaactacg tcacgccgac ggccgaccag 960
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gcgtggtacg acgcggcggg caacttccgc atccacccgc aggcccgcgc catcatggac 1260
ttcgcggcgg agaacgacct gcgcgtcttc ggtcacgtcc tggtgtggca cggccagacc 1320
ccggacttct tcttcacgca cgcggacggc accccgctga cctcgagcga ggccgaccag 1380
gcgatcctgc gcgaccgcat gcgcacgcac atcttcaacg tcgccgaggc cctctccgag 1440
tggggcgagt acggcggcga caacccgctc gtggcctggg acgtcgtcaa cgaggtcgtc 1500
tccgacagcg gcgagcacag cgacggcctg cgccgtagcc gctggtacga cgtgctgggc 1560
gaggagttca tcgacctggc gttcatctac gcgaaccagg cgttcaacgg tgagttcgcc 1620
gctgacgacg ccaaccaccc ggtcacgctc ttcatcaacg actacaacac cgagcagtcc 1680
ggcaagcaga accggtacgc cgcgctcatc gaccgcctca tcgagcgcga ggtcccgatc 1740
gacgccgtgg ggcaccagtt ccacgtcagc ctggccatgc ccatcgcgaa cctgcgcggc 1800
gccctcgagc gcttccagga caccgggctg atccagggcg tcaccgagct cgacgtcacc 1860
gtcggcaaca acccgaccga ggcgctgctc gtcgagcagg gctactacta ccgggacgcc 1920
ttccggctgt tccgtgagtt cacggaggac ctctactcgg tcaccgtgtg ggtctcacc 1980
gacgaccgca gctggcgcag cgctcaggcg ccgctgctgt tcgacgcggg cctgcaggcc 2040
aagccggcct actacggcgc catcgacgcc gacctggacg cacgcgtgcg tgcggcctac 2100
gtgttcgccg aggacatcgc cctcgacgag gccgcgctga cgagccccac ctgggaccgt 2160
ctgccgctgc accagatcga cggggccggc gagttccagc tccgctgggc ggccgaccac 2220
ctcacggtgt tcgtccacgt caccgacggt gacgaggtcg agatcgtgct cggcgacgag 2280
acctacacgg tctcgtcgga cggcgagggc gacctggacg cggtcaccgc ggccggggag 2340
aacggctcct ggaccgctgt ggtccgcgtg ccgctcacgg ccgagcaggg cgacaccgcc 2400
cagttcgacc tccggatcat cgacggcgcc accacctccg ggtggaacgt cgaaggtgtc 2460
ctgggcaccc tgaccctggt cgaggagctg tccttcgtcg aggtcgtcga ggcggccgac 2520
cggccgacca tcgacggcga gatcgacgcc gtgtgggagg acgccaacgt cgtcaccacg 2580
gacgtccgta tcgagggcgc tgctgacggc gcgaaggccg agatccggac cctgtgggac 2640
aacaacacgc tgttcgtcct cgcggagatc gccgacccgg tgatcgacgt gacggcctcc 2700
agcccgtggg agcaggactc gctc 2724

<210> 360
<211> 908
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(31)

<400> 360
Met Thr Arg Ser Val Arg Pro Arg Ala Trp Gly Ala Gly Leu Leu Ala
1 5 10 15
Leu Ala Met Val Ala Thr Val Ala Pro Thr Ala Thr Gly His Ser His
20 25 30
Asp Thr Ala Glu Pro Val Val Val Val Tyr Thr Asp Phe Glu Asn Asp
35 40 45
Ser Ile Glu Pro Trp Ala Gln Ser Gly Gly Pro Thr Leu Asn Ile Val
50 55 60
Glu Val Asp Gly Gly His Ala Leu Arg Val Gly Asn His Gln Asn Thr
65 70 75 80
Trp Asp Gly Ile Gln Thr Gln Pro Ala Thr Thr Arg Ile Glu Pro Gly
85 90 95
Val Glu His Thr Leu Ser Met Arg Val Arg Leu Val Gly Asp Gly Thr
100 105 110
Ala Thr Thr Pro Ala Arg Trp Ile Gly Arg Asp Pro Gly Ala Glu Asn

Tyr Phe Asp Val Val Pro Pro His Arg Arg Gly Gly Ile Ser Val Trp
565 570 575
Gly Ile Ala Asp His Tyr Ser Trp Tyr Tyr Thr His Glu Gly Tyr Val
580 585 590
Asp Trp Pro Leu Leu Trp Asp Arg Asn Leu Gln Pro Lys Pro Ala Tyr
595 600 605
Asn Ala Val Tyr Glu Ala Leu Gln Gln Gly Gln
610 615

<210> 353
<211> 1983
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 353
atggtttgct cggccgccct cggggcgacc gccgtcagtg cccaaacctt gagcaacaac 60
tcaaccggta ccaacaacgg tttctactac accttttgga aggactcggg cagcgcgacc 120
atgaccctcg cagcgggtgg tcgttacacc tcccaatgga ccaacaacac caataactgg 180
gtgggtggta aaggctggaa cccgggcaat agcacccgcg tgatcagcta ttccggtaac 240
tatggcgtca gcaatagcca aaattcctac ctggccttgt acggctggac ccgcagcccg 300
ctgattgaat actacgtgat cgaaagctac ggctcctaca acccggcatc ctgctctggc 360
ggtaccaata tgggtagctt ccagagtgat ggcgcgacct acgatgtgcg ccgttgccag 420
cgcgtgcaac agccatccat cgatggcacc caaaccttct accaatattt cagcgtgcgc 480
aatccgaaaa aaggcttcgg ccaaatttcc ggcaccatca cctttgctaa ccacgcagcc 540
ttttgggcga gcaagggcat gaacctgggt gcccataact atcaagtaat ggcgaccgag 600
ggttatcaaa gtaccggcag ttccgatatc acagtgagtg aaggccccat caacggcggc 660
accagcagca cgcccccggt aacaaccagc agcagtgcca gctcagtggc aacgggcggt 720
ggtaacaccg gtagtggcgt agtggtgcgc gcgcgcggcg tcgcgggcgg cgagcatatt 780
aacctgcgta tcggtggcaa taccgtcgcc agctggaacc tcaccaccag cttccaggat 840
ctcagctaca gcggcaccgc gtcgggcgat atccaggtgc aatatgacaa cgacggcggc 900
agccgcgatg tcgtagtgga ttacatccgc gttaacggcg aaacccgcca ggcggaggat 960
atgagctaca acaccgcctt gtacgcgaat ggttcctgcg gtggcggcgg caattccgaa 1020
ctgatgcact gcaatggcgt gatcggtttt ggctacacct atgattgctt cagcggcaac 1080
tgctccggcg gcagcacggg gggtggcaac actggcacca gcagcagcgc ggcgagcgcc 1140
ggtggtggca acagcaactg ctccggctat gttggtatta ctttcgacga tggcccaacc 1200
gctaacactc ccaccctggt taacctgttg aagcaaaaca acctgacgcc ggtaacctgg 1260
ttcaaccagg gcaacaacgt ggttgccaat gccaattaca tggcccagca attgagcgtt 1320
ggtgaagtac ataaccacag ctacagccat ccgcaaatgg gcagcatgac ctaccaacag 1380
gtttatgacg agttgaaccg tgccaaccag gctatccaaa ccgcgggtgc acccaagcca 1440
accctgttcc gcccacctta tggcaccgtt aactccacca tccaacaagc ggcccaggcc 1500
ttgggtttgc gggtgatcac ctgggatgtg gattcgcaag actggaatgg cgccactgcc 1560
tcggccatcg ccagcgcagc taaccgcctg acaaacggcc aggtaatcct gatgcacgac 1620
ggcagctaca ccaacaccaa tgccgctatt gcccagatcg cctccagcct gcgcgccaag 1680
ggcttgtgcc cgggtcgtat cgatccggca accggccgag ccgttgctcc tgcgggtggc 1740
aatactggcg gcggtactgt gtcaagcagc actcgcagca gcactccggt agtggtaagc 1800
agcagccgta gcagcagtag tgttgccgct ggcggcgcct gccaatgcaa ttggtggggc 1860
acccgttacc cgatctgtac gtccactgcc agtggttggg gttgggagaa caaccgcagc 1920
tgtatcacca ccagcacctg taacagtcag ggccctggcg gtggtggggt agtgtgtaac 1980
taa 1983

<210> 354
<211> 660
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(18)

<400> 354
Met Val Cys Ser Ala Ala Leu Gly Ala Thr Ala Val Ser Ala Gln Thr
1 5 10 15
Leu Ser Asn Asn Ser Thr Gly Thr Asn Asn Gly Phe Tyr Tyr Thr Phe
20 25 30

```
            580                 585                 590
Ser Ser Thr Pro Val Val Val Ser Ser Ser Arg Ser Ser Ser Ser Val
        595                 600                 605
Ala Ala Gly Gly Ala Cys Gln Cys Asn Trp Trp Gly Thr Arg Tyr Pro
    610                 615                 620
Ile Cys Thr Ser Thr Ala Ser Gly Trp Gly Trp Glu Asn Asn Arg Ser
625                 630                 635                 640
Cys Ile Thr Thr Ser Thr Cys Asn Ser Gln Gly Pro Gly Gly Gly Gly
                645                 650                 655
Val Val Cys Asn
            660
```

<210> 355
<211> 1125
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 355

```
atgaaacgaa ccatcttctt aagactctta gccggcgccc tcctctccgc cgcggccctc      60
gcggccgggg ggtgccggcc ctctagtccc ccgaaggtcg agatcgaggc caatatcccc     120
tccctcaaag aggtctgcgc ttcttatttc gagatcggcg cggccgtcga gccgtatcag     180
ttatcctctc caccccacga tgcccttctg cggaaacatt ttaactgcct cgtggcggag     240
aacgtcatga agcccgcctc catccagcct tcggaggggt atttcaactg gaccgaagca     300
gacaagatcg tgaactacgc caaagcccac gggatgaagc tccgcttcca taccctcgtc     360
tggcataatc aggtcccgga ttggttcttc gcgggtaacg acaaaaccct ccttttgcag     420
cgcttggaga atcatatccg gactatcatt aaaagatatg gcgataaggt cgactattgg     480
gacgtggtaa atgaggctat agacccgagc caaccggatg gcatgaggag gagcaaatgg     540
taccagatca ccgggaagga ctacatcaag accgccttcc gggtggcaga cgacgagctc     600
aggaagaatg ggtggaggaa agaaggtcgt cagctctata tcaacgacta caacacccat     660
gatccgacga agagagagta catctggcgc ttgatcgatg agcttcaaac ggaagggatt     720
cccgtcgacg gagtaggcca ccagacgcat atcaatatcg aatggccgcc cgtaaaccag     780
atcgtggact cgatccgctt cttcggggaa aaaggcctcg ataaccaggt gaccgagctg     840
gatgtgagca tatatacgga tagatccagt tcctacggga gttaccaagc gatcccgcag     900
gaagtcttca tcaagcaggg taatcgctac aaggaactct ttgaagggct aaaaagtgta     960
aaaaactacc tcagcaacgt caccttctgg ggcatggcgg acgatcatac ctggctgaac    1020
cattggccca tcgaacggcc cgatgctcct cttcctttcg atatctatct caaggccaag    1080
ccggcgtatt gggggatcgt ggatgctttg aagctttcgc ggtga                    1125
```

<210> 356
<211> 374
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(21)

<400> 356

```
Met Lys Arg Thr Ile Phe Leu Arg Leu Leu Ala Gly Ala Leu Leu Ser
 1               5                  10                  15
Ala Ala Ala Leu Ala Ala Gly Gly Cys Arg Pro Ser Ser Pro Pro Lys
            20                  25                  30
Val Glu Ile Glu Ala Asn Ile Pro Ser Leu Lys Glu Val Cys Ala Ser
        35                  40                  45
Tyr Phe Glu Ile Gly Ala Ala Val Glu Pro Tyr Gln Leu Ser Ser Pro
    50                  55                  60
Pro His Asp Ala Leu Leu Arg Lys His Phe Asn Cys Leu Val Ala Glu
65                  70                  75                  80
Asn Val Met Lys Pro Ala Ser Ile Gln Pro Ser Glu Gly Tyr Phe Asn
                85                  90                  95
Trp Thr Glu Ala Asp Lys Ile Val Asn Tyr Ala Lys Ala His Gly Met
            100                 105                 110
Lys Leu Arg Phe His Thr Leu Val Trp His Asn Gln Val Pro Asp Trp
        115                 120                 125
```

<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(25)

<400> 358
Met Asn Asn Phe Arg Asn Thr Phe Leu Ile Val Val Val Leu Ala Val
1 5 10 15
Val Val Gly Val Leu Pro Ala Cys Glu Ala Gly Pro Pro Glu Asn Thr
20 25 30
Ser Ser Ser Leu Gln Glu Ala Tyr Ala Asp Val Phe Leu Ile Gly Thr
35 40 45
Ala Leu Asn Leu Ala Gln Ile Asp Gly Arg Asp Glu Gln Gly Val Arg
50 55 60
Leu Val Glu Arg His Phe Asn Ala Ile Thr Pro Glu Asn Ile Thr Lys
65 70 75 80
Trp Gly Pro Ile His Pro Ala Pro Gly Glu Tyr Asn Phe Gly Pro Ala
85 90 95
Asp Arg Phe Val Glu Phe Gly Glu Ala His Asp Met Phe Met Ile Gly
100 105 110
His Thr Leu Val Trp His Ser Gln Thr Pro Gly Trp Val Phe Glu Asp
115 120 125
Glu Ala Gly Asn Pro Leu Gly Arg Asp Glu Leu Ile Glu Arg Met Arg
130 135 140
Asp His Ile His Thr Val Val Gly Arg Tyr Arg Gly Arg Ile His Ala
145 150 155 160
Trp Asp Val Val Asn Glu Ala Leu Asn Glu Asp Gly Thr Leu Arg Glu
165 170 175
Ser Pro Trp Tyr Arg Ile Ile Gly Glu Asp Tyr Leu Leu Lys Ala Phe
180 185 190
Glu Phe Ala His Glu Ala Asp Pro Asp Ala Glu Leu Tyr Tyr Asn Asp
195 200 205
Tyr Ser Leu Glu Asn Pro Ala Lys Arg Ala Gly Ala Val Arg Leu Val
210 215 220
Arg Tyr Leu Gln Glu Asn Gly Ala Pro Ile His Gly Ile Gly Thr Gln
225 230 235 240
Gly His Tyr Ser Leu Asp Trp Pro Ser Leu Asp Glu Ile Glu Arg Thr
245 250 255
Ile Thr Asp Phe Ala Ala Leu Asp Val Asp Val Met Val Thr Glu Leu
260 265 270
Glu Ile Asp Val Leu Pro Ser Ala Phe Glu Tyr Gln Gly Ala Asp Ile
275 280 285
Ala Met Arg Ala Glu Leu Glu Glu Arg Leu Asn Pro Tyr Pro Asp Glu
290 295 300
Leu Pro Ala Glu Val Asp Glu Ala Leu Thr Gln Arg Tyr Arg Asp Ile
305 310 315 320
Phe Glu Val Phe Leu Arg His Ser Asp Val Leu Thr Arg Val Thr Phe
325 330 335
Trp Gly Val Thr Asp Gly Asp Ser Trp Lys Asn Asn Trp Pro Val Pro
340 345 350
Gly Arg Thr Asn Tyr Pro Leu Leu Phe Asp Arg Glu Trp Gln Pro Lys
355 360 365
Pro Ala Phe Tyr Ser Val Ile Glu Val Ala Asp Glu Met Leu Asn Glu
370 375 380

<210> 359
<211> 2724
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 359
atgacccggt ctgtacgacc aagagcatgg ggggccggcc tactggccct cgcgatggtg 60
gcgacagtcg cccccacggc caccggccac agccacgaca cggcagagcc cgtcgtcgtg 120
gtctacaccg acttcgagaa cgacagcatc gagccgtggg cgcagtccgg cggccccgacg 180
ctgaacatcg tcgaggtcga cggcgggcac gcgctgcgcg tcggcaacca ccagaacacc 240
tgggacggca tccagaccca gcccgccacc acgcggatcg agccgggtgt cgagcacacc 300

Phe Phe Ala Gly Asn Asp Lys Thr Leu Leu Leu Gln Arg Leu Glu Asn
    130   135   140
His Ile Arg Thr Ile Ile Lys Arg Tyr Gly Asp Lys Val Asp Tyr Trp
145   150   155   160
Asp Val Val Asn Glu Ala Ile Asp Pro Ser Gln Pro Asp Gly Met Arg
                165   170   175
Arg Ser Lys Trp Tyr Gln Ile Thr Gly Lys Asp Tyr Ile Lys Thr Ala
            180   185   190
Phe Arg Val Ala Asp Asp Glu Leu Arg Lys Asn Gly Trp Arg Lys Glu
        195   200   205
Gly Arg Gln Leu Tyr Ile Asn Asp Tyr Asn Thr His Asp Pro Thr Lys
    210   215   220
Arg Glu Tyr Ile Trp Arg Leu Ile Asp Glu Leu Gln Thr Glu Gly Ile
225   230   235   240
Pro Val Asp Gly Val Gly His Gln Thr His Ile Asn Ile Glu Trp Pro
                245   250   255
Pro Val Asn Gln Ile Val Asp Ser Ile Arg Phe Phe Gly Glu Lys Gly
            260   265   270
Leu Asp Asn Gln Val Thr Glu Leu Asp Val Ser Ile Tyr Thr Asp Arg
        275   280   285
Ser Ser Ser Tyr Gly Ser Tyr Gln Ala Ile Pro Gln Glu Val Phe Ile
    290   295   300
Lys Gln Gly Asn Arg Tyr Lys Glu Leu Phe Glu Gly Leu Lys Ser Val
305   310   315   320
Lys Asn Tyr Leu Ser Asn Val Thr Phe Trp Gly Met Ala Asp Asp His
                325   330   335
Thr Trp Leu Asn His Trp Pro Ile Glu Arg Pro Asp Ala Pro Leu Pro
            340   345   350
Phe Asp Ile Tyr Leu Lys Ala Lys Pro Ala Tyr Trp Gly Ile Val Asp
        355   360   365
Ala Leu Lys Leu Ser Arg
    370

<210> 357
<211> 1155
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 357
atgaataact tcagaaatac atttctaatc gtcgttgtac tggcggtcgt cgtcggcgtg 60
ctgccggcct gcgaagccgg tccgccggaa aatacaagtt cgtccctgca ggaggcatat 120
gcagatgtgt ttctgatcgg caccgcgctc aatctggcac agatcgacgg aagggatgaa 180
caaggcgtac gtctggtgga gcggcatttt aatgcgatta caccagagaa cattacaaaa 240
tggggaccga tacatccggc gccgggcgaa tataatttcg gaccggccga ccggtttgtt 300
gaattcggtg aagcccacga catgttcatg ataggccata cgcttgtatg gcacagccag 360
acgcccggat gggtattcga ggatgaagcc ggaaatccgc tcggccgcga cgagctcatc 420
gaacgcatgc gcgatcatat ccataccgtc gtcggacggt accggggtag aatacacgca 480
tgggacgtcg tcaacgaagc gttgaatgaa gacggaaccc tgcgggaatc cccctggtac 540
cgtatcatcg gcgaggatta cctgttgaaa gcgttcgagt tcgcgcatga agcggacccg 600
gatgccgagc tgtactataa cgattattct ctcgaaaatc ccgccaagcg ggcgggggcg 660
gtacgcctgg tccggtacct gcaggagaac ggggcgccga tacacgggat cggtacccag 720
ggacactact ctcttgactg gccatcgctc gacgagatcg aaagaaccat caccgatttc 780
gccgcgttgg acgtggacgt catggttacc gaacttgaaa tcgacgtcct cccttccgcg 840
ttcgagtatc agggggccga tattgcgatg cggcggaac tcgaagagcg gttgaatccg 900
tatcccgacg aactgccggc cgaggtcgat gaagcgctta cacagcggta tcgggacatc 960
ttcgaggtat ttctgcggca cagcgacgtt cttacgcgcg taacgttctg gggggtgacc 1020
gatggagatt cgtggaagaa taactggccg gtaccgggaa ggacgaatta tccgctgctg 1080
ttcgaccgcg aatggcagcc aaaaccagca ttttattccg tgatcgaagt tgcggatgag 1140
atgctgaatg aataa 1155

<210> 358
<211> 384
<212> PRT
<213> Unknown

<220>

Asp Phe Leu Met Trp Gly Phe Trp Glu Gly Ser His Trp Lys Pro Leu
500 505 510
Gly Ala Met Ile Arg Arg Asp Trp Ser Glu Lys Pro Met Tyr Arg Val
515 520 525
Trp Arg Glu Leu Ile Phe Glu Arg Trp Gln Thr Asp Glu Thr Gly Val
530 535 540
Thr Pro Glu His Gly Ala Ile Tyr Val Arg Gly Phe Lys Gly Asp Tyr
545 550 555 560
Glu Ile Thr Val Lys Ala Gly Gly Gln Glu Val Arg Val Pro Tyr Thr
565 570 575
Leu Lys Glu Asp Gly Gln Val Leu Trp Val Thr Val Gly Gly Thr Ser
580 585 590
Glu Glu Gln Ala Pro
595

<210> 351
<211> 1860
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 351
atgcaccttc caaattaccg ctcgctcgca acggcgctca gtcgctacag ttgctcggcg 60
ctgctggccg tcagtcttgt ggcctgcggg ggcaataatg accaagatcc gccgaccccg 120
gagccaactc cggtcccaac gccgactcca actccaaccc cgaccccgac tccggagcca 180
accccgactc cgactccgga gcccactccg actccagagc caactccgac gccgaccccg 240
gaaccaacac cgacgccgga gccgacgcca acaccggatc ccggggccga ctaccagccg 300
cccagcaatg acattgccgt caatggcgac gtggaaagcg gtactaccaa ctggggtgca 360
cgcggttcgg catccattag ccgagtcact ttagagagct ttgaaggtga tgccagcttg 420
agtgttaccg gccgagaaga cgactggcat ggcgccacct tctctgtagg ccatctgacc 480
ccgggtaata gctatgaagt ggctgcgtgg gtcaagttag cctcaggcga gcccaacaca 540
gtggtcaaaa tcacgggtaa gcgcgagggc gagagcgcga cttacgaaga gtacacggat 600
gtcggtacgg cattggctac cgacggtagc tggaccgaaa ttaccggcac ttatattcct 660
gatagcgcca gcccatttga atattttatt gtggagaccc aagagggtgg accgaccgtt 720
agcttctacg tggacgcgtt ttcagtggcc ggtgaggtgg aagatacgcc agcgccaacg 780
ccgcccccaa ccgctccgcc accgagtggc tcaggcctag cggaactagt ggatttcccg 840
gtgggcgttg ccgttgcggt agctagtttt gccaataacg atttcctgag taacacgcaa 900
caacaagata tcgtgcttaa caattttagt gaaattgttg cggagaatca gatgaagatg 960
gaatatttca acgatgacta ctccaacccc agggcagatc aactggtcag ctgggccaat 1020
gagcgaggta ttcgggttca cggccacgct ttggtctggc acgcgcaagc agcgtcatgg 1080
gtcagtcctc cggtaagcaa ctttcgcgag cgttatgtca accatgttcg tggtgtggca 1140
tcccggtatg cggacacggt agtaagctgg gatgtcgtca atgaagcttt gaccgatgat 1200
gatgtctccc cgggtggaag ctactaccgg caatctgagt tctaccgaca gttcaatggc 1260
ccagagttca ttgatatcgc tttccgtgaa gctcgagagg cagcccccaa tgcgctgctt 1320
tactacaacg actacaatat tgagaacgga ctggacaaaa ccgatggttt gattcagcta 1380
cttgagaggt tgagggataa tgacgtgccc attgatggcg tgggcttcca aatgcatgtt 1440
ttgttggatt ggcccgatat cagcactatt cgacgttcct gggagcgcgc attagcggtt 1500
gaccccgatg accgtatgct tttaaaaata acggaactcg atgtgcgtat caacaatccc 1560
tacgacgata atctcgaaag aggcatcgtt cactccagcc ggggtgactg cgatgacatt 1620
tccggggtct gcgaaggctt tgagcggcaa gccgctcgtt accgggagat tattgaggcc 1680
tactttgacg tcgtgccacc gcaccgccga ggtggcatca gtgtttgggg tattgccgac 1740
cattatagtt ggtattatac ccatgaaggc tatgtcgatt ggcccctttt gtgggacagg 1800
aacctacagc caaagcctgc ttacaacgct gtttatgaag ctctgcagca gggccaataa 1860

<210> 352
<211> 619
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(73)

<400> 352
Met His Leu Pro Asn Tyr Arg Ser Leu Ala Thr Ala Leu Ser Arg Tyr

1 5 10 15
Ser Cys Ser Ala Leu Leu Ala Val Ser Leu Val Ala Cys Gly Gly Asn
20 25 30
Asn Asp Gln Asp Pro Pro Thr Pro Glu Pro Thr Pro Val Pro Thr Pro
35 40 45
Thr Pro Thr Pro Thr Pro Thr Pro Thr Pro Glu Pro Thr Pro Thr Pro
50 55 60
Thr Pro Glu Pro Thr Pro Thr Pro Glu Pro Thr Pro Thr Pro Thr Pro
65 70 75 80
Glu Pro Thr Pro Thr Pro Glu Pro Thr Pro Thr Pro Asp Pro Gly Ala
85 90 95
Asp Tyr Gln Pro Pro Ser Asn Asp Ile Ala Val Asn Gly Asp Val Glu
100 105 110
Ser Gly Thr Thr Asn Trp Gly Ala Arg Gly Ser Ala Ser Ile Ser Arg
115 120 125
Val Thr Leu Glu Ser Phe Glu Gly Asp Ala Ser Leu Ser Val Thr Gly
130 135 140
Arg Glu Asp Asp Trp His Gly Ala Thr Phe Ser Val Gly His Leu Thr
145 150 155 160
Pro Gly Asn Ser Tyr Glu Val Ala Ala Trp Val Lys Leu Ala Ser Gly
165 170 175
Glu Pro Asn Thr Val Val Lys Ile Thr Gly Lys Arg Glu Gly Glu Ser
180 185 190
Ala Thr Tyr Glu Glu Tyr Thr Asp Val Gly Thr Ala Leu Ala Thr Asp
195 200 205
Gly Ser Trp Thr Glu Ile Thr Gly Thr Tyr Ile Pro Asp Ser Ala Ser
210 215 220
Pro Phe Glu Tyr Phe Ile Val Glu Thr Gln Glu Gly Gly Pro Thr Val
225 230 235 240
Ser Phe Tyr Val Asp Ala Phe Ser Val Ala Gly Glu Val Glu Asp Thr
245 250 255
Pro Ala Pro Thr Pro Pro Pro Thr Ala Pro Pro Pro Ser Gly Ser Gly
260 265 270
Leu Ala Glu Leu Val Asp Phe Pro Val Gly Val Ala Val Ala Val Ala
275 280 285
Ser Phe Ala Asn Asn Asp Phe Leu Ser Asn Thr Gln Gln Gln Asp Ile
290 295 300
Val Leu Asn Asn Phe Ser Glu Ile Val Ala Glu Asn Gln Met Lys Met
305 310 315 320
Glu Tyr Phe Asn Asp Asp Tyr Ser Asn Pro Arg Ala Asp Gln Leu Val
325 330 335
Ser Trp Ala Asn Glu Arg Gly Ile Arg Val His Gly His Ala Leu Val
340 345 350
Trp His Ala Gln Ala Ala Ser Trp Val Ser Pro Pro Val Ser Asn Phe
355 360 365
Arg Glu Arg Tyr Val Asn His Val Arg Gly Val Ala Ser Arg Tyr Ala
370 375 380
Asp Thr Val Val Ser Trp Asp Val Val Asn Glu Ala Leu Thr Asp Asp
385 390 395 400
Asp Val Ser Pro Gly Gly Ser Tyr Tyr Arg Gln Ser Glu Phe Tyr Arg
405 410 415
Gln Phe Asn Gly Pro Glu Phe Ile Asp Ile Ala Phe Arg Glu Ala Arg
420 425 430
Glu Ala Ala Pro Asn Ala Leu Leu Tyr Tyr Asn Asp Tyr Asn Ile Glu
435 440 445
Asn Gly Leu Asp Lys Thr Asp Gly Leu Ile Gln Leu Leu Glu Arg Leu
450 455 460
Arg Asp Asn Asp Val Pro Ile Asp Gly Val Gly Phe Gln Met His Val
465 470 475 480
Leu Leu Asp Trp Pro Asp Ile Ser Thr Ile Arg Arg Ser Trp Glu Arg
485 490 495
Ala Leu Ala Val Asp Pro Asp Asp Arg Met Leu Leu Lys Ile Thr Glu
500 505 510
Leu Asp Val Arg Ile Asn Asn Pro Tyr Asp Asp Asn Leu Glu Arg Gly
515 520 525
Ile Val His Ser Ser Arg Gly Asp Cys Asp Asp Ile Ser Gly Val Cys
530 535 540
Glu Gly Phe Glu Arg Gln Ala Ala Arg Tyr Arg Glu Ile Ile Glu Ala
545 550 555 560

Trp Lys Asp Ser Gly Ser Ala Thr Met Thr Leu Ala Ala Gly Gly Arg
35 40 45
Tyr Thr Ser Gln Trp Thr Asn Asn Thr Asn Asn Trp Val Gly Gly Lys
50 55 60
Gly Trp Asn Pro Gly Asn Ser Thr Arg Val Ile Ser Tyr Ser Gly Asn
65 70 75 80
Tyr Gly Val Ser Asn Ser Gln Asn Ser Tyr Leu Ala Leu Tyr Gly Trp
85 90 95
Thr Arg Ser Pro Leu Ile Glu Tyr Tyr Val Ile Glu Ser Tyr Gly Ser
100 105 110
Tyr Asn Pro Ala Ser Cys Ser Gly Gly Thr Asn Met Gly Ser Phe Gln
115 120 125
Ser Asp Gly Ala Thr Tyr Asp Val Arg Arg Cys Gln Arg Val Gln Gln
130 135 140
Pro Ser Ile Asp Gly Thr Gln Thr Phe Tyr Gln Tyr Phe Ser Val Arg
145 150 155 160
Asn Pro Lys Lys Gly Phe Gly Gln Ile Ser Gly Thr Ile Thr Phe Ala
165 170 175
Asn His Ala Ala Phe Trp Ala Ser Lys Gly Met Asn Leu Gly Ala His
180 185 190
Asn Tyr Gln Val Met Ala Thr Glu Gly Tyr Gln Ser Thr Gly Ser Ser
195 200 205
Asp Ile Thr Val Ser Glu Gly Pro Ile Asn Gly Gly Thr Ser Ser Thr
210 215 220
Pro Pro Val Thr Thr Ser Ser Ser Ala Ser Ser Val Ala Thr Gly Gly
225 230 235 240
Gly Asn Thr Gly Ser Gly Val Val Val Arg Ala Arg Gly Val Ala Gly
245 250 255
Gly Glu His Ile Asn Leu Arg Ile Gly Gly Asn Thr Val Ala Ser Trp
260 265 270
Asn Leu Thr Thr Ser Phe Gln Asp Leu Ser Tyr Ser Gly Thr Ala Ser
275 280 285
Gly Asp Ile Gln Val Gln Tyr Asp Asn Asp Gly Gly Ser Arg Asp Val
290 295 300
Val Val Asp Tyr Ile Arg Val Asn Gly Glu Thr Arg Gln Ala Glu Asp
305 310 315 320
Met Ser Tyr Asn Thr Ala Leu Tyr Ala Asn Gly Ser Cys Gly Gly Gly
325 330 335
Gly Asn Ser Glu Leu Met His Cys Asn Gly Val Ile Gly Phe Gly Tyr
340 345 350
Thr Tyr Asp Cys Phe Ser Gly Asn Cys Ser Gly Gly Ser Thr Gly Gly
355 360 365
Gly Asn Thr Gly Thr Ser Ser Ser Ala Ala Ser Ala Gly Gly Gly Asn
370 375 380
Ser Asn Cys Ser Gly Tyr Val Gly Ile Thr Phe Asp Asp Gly Pro Thr
385 390 395 400
Ala Asn Thr Pro Thr Leu Val Asn Leu Leu Lys Gln Asn Asn Leu Thr
405 410 415
Pro Val Thr Trp Phe Asn Gln Gly Asn Asn Val Val Ala Asn Ala Asn
420 425 430
Tyr Met Ala Gln Gln Leu Ser Val Gly Glu Val His Asn His Ser Tyr
435 440 445
Ser His Pro Gln Met Gly Ser Met Thr Tyr Gln Gln Val Tyr Asp Glu
450 455 460
Leu Asn Arg Ala Asn Gln Ala Ile Gln Thr Ala Gly Ala Pro Lys Pro
465 470 475 480
Thr Leu Phe Arg Pro Pro Tyr Gly Thr Val Asn Ser Thr Ile Gln Gln
485 490 495
Ala Ala Gln Ala Leu Gly Leu Arg Val Ile Thr Trp Asp Val Asp Ser
500 505 510
Gln Asp Trp Asn Gly Ala Thr Ala Ser Ala Ile Ala Ser Ala Ala Asn
515 520 525
Arg Leu Thr Asn Gly Gln Val Ile Leu Met His Asp Gly Ser Tyr Thr
530 535 540
Asn Thr Asn Ala Ala Ile Ala Gln Ile Ala Ser Ser Leu Arg Ala Lys
545 550 555 560
Gly Leu Cys Pro Gly Arg Ile Asp Pro Ala Thr Gly Arg Ala Val Ala
565 570 575
Pro Ala Gly Gly Asn Thr Gly Gly Gly Thr Val Ser Ser Ser Thr Arg

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(20)

<400> 350
Met Pro Val Leu Phe Ala Leu Phe Leu Val Ala Ser Ser Cys Ala Ala
 1   5   10   15
Gln Ser Leu Ala Gly Pro Val Ser Leu Leu Gly Gly Asp Ala Gly Ala
            20   25   30
Ala Phe Arg Tyr Thr Gly Pro Ser Ala Gly Ala Ala Ser Gly Ser Ala
        35   40   45
Glu Trp Val Ala Val Glu Asn Met Pro Phe Thr His Ala Trp Arg Leu
    50   55   60
Arg Thr Asn Pro Leu Pro Glu Ser Gly Gly Asn Glu Trp Asp Leu Arg
65   70   75   80
Ile Arg Ala Arg Gly Ala Ala Ala Val Ser Ala Gly Asp Lys Ile Leu
                85   90   95
Ala Glu Phe Trp Met Arg Cys Val Glu Pro Glu Asn Gly Asp Cys Ile
            100   105   110
Leu Arg Leu Asn Val Glu Arg Asp Gly Ser Pro Trp Thr Lys Ser Ile
        115   120   125
Ser Asn Pro Tyr Pro Val Gly Arg Glu Trp Arg Arg Phe Arg Val Leu
    130   135   140
Phe Glu Met Arg Glu Ser Tyr Ala Ala Gly Gly Tyr Met Ile Asp Phe
145   150   155   160
Trp Met Gly Gln Gln Val Gln Thr Ala Glu Val Gly Gly Ile Ser Leu
                165   170   175
Leu Asn Tyr Gly Pro Gln Ala Thr Ala Glu Gln Leu Gly Leu Asp Arg
            180   185   190
Phe Tyr Glu Gly Ala Ala Ala Asp Ala Ala Trp Arg Gln Ala Ala Glu
        195   200   205
Gln Arg Ile Glu Glu Ile Arg Lys Ala Gly Met Ile Ile Val Ala Val
    210   215   220
Thr Pro Asp Gly Glu Pro Ile Glu Gly Ala Glu Ile Arg Ala Lys Leu
225   230   235   240
Lys Arg His Ala Phe Gly Trp Gly Thr Ala Val Ala Ala Ser Arg Leu
                245   250   255
Leu Gly Thr Gly Thr Asp Ser Glu Arg Tyr Arg Asn Phe Ile Arg Glu
            260   265   270
Asn Phe Asn Met Ala Val Leu Glu Asn Asp Leu Lys Trp Gly Pro Phe
        275   280   285
Glu Glu Asn Arg Ala Arg Ala Met Asn Ala Leu Arg Trp Leu His Glu
    290   295   300
Asn Gly Ile Thr Trp Ile Arg Gly His Asn Leu Val Trp Pro Gly Trp
305   310   315   320
Arg Trp Met Pro Ser Asp Val Arg Asn Leu Ala Asn Asn Pro Glu Ala
                325   330   335
Leu Arg Gln Arg Ile Leu Asp Arg Ile Arg Asp Thr Ala Thr Ala Thr
            340   345   350
Arg Gly Leu Val Val His Trp Asp Val Val Asn Glu Pro Val Ala Glu
        355   360   365
Arg Asp Val Leu Asn Ile Leu Gly Asp Glu Val Met Ala Asp Trp Phe
    370   375   380
Arg Ala Ala Lys Glu Cys Asp Pro Glu Ala Arg Met Phe Ile Asn Glu
385   390   395   400
Tyr Asp Ile Leu Ala Ala Asn Gly Ala Asn Leu Arg Lys Gln Asn Ala
                405   410   415
Tyr Tyr Arg Met Ile Glu Met Leu Leu Lys Leu Glu Ala Pro Val Glu
            420   425   430
Gly Ile Gly Phe Gln Gly His Phe Asp Thr Ala Thr Pro Pro Glu Arg
        435   440   445
Met Leu Glu Ile Met Asn Arg Tyr Ala Arg Leu Gly Leu Pro Ile Ala
    450   455   460
Ile Thr Glu Tyr Asp Phe Ala Thr Val Asp Glu Glu Leu Gln Ala Gln
465   470   475   480
Phe Thr Arg Asp Leu Met Ile Leu Ala Phe Ser His Pro Ala Val Ser
                485   490   495

```
                420                     425                     430
Leu Ala Trp Thr His Ala Pro Gly Gln Ile Val Thr Ser Gly Trp Asn
        435                     440                     445
Val Thr Ile Ala Gln Ser Gly Ser Ala Val Ser Ala Ser Asn Pro Ala
    450                     455                     460
Gly Tyr Trp Asn Gly Val Ile Gly Ala Asn Gly Gly Lys Ile Ser Phe
465                     470                     475                     480
Gly Phe Gln Gly Ser Leu Ala Gly Gly Ser Ala Val Ala Pro Thr Tyr
                485                     490                     495
Phe Ala Leu Asn Gly Ala Ala Cys Asn Gly Ala Val Leu Pro Pro Thr
            500                     505                     510
Ala Thr Phe Thr Pro Ser Pro Thr Ala Thr Met Cys Pro Gln Ala Thr
        515                     520                     525
Pro Glu Leu Leu Val Val Gln Pro Val Thr Ser Pro Thr Thr Gln Leu
    530                     535                     540
Ser Gln Thr Leu Val Val Arg Leu Gly Asn Gly Glu Trp Val Arg Ala
545                     550                     555                     560
Ala Gly Pro Ala Gly Val Val Thr Val Thr Ala Pro Asp Pro Asp Gly
                565                     570                     575
Tyr Phe Arg Leu Thr Ile Pro Leu Ala Ala Asn Thr Ser Asn Ala Ile
            580                     585                     590
Leu Val Glu Gly Arg Val Arg Val Ile Thr His Ser Asn Gly Cys Thr
        595                     600                     605
Tyr Gly Gly Tyr Thr Leu Ser Arg Thr Val Thr Ile Val Gln Ala Ser
    610                     615                     620
Ser Pro Val Thr Leu Thr Pro Thr Ala Thr Pro Ser Pro Thr Ala Thr
625                     630                     635                     640
Ala Thr Pro Thr Val Thr Ala Thr Ser Pro Ser Gly Ala Cys Thr Val
                645                     650                     655
Ala Tyr Ala Ile Thr Asn Asp Trp Gly Ser Gly Phe Thr Ala Asn Val
            660                     665                     670
Thr Leu Thr Asn Thr Gly Gly Ser Ala Leu Asn Gly Trp Thr Leu Ala
        675                     680                     685
Tyr Ala Phe Pro Gly Asn Gln Thr Ile Ser Asn Ala Trp Asn Gly Thr
    690                     695                     700
Ala Val Gln Ser Gly Ser Ser Val Ser Val Thr Asn Ala Gly Trp Asn
705                     710                     715                     720
Gly Ser Leu Pro Pro Asn Val Ser Ala Ser Phe Gly Phe Gln Ala Ser
                725                     730                     735
Tyr Ser Gly Asn Asn Ser Val Pro Ala Ser Phe Thr Leu Asn Gly Ala
            740                     745                     750
Leu Cys His
        755
```

<210> 331
<211> 1242
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 331

```
gtgttcaagg gcttgcgcta tttgctgttg ctgtgcctga gtgcgggact ggtctttgcc      60
tgtgcgccac ggtctgtgac cgccccaccc gatgggctaa gcgggcaaat taggctcctg     120
cgccaaggaa ccctcactgt ccttgtccag aatgcccaag ggcaacccat tgccaacgcc     180
aaggtggtag ctgctcagca aacccatgcc ttccccttg gtgttgcctt agatacagca      240
atgtttgagc cttccccgcc acccgcagcc aactggtacc gcaacaccgc tcgccaaaat     300
tttaatgccg ctgtccatga aaacgccctc aagtggtatg cccttgaacc ggagcagggc     360
aagctggact ttacgatggc ggatcgcatc ctcgcttgga gtgaagccca aggctggccg     420
atgcgggggc acaccctctt ttgggaagtt gagcaattta accccccatg gctgaaaacg     480
ctgccaccag agcaactgcg ggctgccgtc aagaaccatg ccatgacggt gtgtcgccat     540
taccgcgggc gaatcaatga atttgatgtc aataatgaaa tgctccacgg taactttttc     600
cgcagtcgtt tgggaaacgg catagttaaa gagatgttcg agtggtgccg cgagggtaac     660
cccgaggccg tcctttatgt gaacgactac ggcattattg agggcgatcg cctcgacgac     720
tacgtgcagc agattcgcga tttactgggg caaggggttc ccattggtgg cattggcatt     780
caagcccatt tggaatatcc cttggatgca gccaagatga aacgcgccct tgatacccctt    840
gcccaattca acctgcccct aaaaatcact gaagttagtg tcagccttgc cgacgagcag     900
cagcaggcgg agacactgcg ccaaatctac cgcattggtt ttgcccatcc agccgtcaaa     960
```

gagatcctcc tgtggggatt ttgggaaggc aaccactggc gaccccaagc aggactgtac 1020
cgtcgcgact tttccgccaa acctgctgcc gaagcctatc gacaactcct ctttcaggag 1080
tggtggacca ccagcaacgg caaaactaat gccgatgggc gctggcagac ccgcggctat 1140
gcggggcgct atcgcctcac agtaacggcc aacggccaga ccattaaccg cgacattgac 1200
ctaccagact tggagagaac cgtgaccgta caattcccat ga 1242

<210> 332
<211> 413
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(28)

<400> 332
Met Phe Lys Gly Leu Arg Tyr Leu Leu Leu Leu Cys Leu Ser Ala Gly
1 5 10 15
Leu Val Phe Ala Cys Ala Pro Arg Ser Val Thr Ala Pro Pro Asp Gly
20 25 30
Leu Ser Gly Gln Ile Arg Leu Leu Arg Gln Gly Thr Leu Thr Val Leu
35 40 45
Val Gln Asn Ala Gln Gly Gln Pro Ile Ala Asn Ala Lys Val Val Ala
50 55 60
Ala Gln Gln Thr His Ala Phe Pro Phe Gly Val Ala Leu Asp Thr Ala
65 70 75 80
Met Phe Glu Pro Ser Pro Pro Pro Ala Ala Asn Trp Tyr Arg Asn Thr
85 90 95
Ala Arg Gln Asn Phe Asn Ala Ala Val His Glu Asn Ala Leu Lys Trp
100 105 110
Tyr Ala Leu Glu Pro Glu Gln Gly Lys Leu Asp Phe Thr Met Ala Asp
115 120 125
Arg Ile Leu Ala Trp Ser Glu Ala Gln Gly Trp Pro Met Arg Gly His
130 135 140
Thr Leu Phe Trp Glu Val Glu Gln Phe Asn Pro Pro Trp Leu Lys Thr
145 150 155 160
Leu Pro Pro Glu Gln Leu Arg Ala Ala Val Lys Asn His Ala Met Thr
165 170 175
Val Cys Arg His Tyr Arg Gly Arg Ile Asn Glu Phe Asp Val Asn Asn
180 185 190
Glu Met Leu His Gly Asn Phe Phe Arg Ser Arg Leu Gly Asn Gly Ile
195 200 205
Val Lys Glu Met Phe Glu Trp Cys Arg Glu Gly Asn Pro Glu Ala Val
210 215 220
Leu Tyr Val Asn Asp Tyr Gly Ile Ile Glu Gly Asp Arg Leu Asp Asp
225 230 235 240
Tyr Val Gln Gln Ile Arg Asp Leu Leu Gly Gln Gly Val Pro Ile Gly
245 250 255
Gly Ile Gly Ile Gln Ala His Leu Glu Tyr Pro Leu Asp Ala Ala Lys
260 265 270
Met Lys Arg Ala Leu Asp Thr Leu Ala Gln Phe Asn Leu Pro Leu Lys
275 280 285
Ile Thr Glu Val Ser Val Ser Leu Ala Asp Glu Gln Gln Gln Ala Glu
290 295 300
Thr Leu Arg Gln Ile Tyr Arg Ile Gly Phe Ala His Pro Ala Val Lys
305 310 315 320
Glu Ile Leu Leu Trp Gly Phe Trp Glu Gly Asn His Trp Arg Pro Gln
325 330 335
Ala Gly Leu Tyr Arg Arg Asp Phe Ser Ala Lys Pro Ala Ala Glu Ala
340 345 350
Tyr Arg Gln Leu Leu Phe Gln Glu Trp Trp Thr Thr Ser Asn Gly Lys
355 360 365
Thr Asn Ala Asp Gly Arg Trp Gln Thr Arg Gly Tyr Ala Gly Arg Tyr
370 375 380
Arg Leu Thr Val Thr Ala Asn Gly Gln Thr Ile Asn Arg Asp Ile Asp
385 390 395 400
Leu Pro Asp Leu Glu Arg Thr Val Thr Val Gln Phe Pro

405 410

<210> 333
<211> 1152
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 333
```
atgaaaagac aatttattgg acgattgaga cttgtcacta tcctttcaat catagtgatt      60
atgggatgtg cttcaaacaa aagtgatcag aatgttgata acctaaagga cgccttcgac     120
ggtttgttcc ttattggaac tgccatgaat accccccaga tcaccggaca ggatacccgg     180
acgcttgaat tgatcaaaaa acacatgaac tccattgtgg cagaaaacgt tatgaaaagc     240
ggactaatac agcccagcga aggggagttc gacttctcac ttgccgacca gtttgtgcaa     300
ttcggtgttg acaacaacat gcacatcgta gggcataccc ttatctggca ttcgcaggct     360
ccagggtggt tttttgtgga tgaaaacggt aatgatgtta gtcccgaagt tcttaagcaa     420
aggatgaaag accacatcta cacagtagtt ggccgttaca aaggcaaagt gcacggttgg     480
gatgtggtga atgaatgtat cgttgacgat gggtcatggc gcaacagcaa gtttttaccag    540
atcctgggtg aagactttgt aaagtatgcc ttccagtttg cttcagaagc cgacccgaat     600
gctgaattgt attacaacga ttattccatg gcacttcccg gccgccgcca gggagtcgta     660
aacatggtaa aaaatctaca ggcacaaggt attaaaattg acggaatagg aatgcagggc     720
cacctgatga tcgaccatcc atcccttgaa gatttcgaaa ccagtttgct tgcctttgcc     780
gatctgggtg tacatgttat gatcactgag cttgatgtat ctgtacttcc ttttcctacc     840
cgcaacctcg gtgctgatgt atctctaaac atagcttaca acactgaact gaacccctat     900
cccgatggat tgcctgatga tgtggcccaa aaacttcatg atcgctggct cgatatatat     960
cgtttattta taaaacatca cgacaagatc acccgtgtta ctacctgggg tacagccgat    1020
ggtatgtcat ggaagaacaa ctggcccatt cgtggacgca cagactttcc tttattattc    1080
gaccgcgatt ttcaacccaa accggtagta gctgatatta tcaaagaagc attggctgca    1140
aagagaaaat ag                                                        1152
```

<210> 334
<211> 383
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(30)

<400> 334
```
Met Lys Arg Gln Phe Ile Gly Arg Leu Arg Leu Val Thr Ile Leu Ser
 1               5                  10                  15
Ile Ile Val Ile Met Gly Cys Ala Ser Asn Lys Ser Asp Gln Asn Val
            20                  25                  30
Asp Asn Leu Lys Asp Ala Phe Asp Gly Leu Phe Leu Ile Gly Thr Ala
        35                  40                  45
Met Asn Thr Pro Gln Ile Thr Gly Gln Asp Thr Arg Thr Leu Glu Leu
    50                  55                  60
Ile Lys Lys His Met Asn Ser Ile Val Ala Glu Asn Val Met Lys Ser
65                  70                  75                  80
Gly Leu Ile Gln Pro Ser Glu Gly Glu Phe Asp Phe Ser Leu Ala Asp
                85                  90                  95
Gln Phe Val Gln Phe Gly Val Asp Asn Asn Met His Ile Val Gly His
            100                 105                 110
Thr Leu Ile Trp His Ser Gln Ala Pro Gly Trp Phe Phe Val Asp Glu
        115                 120                 125
Asn Gly Asn Asp Val Ser Pro Glu Val Leu Lys Gln Arg Met Lys Asp
    130                 135                 140
His Ile Tyr Thr Val Val Gly Arg Tyr Lys Gly Lys Val His Gly Trp
145                 150                 155                 160
Asp Val Val Asn Glu Cys Ile Val Asp Asp Gly Ser Trp Arg Asn Ser
                165                 170                 175
Lys Phe Tyr Gln Ile Leu Gly Glu Asp Phe Val Lys Tyr Ala Phe Gln
            180                 185                 190
Phe Ala Ser Glu Ala Asp Pro Asn Ala Glu Leu Tyr Tyr Asn Asp Tyr
```

```
            195                     200                     205
Ser Met Ala Leu Pro Gly Arg Arg Gln Gly Val Val Asn Met Val Lys
    210                     215                     220
Asn Leu Gln Ala Gln Gly Ile Lys Ile Asp Gly Ile Gly Met Gln Gly
225                     230                     235                 240
His Leu Met Ile Asp His Pro Ser Leu Glu Asp Phe Glu Thr Ser Leu
                245                     250                     255
Leu Ala Phe Ala Asp Leu Gly Val His Val Met Ile Thr Glu Leu Asp
                260                     265                     270
Val Ser Val Leu Pro Phe Pro Thr Arg Asn Leu Gly Ala Asp Val Ser
        275                     280                     285
Leu Asn Ile Ala Tyr Asn Thr Glu Leu Asn Pro Tyr Pro Asp Gly Leu
    290                     295                     300
Pro Asp Asp Val Ala Gln Lys Leu His Asp Arg Trp Leu Asp Ile Tyr
305                     310                     315                 320
Arg Leu Phe Ile Lys His His Asp Lys Ile Thr Arg Val Thr Thr Trp
                325                     330                     335
Gly Thr Ala Asp Gly Met Ser Trp Lys Asn Asn Trp Pro Ile Arg Gly
            340                     345                     350
Arg Thr Asp Phe Pro Leu Leu Phe Asp Arg Asp Phe Gln Pro Lys Pro
        355                     360                     365
Val Val Ala Asp Ile Ile Lys Glu Ala Leu Ala Ala Lys Arg Lys
    370                     375                     380
```

<210> 335
<211> 849
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 335

```
atgattccaa ggatcgtcct ggccgtccgc atatccccta cttttctcag cccacaaaaa     60
ggggtaataa aaatgataaa gcgggctttt atgataaccc tggcggcctt cctcctcctt    120
ttcgccctaa attccctgcc tatccatgcc ggggccgaag gcggggagga aaagtttacc    180
cccaaggtca tcgtggagca cggtttcgag aataacgact tccacggttg ggtcccccgg    240
ggcggggtcg ggaccatttc cattaccaat gaggcggccc atagcgggtc ctcctgcctg    300
aagatcaccg gccggactca agcttggcat atgccgcggg tggagatcac caagtactta    360
gaaaagggag ctaagtataa gatcgaattg tacgtcaagc tccccgcggg cacctcgccg    420
cgcaagttcc agctggcggt tctcacccgt tatctcgaag gcaaccagac cagggacaaa    480
gaggactcca tctcggacga ggtggaggtg accgccgata cctggaccaa ggtcgagggc    540
gagtacgtct tcgacccggc ggccatcggc gcctacgtct acccctacct caagggcgac    600
cccgcagggg cctatgcccc ctatctcatc gatgatttca agatcaccac gatcgccccc    660
gcccccaaga agaccgccgc taccgccgcg gcaaaagagg cagaagagcc cttaatcgag    720
accgatatac catccttaaa agacgtctgc gcgtcctact tcgagatcgg cgcggccatc    780
gagccatatg agttattctc caagccccac gatcagctgc tccggaaaca tttcaacacc    840
gttggttga                                                            849
```

<210> 336
<211> 282
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(50)

<400> 336

```
Met Ile Pro Arg Ile Val Leu Ala Val Arg Ile Ser Pro Thr Phe Leu
 1               5                  10                  15
Ser Pro Gln Lys Gly Val Ile Lys Met Ile Lys Arg Ala Phe Met Ile
            20                  25                  30
Thr Leu Ala Ala Phe Leu Leu Leu Phe Ala Leu Asn Ser Leu Pro Ile
        35                  40                  45
His Ala Gly Ala Glu Gly Gly Glu Glu Lys Phe Thr Pro Lys Val Ile
    50                  55                  60
```

Val Glu His Gly Phe Glu Asn Asn Asp Phe His Gly Trp Val Pro Arg
65 70 75 80
Gly Gly Val Gly Thr Ile Ser Ile Thr Asn Glu Ala Ala His Ser Gly
85 90 95
Ser Ser Cys Leu Lys Ile Thr Gly Arg Thr Gln Ala Trp His Met Pro
100 105 110
Arg Val Glu Ile Thr Lys Tyr Leu Glu Lys Gly Ala Lys Tyr Lys Ile
115 120 125
Glu Leu Tyr Val Lys Leu Pro Ala Gly Thr Ser Pro Arg Lys Phe Gln
130 135 140
Leu Ala Val Leu Thr Arg Tyr Leu Glu Gly Asn Gln Thr Arg Asp Lys
145 150 155 160
Glu Asp Ser Ile Ser Asp Glu Val Glu Val Thr Ala Asp Thr Trp Thr
165 170 175
Lys Val Glu Gly Glu Tyr Val Phe Asp Pro Ala Ala Ile Gly Ala Tyr
180 185 190
Val Tyr Pro Tyr Leu Lys Gly Asp Pro Ala Gly Ala Tyr Ala Pro Tyr
195 200 205
Leu Ile Asp Asp Phe Lys Ile Thr Thr Ile Ala Pro Ala Pro Lys Lys
210 215 220
Thr Ala Ala Thr Ala Ala Ala Lys Glu Ala Glu Glu Pro Leu Ile Glu
225 230 235 240
Thr Asp Ile Pro Ser Leu Lys Asp Val Cys Ala Ser Tyr Phe Glu Ile
245 250 255
Gly Ala Ala Ile Glu Pro Tyr Glu Leu Phe Ser Lys Pro His Asp Gln
260 265 270
Leu Leu Arg Lys His Phe Asn Thr Val Gly
275 280

<210> 337
<211> 870
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 337
atgaagcccg acagcgtgct ggatgtaaac gccagcaaaa agctctccgc ccaggatgaa 60
accgccgtgg cggtgaaatt cgacgccgcc cgcgccctgc tggattttgt caaggaaaac 120
gggctcaagg tgcacggtca cgtgctggta tggcattccc agacgccgga agccttcttc 180
cacgagggct atgatgccgc caggccctac gtggggcggg acgtgatgct ggggcgcatg 240
aaaaactaca tcaaggccgt gtttgaatac actgagacca attaccccgg cgtcatcgtc 300
tcctgggacg tagtgaacga agccatcgac gacggcacca acaagctgcg ccagtccaac 360
tggttcaaaa ccgttggcga ggatttcgtg ctccgcgcct ttgaatacgc caggaaatac 420
gcccccgaag gcacgctgct ttattacaac gattacaaca ccgccatgcc cggcaagctg 480
aacggcatcg ccaatctgct caaagccctc atcgccgagg gcaacatcga cggctacggc 540
ttccaaatgc accacagcgt gggcttcccc tccatggaaa tgatttccgc gtctgtggag 600
cgcatcgccg gcatgggcct taagctccgg gtcagcgaat tggacgtggg caccgacgga 660
aacaccgaaa gcagcttcac caagcaggcg gaaaaatacg ccgccatcat gcggctgctg 720
ctggattata aggatcaaat ggaagccgtg caggtatggg gcctcaccga cgatatgagc 780
tggcgccggg ccaactatcc cctgctcttc gacggcaaat tcaaccccaa gcccgccttc 840
tacgccgtgg ctgacccata cgcaaaataa 870

<210> 338
<211> 289
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 338
Met Lys Pro Asp Ser Val Leu Asp Val Asn Ala Ser Lys Lys Leu Ser
1 5 10 15
Ala Gln Asp Glu Thr Ala Val Ala Val Lys Phe Asp Ala Ala Arg Ala
20 25 30
Leu Leu Asp Phe Val Lys Glu Asn Gly Leu Lys Val His Gly His Val
35 40 45

Leu Val Trp His Ser Gln Thr Pro Glu Ala Phe Phe His Glu Gly Tyr
50 55 60
Asp Ala Ala Arg Pro Tyr Val Gly Arg Asp Val Met Leu Gly Arg Met
65 70 75 80
Lys Asn Tyr Ile Lys Ala Val Phe Glu Tyr Thr Glu Thr Asn Tyr Pro
85 90 95
Gly Val Ile Val Ser Trp Asp Val Val Asn Glu Ala Ile Asp Asp Gly
100 105 110
Thr Asn Lys Leu Arg Gln Ser Asn Trp Phe Lys Thr Val Gly Glu Asp
115 120 125
Phe Val Leu Arg Ala Phe Glu Tyr Ala Arg Lys Tyr Ala Pro Glu Gly
130 135 140
Thr Leu Leu Tyr Tyr Asn Asp Tyr Asn Thr Ala Met Pro Gly Lys Leu
145 150 155 160
Asn Gly Ile Ala Asn Leu Leu Lys Ala Leu Ile Ala Glu Gly Asn Ile
165 170 175
Asp Gly Tyr Gly Phe Gln Met His His Ser Val Gly Phe Pro Ser Met
180 185 190
Glu Met Ile Ser Ala Ser Val Glu Arg Ile Ala Gly Met Gly Leu Lys
195 200 205
Leu Arg Val Ser Glu Leu Asp Val Gly Thr Asp Gly Asn Thr Glu Ser
210 215 220
Ser Phe Thr Lys Gln Ala Glu Lys Tyr Ala Ala Ile Met Arg Leu Leu
225 230 235 240
Leu Asp Tyr Lys Asp Gln Met Glu Ala Val Gln Val Trp Gly Leu Thr
245 250 255
Asp Asp Met Ser Trp Arg Arg Ala Asn Tyr Pro Leu Leu Phe Asp Gly
260 265 270
Lys Phe Asn Pro Lys Pro Ala Phe Tyr Ala Val Ala Asp Pro Tyr Ala
275 280 285
Lys

<210> 339
<211> 1125
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 339
atgcctatgg agcgacccac tttcttgcgg tttcttgcct tttttcttct ttttaccatg 60
attttcgccg ccggagggtg ccgacccctt gccccttcac ggatggagat cgagacggat 120
atcccctccc tcaaggaagt cgccgcttct tatttcgaga tcggcgcggc cgtcgagccg 180
tatcagttat cctctccacc ccacgatgcc cttctgcgga aacattttaa ctgcctcgtg 240
gcggagaacg tcatgaagcc cgcctccatc cagccatcgg aggggtattt caactggacc 300
gaagcggaca agatcgtgaa ctacgccaaa gcccacggga tgaagctccg cttccatacc 360
ctcgtctggc ataatcaggt cccggattgg ttcttcgcgg gtaacgacaa aacccgcctt 420
ttgcagcgct tggagaatca tatccggact atcattaaaa gatatggcga taaggtcgac 480
tattgggacg tggtgaacga agtaatagac gacaacggcg gtatgcgaaa cagcaagtgg 540
taccagatca ccgggaagga ctacatcaag accgccttcc gggtggcaga cgacgagctc 600
aggaagaatg ggtggaggaa agaaggtcgt cagctctata tcaacgacta caacacccat 660
aacccaacga agagagaggg gatctggcgc ttgatccaag agctccgggc ggaagggatt 720
cccgtcgacg gagtaggcca ccagacgcat atcaatatcg aatggccgcc cgtaagccag 780
atcgtggaat cgatccgctt cttcggcgaa aaaggcctcg ataaccaggt gaccgagctg 840
gatgtgagca tctatacgaa tgacaaggat tcacatggta gttatcaggc catccccgcag 900
gaagtcttca tcaagcaggg taatcgctac aaggaactct ttgaagggct aaaaagtgta 960
aaaaactacc tcagcaacgt caccttctgg ggcatggcgg acgatcatac ctggctgaac 1020
cgttggccca tcgaacggcc cgatgctcct cttcctttcg atatctatct caaggccaag 1080
ccggcgtatt gggggatcgt ggatgctttg aagctttcgc ggtga 1125

<210> 340
<211> 374
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(23)

<400> 340
Met Pro Met Glu Arg Pro Thr Phe Leu Arg Phe Leu Ala Phe Phe Leu
1 5 10 15
Leu Phe Thr Met Ile Phe Ala Ala Gly Gly Cys Arg Pro Leu Ala Pro
20 25 30
Ser Arg Met Glu Ile Glu Thr Asp Ile Pro Ser Leu Lys Glu Val Ala
35 40 45
Ala Ser Tyr Phe Glu Ile Gly Ala Ala Val Glu Pro Tyr Gln Leu Ser
50 55 60
Ser Pro Pro His Asp Ala Leu Leu Arg Lys His Phe Asn Cys Leu Val
65 70 75 80
Ala Glu Asn Val Met Lys Pro Ala Ser Ile Gln Pro Ser Glu Gly Tyr
85 90 95
Phe Asn Trp Thr Glu Ala Asp Lys Ile Val Asn Tyr Ala Lys Ala His
100 105 110
Gly Met Lys Leu Arg Phe His Thr Leu Val Trp His Asn Gln Val Pro
115 120 125
Asp Trp Phe Phe Ala Gly Asn Asp Lys Thr Arg Leu Leu Gln Arg Leu
130 135 140
Glu Asn His Ile Arg Thr Ile Ile Lys Arg Tyr Gly Asp Lys Val Asp
145 150 155 160
Tyr Trp Asp Val Val Asn Glu Val Ile Asp Asp Asn Gly Gly Met Arg
165 170 175
Asn Ser Lys Trp Tyr Gln Ile Thr Gly Lys Asp Tyr Ile Lys Thr Ala
180 185 190
Phe Arg Val Ala Asp Asp Glu Leu Arg Lys Asn Gly Trp Arg Lys Glu
195 200 205
Gly Arg Gln Leu Tyr Ile Asn Asp Tyr Asn Thr His Asn Pro Thr Lys
210 215 220
Arg Glu Gly Ile Trp Arg Leu Ile Gln Glu Leu Arg Ala Glu Gly Ile
225 230 235 240
Pro Val Asp Gly Val Gly His Gln Thr His Ile Asn Ile Glu Trp Pro
245 250 255
Pro Val Ser Gln Ile Val Glu Ser Ile Arg Phe Phe Gly Glu Lys Gly
260 265 270
Leu Asp Asn Gln Val Thr Glu Leu Asp Val Ser Ile Tyr Thr Asn Asp
275 280 285
Lys Asp Ser His Gly Ser Tyr Gln Ala Ile Pro Gln Glu Val Phe Ile
290 295 300
Lys Gln Gly Asn Arg Tyr Lys Glu Leu Phe Glu Gly Leu Lys Ser Val
305 310 315 320
Lys Asn Tyr Leu Ser Asn Val Thr Phe Trp Gly Met Ala Asp Asp His
325 330 335
Thr Trp Leu Asn Arg Trp Pro Ile Glu Arg Pro Asp Ala Pro Leu Pro
340 345 350
Phe Asp Ile Tyr Leu Lys Ala Lys Pro Ala Tyr Trp Gly Ile Val Asp
355 360 365
Ala Leu Lys Leu Ser Arg
370

<210> 341
<211> 1347
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 341
atgacaatta acaacaaaac tacagcgagt cctagtattc ccagcaccca caattccctc 60
ccgtcgcttc gcacactgtt taccaccagc ctgctcacgc tggccctgac cgcctgcggt 120
ggttcttcca gcagcgacaa ggacccttca agctccagct ccagtgaatc atcaagttcc 180
agcgaatcct cgagctcagc ttccagcgaa tcctcgagca gtgagtccag cagtagctct 240
tccgcgggcc atttctccat cgagccggac ttccagctct acagcctggc caacttcccg 300
gtgggcgtgg cggtctccgc cgccaacgag aacgacagca tcttcaacag tccggatgcc 360

gccgaacgtc aggccgttat tattgagcac ttctctcagc tcaccgccgg caacatcatg 420
aaaatgagct acctgcagcc gagtcaaggc aacttcacct tcgatgacgc cgacgagttg 480
gttaacttcg cccaagccaa tggcatgacc gtacacggcc actccaccat ctggcacgcg 540
gactaccaag taccgaactt catgagaaac tttgaaggtg accaggagga atgggcagaa 600
attctgaccg atcacgtcac taccatcatc gagcacttcc ccgacgatgt ggtcatcagc 660
tgggacgtgg tgaacgaggc tgtcgatcaa ggcacggcga acggctggcg ccattcggtg 720
ttctacaatg cattcgacgc cccggaagaa ggcgacattc ccgaatacat caaagtcgct 780
ttccgcgccg cgcgcgaggc tgacgccaac gtagacctct actacaacga ctacgacaat 840
accgccaatg cccagcgcct ggccaaaaca ctgcaaattg ccgaggtact ggacgccgaa 900
ggcaccattg acggcgtcgg tttccagatg cacgcctaca tggattaccc gagcctgacc 960
cattttgaaa acgccttccg gcaagtcgtc gacctggggc tcaaagtgaa agttaccgag 1020
ctggacgtat ccgtagtcaa cccctacggc ggcgaagcac ctccacaacc ggaatacgac 1080
aaagaactgg ccggcgcgca aaaactgcgc ttctgccaaa tcgccgaagt ttacatgaac 1140
actgtacccg aggagttacg cggtggcttc accgtctggg gcctgaccga tgatgaaagt 1200
tggctgatgc aacagttcag aaacgccacc ggcgccgact acgacgacgt ctggccgtta 1260
ctgttcaatg ccgacaaatc cgccaaaccg gcactgcaag gcgtggccga cgcctttacc 1320
ggacaaacct gcacctccga gttctaa 1347

<210> 342
<211> 448
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(45)

<400> 342
Met Thr Ile Asn Asn Lys Thr Thr Ala Ser Pro Ser Ile Pro Ser Thr
1 5 10 15
His Asn Ser Leu Pro Ser Leu Arg Thr Leu Phe Thr Thr Ser Leu Leu
20 25 30
Thr Leu Ala Leu Thr Ala Cys Gly Gly Ser Ser Ser Ser Asp Lys Asp
35 40 45
Pro Ser Ser Ser Ser Ser Ser Glu Ser Ser Ser Ser Ser Glu Ser Ser
50 55 60
Ser Ser Ala Ser Ser Glu Ser Ser Ser Ser Glu Ser Ser Ser Ser Ser
65 70 75 80
Ser Ala Gly His Phe Ser Ile Glu Pro Asp Phe Gln Leu Tyr Ser Leu
85 90 95
Ala Asn Phe Pro Val Gly Val Ala Val Ser Ala Ala Asn Glu Asn Asp
100 105 110
Ser Ile Phe Asn Ser Pro Asp Ala Ala Glu Arg Gln Ala Val Ile Ile
115 120 125
Glu His Phe Ser Gln Leu Thr Ala Gly Asn Ile Met Lys Met Ser Tyr
130 135 140
Leu Gln Pro Ser Gln Gly Asn Phe Thr Phe Asp Asp Ala Asp Glu Leu
145 150 155 160
Val Asn Phe Ala Gln Ala Asn Gly Met Thr Val His Gly His Ser Thr
165 170 175
Ile Trp His Ala Asp Tyr Gln Val Pro Asn Phe Met Arg Asn Phe Glu
180 185 190
Gly Asp Gln Glu Glu Trp Ala Glu Ile Leu Thr Asp His Val Thr Thr
195 200 205
Ile Ile Glu His Phe Pro Asp Asp Val Val Ile Ser Trp Asp Val Val
210 215 220
Asn Glu Ala Val Asp Gln Gly Thr Ala Asn Gly Trp Arg His Ser Val
225 230 235 240
Phe Tyr Asn Ala Phe Asp Ala Pro Glu Glu Gly Asp Ile Pro Glu Tyr
245 250 255
Ile Lys Val Ala Phe Arg Ala Ala Arg Glu Ala Asp Ala Asn Val Asp
260 265 270
Leu Tyr Tyr Asn Asp Tyr Asp Asn Thr Ala Asn Ala Gln Arg Leu Ala
275 280 285
Lys Thr Leu Gln Ile Ala Glu Val Leu Asp Ala Glu Gly Thr Ile Asp
290 295 300
Gly Val Gly Phe Gln Met His Ala Tyr Met Asp Tyr Pro Ser Leu Thr

305 310 315 320
His Phe Glu Asn Ala Phe Arg Gln Val Val Asp Leu Gly Leu Lys Val
325 330 335
Lys Val Thr Glu Leu Asp Val Ser Val Val Asn Pro Tyr Gly Gly Glu
340 345 350
Ala Pro Pro Gln Pro Glu Tyr Asp Lys Glu Leu Ala Gly Ala Gln Lys
355 360 365
Leu Arg Phe Cys Gln Ile Ala Glu Val Tyr Met Asn Thr Val Pro Glu
370 375 380
Glu Leu Arg Gly Gly Phe Thr Val Trp Gly Leu Thr Asp Asp Glu Ser
385 390 395 400
Trp Leu Met Gln Gln Phe Arg Asn Ala Thr Gly Ala Asp Tyr Asp Asp
405 410 415
Val Trp Pro Leu Leu Phe Asn Ala Asp Lys Ser Ala Lys Pro Ala Leu
420 425 430
Gln Gly Val Ala Asp Ala Phe Thr Gly Gln Thr Cys Thr Ser Glu Phe
435 440 445

<210> 343
<211> 2217
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 343
atggtggagc acgaagctga gcttcatgat taccgcgaac gaatatgcga agttgcttgg 60
caattcgctg ggcctggagg gcgagaaggc aaagcggatt ttgcgggaaa tcaacaactg 120
gctgttttga agatgaaatt atcgagaggg agggggcatg gcgttttgaa acgagcaggt 180
ctgattgggc ttattgcagc gatattgggc tgcgcggcgc tgcttatgca caatgagatc 240
tcatccctgg gaattcagct gagatcatgg ctcagaggga gcgacaatgt gaacgctagc 300
tgggaaaagg attggaagac ggctgctaac gagcaaatcg agcagctccg caagcgcaat 360
gtggagatcg aggtcgtcga tctgaacgga aacccgctgc ctggggctac cgttcgcgcg 420
gttcagcgca cgcatcagtt tggcttcggc accgccatca accgaacggc gttgagcaat 480
ccggtgtacg ccgattttgt caaaaaccgt ttcgaatggg tgaccttcga gaacgaggcc 540
aagtggctct ggaatgaggc cgtacaaggg cgggtctatt atcgggaggc cgatcagctg 600
ctcgaatttg ccaggcaaaa cgggctgaag gtgcgcggac ataatctgtt ctgggaggcg 660
gagaaatatc agccgcagtg ggtgaagagt ctgacgggcg ctgcgctgaa ggaagcgatc 720
gataaccggc tgaacagcgc cgtcctgcat tttaagggca attttctgca ctgggacgtc 780
aacaacgaaa tgtttcacgg cagcttcttc aaggatcgcc tgggggaaga aatctggacc 840
tatatgtata agcgaacccg ggaactcgat cccggcgtca agctgttcgt caacgattac 900
aattttatcg agtacccgcc ggagcgggat tataaccagg tcattcaagc gctcatcgat 960
cgggggatgc cgattgacgg catcggcgcg caagggcatt ttaacggagt catcgatccc 1020
ttgttcgtta agggaagact ggataagctg gctgagctga atctgccgat ctggattacc 1080
gaattcgatt ccacgcataa ggacgagaga gtccgtgccg ataatctgga gaagatgtat 1140
cggctggcgt tcgcccatcc ggcggtcgaa gggattgtca tgtggggctt ctgggcgggc 1200
tcccattgga agggcactga cggcgcgatc gtgaatcaag actggacgct caatgccgcc 1260
ggacagcgat accagcagct tatggatgaa tggacgacgg tcgtcgaagg cacgaccgat 1320
cagcgcggca tgttttcgtt ccggggggttc cacggaacct acgatatgct ggtcgattac 1380
cctggagcgg cggctgtgaa gcagtccttt accttggagc ccggctctgg caatgcgaag 1440
ctgcacattc cgttcgacgt tcaggacaag tccatcccgg aggctcctgc caagctcagc 1500
gccgctgccg cggattccca ggttatgctg agctggagca aggtcaacgg ggcaaccggc 1560
tatacggtta aaagcgcggt cagcgccgac ggtccctata cgccgattgc ccatcagctg 1620
ctcaccgaga ccttcacgca catcggtcta gtgaaccgga aagattatta ttacgtggtg 1680
agcgccagca accatctagg tgagagcccg gattccgccc cgatccgggc cactccgcgt 1740
gccgcgggcg agttacaaac gaatctcgtg cttcagtacc gctccgctga tggagataac 1800
aactatcaaa tgaagcctca gttcacgatc aagaacgcag gcaaagtgcc catcccgtta 1860
agcgagctga cgatccgcta ctatttcacg ccggagagca cgcagccggt ggataccagg 1920
atcgactggg cccaattcgg agcagagcat gtccagacga cggtcgttcc gccatccgat 1980
gccgcggcgc acgcctatgt cgagctcagc ttcctggagt cggcaggggc catcccttcc 2040
gatacgacat taggcaatat tcagctgcgc atctttaaca gcgatggctc ttcgttcgat 2100
aaaacgaacg attattcctt cgacccgacg aaaaaggctt atacggcgtg ggagaaggtc 2160
acgctttatc ggaacgggga actggtttgg gggatagagc cttggggcgc gaagtaa 2217

<210> 344
<211> 738
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 344
Met Val Glu His Glu Ala Glu Leu His Asp Tyr Arg Glu Arg Ile Cys
1   5   10   15
Glu Val Ala Trp Gln Phe Ala Gly Pro Gly Gly Arg Glu Gly Lys Ala
            20   25   30
Asp Phe Ala Gly Asn Gln Gln Leu Ala Val Leu Lys Met Lys Leu Ser
        35   40   45
Arg Gly Arg Gly His Gly Val Leu Lys Arg Ala Gly Leu Ile Gly Leu
    50   55   60
Ile Ala Ala Ile Leu Gly Cys Ala Ala Leu Leu Met His Asn Glu Ile
65   70   75   80
Ser Ser Leu Gly Ile Gln Leu Arg Ser Trp Leu Arg Gly Ser Asp Asn
                85   90   95
Val Asn Ala Ser Trp Glu Lys Asp Trp Lys Thr Ala Ala Asn Glu Gln
            100   105   110
Ile Glu Gln Leu Arg Lys Arg Asn Val Glu Ile Glu Val Val Asp Leu
        115   120   125
Asn Gly Asn Pro Leu Pro Gly Ala Thr Val Arg Ala Val Gln Arg Thr
    130   135   140
His Gln Phe Gly Phe Gly Thr Ala Ile Asn Arg Thr Ala Leu Ser Asn
145   150   155   160
Pro Val Tyr Ala Asp Phe Val Lys Asn Arg Phe Glu Trp Val Thr Phe
                165   170   175
Glu Asn Glu Ala Lys Trp Leu Trp Asn Glu Ala Val Gln Gly Arg Val
            180   185   190
Tyr Tyr Arg Glu Ala Asp Gln Leu Leu Glu Phe Ala Arg Gln Asn Gly
        195   200   205
Leu Lys Val Arg Gly His Asn Leu Phe Trp Glu Ala Glu Lys Tyr Gln
    210   215   220
Pro Gln Trp Val Lys Ser Leu Thr Gly Ala Ala Leu Lys Glu Ala Ile
225   230   235   240
Asp Asn Arg Leu Asn Ser Ala Val Leu His Phe Lys Gly Asn Phe Leu
                245   250   255
His Trp Asp Val Asn Asn Glu Met Phe His Gly Ser Phe Phe Lys Asp
            260   265   270
Arg Leu Gly Glu Glu Ile Trp Thr Tyr Met Tyr Lys Arg Thr Arg Glu
        275   280   285
Leu Asp Pro Gly Val Lys Leu Phe Val Asn Asp Tyr Asn Phe Ile Glu
    290   295   300
Tyr Pro Pro Glu Arg Asp Tyr Asn Gln Val Ile Gln Ala Leu Ile Asp
305   310   315   320
Arg Gly Met Pro Ile Asp Gly Ile Gly Ala Gln Gly His Phe Asn Gly
                325   330   335
Val Ile Asp Pro Leu Phe Val Lys Gly Arg Leu Asp Lys Leu Ala Glu
            340   345   350
Leu Asn Leu Pro Ile Trp Ile Thr Glu Phe Asp Ser Thr His Lys Asp
        355   360   365
Glu Arg Val Arg Ala Asp Asn Leu Glu Lys Met Tyr Arg Leu Ala Phe
    370   375   380
Ala His Pro Ala Val Glu Gly Ile Val Met Trp Gly Phe Trp Ala Gly
385   390   395   400
Ser His Trp Lys Gly Thr Asp Gly Ala Ile Val Asn Gln Asp Trp Thr
                405   410   415
Leu Asn Ala Ala Gly Gln Arg Tyr Gln Gln Leu Met Asp Glu Trp Thr
            420   425   430
Thr Val Val Glu Gly Thr Thr Asp Gln Arg Gly Met Phe Ser Phe Arg
        435   440   445
Gly Phe His Gly Thr Tyr Asp Met Leu Val Asp Tyr Pro Gly Ala Ala
    450   455   460
Ala Val Lys Gln Ser Phe Thr Leu Glu Pro Gly Ser Gly Asn Ala Lys
465   470   475   480
Leu His Ile Pro Phe Asp Val Gln Asp Lys Ser Ile Pro Glu Ala Pro
                485   490   495
Ala Lys Leu Ser Ala Ala Ala Ala Asp Ser Gln Val Met Leu Ser Trp
            500   505   510

Ser Lys Val Asn Gly Ala Thr Gly Tyr Thr Val Lys Ser Ala Val Ser
        515   520   525
Ala Asp Gly Pro Tyr Thr Pro Ile Ala His Gln Leu Leu Thr Glu Thr
    530   535   540
Phe Thr His Ile Gly Leu Val Asn Arg Lys Asp Tyr Tyr Tyr Val Val
545   550   555   560
Ser Ala Ser Asn His Leu Gly Glu Ser Pro Asp Ser Ala Pro Ile Arg
                565   570   575
Ala Thr Pro Arg Ala Ala Gly Glu Leu Gln Thr Asn Leu Val Leu Gln
            580   585   590
Tyr Arg Ser Ala Asp Gly Asp Asn Asn Tyr Gln Met Lys Pro Gln Phe
        595   600   605
Thr Ile Lys Asn Ala Gly Lys Val Pro Ile Pro Leu Ser Glu Leu Thr
    610   615   620
Ile Arg Tyr Tyr Phe Thr Pro Glu Ser Thr Gln Pro Val Asp Thr Arg
625   630   635   640
Ile Asp Trp Ala Gln Phe Gly Ala Glu His Val Gln Thr Thr Val Val
                645   650   655
Pro Pro Ser Asp Ala Ala Ala His Ala Tyr Val Glu Leu Ser Phe Leu
            660   665   670
Glu Ser Ala Gly Ala Ile Pro Ser Asp Thr Thr Leu Gly Asn Ile Gln
        675   680   685
Leu Arg Ile Phe Asn Ser Asp Gly Ser Ser Phe Asp Lys Thr Asn Asp
    690   695   700
Tyr Ser Phe Asp Pro Thr Lys Lys Ala Tyr Thr Ala Trp Glu Lys Val
705   710   715   720
Thr Leu Tyr Arg Asn Gly Glu Leu Val Trp Gly Ile Glu Pro Trp Gly
                725   730   735
Ala Lys

<210> 345
<211> 849
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 345
atgaagatga cctacatgca tccggctgaa gatacttact cgtttggtca agcggatcag 60
ttggtcaact gggcgaaagc gaatggtatt ggcgtgcacg gccacactct ggtttggcac 120
tccgaatacc aggtacccaa ttggatgaaa aattactctg gtgatgcaac tgcattccaa 180
accatgctca acacccatgt gaaaactgtg gctgagcatt ttgctggcga actggacagc 240
tgggacgttg tgaatgaagt gctggagccg ggctccaatg gttgctggcg tgaaaactct 300
ctgttctacc agaagcttgg caaagacttt gtcgcgaacg cattccgtgc agctcgcgag 360
ggcgatccca atgcagactt gtattacaac gattactcga ctgaaaatgg tgtaacttcc 420
gatgagaagt tcagttgttt gttggaacta gtcgatgagc ttctggaagc ggacgtgccg 480
attacaggtg ttggtttcca aatgcacgtg caggcgacgt ggcctagcaa tgccaacatc 540
ggcaaggcat tcaaagccat cgcggatcgc ggtctgaaag ttaaaatttc tgagctcgat 600
gttcctgtta acaaccctta cggaaccact aatttcccgc aatacagcag ttttaccgcg 660
gaagccgccg agctgcagaa gcagcgctac aagggcatta tgcaagcgta ccttgataac 720
gtaccggcca acctgcgtgg tggtttcacc gtgtggggcg tttgggatgg cgatagctgg 780
atcatgacgt tcagccagta caccaacgct aacgccaacg actggccact gttgttcacc 840
gggccgtag 849

<210> 346
<211> 282
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 346
Met Lys Met Thr Tyr Met His Pro Ala Glu Asp Thr Tyr Ser Phe Gly
1   5   10   15
Gln Ala Asp Gln Leu Val Asn Trp Ala Lys Ala Asn Gly Ile Gly Val
            20   25   30

His Gly His Thr Leu Val Trp His Ser Glu Tyr Gln Val Pro Asn Trp
        35   40   45
Met Lys Asn Tyr Ser Gly Asp Ala Thr Ala Phe Gln Thr Met Leu Asn
    50   55   60
Thr His Val Lys Thr Val Ala Glu His Phe Ala Gly Glu Leu Asp Ser
65   70   75   80
Trp Asp Val Val Asn Glu Val Leu Glu Pro Gly Ser Asn Gly Cys Trp
                85   90   95
Arg Glu Asn Ser Leu Phe Tyr Gln Lys Leu Gly Lys Asp Phe Val Ala
            100   105   110
Asn Ala Phe Arg Ala Ala Arg Glu Gly Asp Pro Asn Ala Asp Leu Tyr
        115   120   125
Tyr Asn Asp Tyr Ser Thr Glu Asn Gly Val Thr Ser Asp Glu Lys Phe
    130   135   140
Ser Cys Leu Leu Glu Leu Val Asp Glu Leu Leu Glu Ala Asp Val Pro
145   150   155   160
Ile Thr Gly Val Gly Phe Gln Met His Val Gln Ala Thr Trp Pro Ser
                165   170   175
Asn Ala Asn Ile Gly Lys Ala Phe Lys Ala Ile Ala Asp Arg Gly Leu
            180   185   190
Lys Val Lys Ile Ser Glu Leu Asp Val Pro Val Asn Asn Pro Tyr Gly
        195   200   205
Thr Thr Asn Phe Pro Gln Tyr Ser Ser Phe Thr Ala Glu Ala Ala Glu
    210   215   220
Leu Gln Lys Gln Arg Tyr Lys Gly Ile Met Gln Ala Tyr Leu Asp Asn
225   230   235   240
Val Pro Ala Asn Leu Arg Gly Gly Phe Thr Val Trp Gly Val Trp Asp
                245   250   255
Gly Asp Ser Trp Ile Met Thr Phe Ser Gln Tyr Thr Asn Ala Asn Ala
            260   265   270
Asn Asp Trp Pro Leu Leu Phe Thr Gly Pro
        275   280

<210> 347
<211> 1794
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 347
atgcccgttt tgttcgccct gtttcttgtt gcctcgtcct gcgcggcgca gtcgctggcc 60
gggccggttt ccctgcttgg cggagatgcg ggcgcggcgt tccgctatac cgggccatcg 120
gcgggcgcgg cgagcggctc ggccgaatgg gtggcggtgg agaacatgcc gttcacgcac 180
gcctggcggc tgcgcacgaa tccgctgccg gagagcggcg gcaacgaatg ggacctgcgc 240
atccgcgccc gcggagcggc ggctgtttcg gcaggggaca agatcctggc cgagttctgg 300
atgcgctgcg tggagcccga aaacggcgac tgcattctgc gcctgaacgt ggagcgcgac 360
gggtcgccgt ggaccaaatc catcagcaac ccctacccgg tgggccggga gtggcggcgg 420
ttccgcgtgc tgttcgagat gcgggagagc tacgccgccg gcggctacat gatcgatttc 480
tggatgggcc agcaggtgca gacggcggaa gtgggcggga tttccctgct gaattacggt 540
ccgcaggcca cggccgagca gcttggcctg gaccggtttt atgagggcgc ggcggcggac 600
gccgcgtggc ggcaggcggc cgagcagcgg atcgaggaga tccggaaagc gggcatgatc 660
atcgtggcgg tgacgccgga cggcgagccg atcgagggcg ctgaaatccg ggcgaagctg 720
aagcggcacg cgttcgggtg gggcacggct gtggcggcat cacggcttct ggggacggga 780
acggacagcg agcgctaccg caacttcatc cgcgagaact tcaacatggc ggtgctcgag 840
aacgacctga aatggggccc gttcgaagag aaccgcaacc gcgcgatgaa cgcgctgcgc 900
tggctgcatg agaacgggat cacgtggatc cgcgggcaca atctcgtctg gccgggctgg 960
cggtggatgc cgaacgacgt gcgcaacctg gcgaacaatc ccgaggcgct gcggcagcgg 1020
attctggacc gcatccggga cacggccacg gccacgcgcg ggctggtggt gcactgggac 1080
gtcgtcaacg agccggtggc cgagcgcgac gtgctgaaca ttctgggcga cgaggtgatg 1140
gcggactggt tccgcgccgc gaaggagtgc gatcccgagg cgaggatgtt catcaatgag 1200
tacgacattc tggcggcgaa cgggggccaat ctgcggaagc agaacgcgta ttaccgcatg 1260
atcgagatgc tgttgaagct cgaggcgccg gtggagggca tcggcttcca gggccacttc 1320
gacacggcca cgccgccgga gcggatgctg gagatcatga accggtacgc ccggctcggg 1380
ctgccgatcg ccatcaccga gtacgatttc gccacggcgg acgaggagct gcaggcgcag 1440
ttcacgcgcg acctgatgat tctcgccttc agccatccgg cggtttcgga cttcctgatg 1500
tggggcttct gggaagggag ccactggaag ccgctgggcg ccatgatccg gcgcgactgg 1560
agcgagaagc cgatgtaccg cgtctggcgc gagctgatct tcgagcgctg gcagacggat 1620

gaaacaggcg tgacgccgga gcacggtgcc atctacgtgc ggggcttcaa gggcgactac 1680
gagatcacgg tgaaggcggg cgggcaggaa gtccgggtgc cgtacacgct gaaagaagac 1740
ggccaggtgc tgtgggtgac ggtgggcggg gcttctgaag agcgcgtgca gtaa 1794

<210> 348
<211> 597
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(20)

<400> 348
Met Pro Val Leu Phe Ala Leu Phe Leu Val Ala Ser Ser Cys Ala Ala
1 5 10 15
Gln Ser Leu Ala Gly Pro Val Ser Leu Leu Gly Gly Asp Ala Gly Ala
20 25 30
Ala Phe Arg Tyr Thr Gly Pro Ser Ala Gly Ala Ala Ser Gly Ser Ala
35 40 45
Glu Trp Val Ala Val Glu Asn Met Pro Phe Thr His Ala Trp Arg Leu
50 55 60
Arg Thr Asn Pro Leu Pro Glu Ser Gly Gly Asn Glu Trp Asp Leu Arg
65 70 75 80
Ile Arg Ala Arg Gly Ala Ala Ala Val Ser Ala Gly Asp Lys Ile Leu
85 90 95
Ala Glu Phe Trp Met Arg Cys Val Glu Pro Glu Asn Gly Asp Cys Ile
100 105 110
Leu Arg Leu Asn Val Glu Arg Asp Gly Ser Pro Trp Thr Lys Ser Ile
115 120 125
Ser Asn Pro Tyr Pro Val Gly Arg Glu Trp Arg Arg Phe Arg Val Leu
130 135 140
Phe Glu Met Arg Glu Ser Tyr Ala Ala Gly Gly Tyr Met Ile Asp Phe
145 150 155 160
Trp Met Gly Gln Gln Val Gln Thr Ala Glu Val Gly Gly Ile Ser Leu
165 170 175
Leu Asn Tyr Gly Pro Gln Ala Thr Ala Glu Gln Leu Gly Leu Asp Arg
180 185 190
Phe Tyr Glu Gly Ala Ala Ala Asp Ala Ala Trp Arg Gln Ala Ala Glu
195 200 205
Gln Arg Ile Glu Glu Ile Arg Lys Ala Gly Met Ile Ile Val Ala Val
210 215 220
Thr Pro Asp Gly Glu Pro Ile Glu Gly Ala Glu Ile Arg Ala Lys Leu
225 230 235 240
Lys Arg His Ala Phe Gly Trp Gly Thr Ala Val Ala Ala Ser Arg Leu
245 250 255
Leu Gly Thr Gly Thr Asp Ser Glu Arg Tyr Arg Asn Phe Ile Arg Glu
260 265 270
Asn Phe Asn Met Ala Val Leu Glu Asn Asp Leu Lys Trp Gly Pro Phe
275 280 285
Glu Glu Asn Arg Asn Arg Ala Met Asn Ala Leu Arg Trp Leu His Glu
290 295 300
Asn Gly Ile Thr Trp Ile Arg Gly His Asn Leu Val Trp Pro Gly Trp
305 310 315 320
Arg Trp Met Pro Asn Asp Val Arg Asn Leu Ala Asn Asn Pro Glu Ala
325 330 335
Leu Arg Gln Arg Ile Leu Asp Arg Ile Arg Asp Thr Ala Thr Ala Thr
340 345 350
Arg Gly Leu Val Val His Trp Asp Val Val Asn Glu Pro Val Ala Glu
355 360 365
Arg Asp Val Leu Asn Ile Leu Gly Asp Glu Val Met Ala Asp Trp Phe
370 375 380
Arg Ala Ala Lys Glu Cys Asp Pro Glu Ala Arg Met Phe Ile Asn Glu
385 390 395 400
Tyr Asp Ile Leu Ala Ala Asn Gly Ala Asn Leu Arg Lys Gln Asn Ala
405 410 415
Tyr Tyr Arg Met Ile Glu Met Leu Leu Lys Leu Glu Ala Pro Val Glu

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                420                     425                     430
Gly Ile Gly Phe Gln Gly His Phe Asp Thr Ala Thr Pro Pro Glu Arg
            435                     440                     445
Met Leu Glu Ile Met Asn Arg Tyr Ala Arg Leu Gly Leu Pro Ile Ala
    450                     455                     460
Ile Thr Glu Tyr Asp Phe Ala Thr Ala Asp Glu Glu Leu Gln Ala Gln
465                     470                     475                     480
Phe Thr Arg Asp Leu Met Ile Leu Ala Phe Ser His Pro Ala Val Ser
                485                     490                     495
Asp Phe Leu Met Trp Gly Phe Trp Glu Gly Ser His Trp Lys Pro Leu
                500                     505                     510
Gly Ala Met Ile Arg Arg Asp Trp Ser Glu Lys Pro Met Tyr Arg Val
            515                     520                     525
Trp Arg Glu Leu Ile Phe Glu Arg Trp Gln Thr Asp Glu Thr Gly Val
    530                     535                     540
Thr Pro Glu His Gly Ala Ile Tyr Val Arg Gly Phe Lys Gly Asp Tyr
545                     550                     555                     560
Glu Ile Thr Val Lys Ala Gly Gly Gln Glu Val Arg Val Pro Tyr Thr
                565                     570                     575
Leu Lys Glu Asp Gly Gln Val Leu Trp Val Thr Val Gly Gly Ala Ser
                580                     585                     590
Glu Glu Arg Val Gln
            595
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<210> 349
<211> 1794
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 349

```
atgcccgttt tgttcgccct gtttcttgtt gcctcgtcct gcgcggcgca gtcgctggcc      60
gggccggttt ccctgcttgg cggagatgcg ggcgcggcgt tccgctatac cgggccatcg     120
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<210> 350
<211> 597
<212> PRT
<213> Unknown

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<210> 362
<211> 1680
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(26)

<400> 362
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Val Pro Arg Val Ile Phe Glu Thr Gly Phe Glu Thr Gly Leu Asp Gly
        35   40   45
Phe Lys Gly Arg Gly Ser Ala Thr Leu Thr Arg Thr Thr Asp Glu Thr
    50   55   60
Gln Ala Gly Asp Tyr Ser Val Leu Val Ser Asn Arg Leu Glu His Trp
65   70   75   80
Asn Gly Ala Ser Leu Pro Leu Thr Gly Phe Val Leu Pro Gly Asn Thr
                85   90   95
Tyr Glu Phe Val Gly Tyr Ile Lys Ala Lys Ala Asp Val Ala Asp Asn
            100   105   110
Tyr Val Met Ser Gly Glu Tyr Asn Glu Gly Ile Ser Gly Asn Gln Tyr
        115   120   125
Pro Trp Ile Ser Asn Arg Leu Leu Thr Val Gln Asp Gly Phe Val Glu
    130   135   140
Phe Arg Gly Glu Leu Thr Ile Leu Glu Asp Met Thr Ser Phe Asn Leu
145   150   155   160
Asn Phe Glu His Gln Asn Ala Glu Val Glu Phe Tyr Leu Asp Ser Val
                165   170   175
Gln Val Ile Leu Ile Glu Glu Gly Gln Val Asn Asp Leu Pro Met Asn
            180   185   190
Val Arg Arg Ala Pro Leu Thr Leu Ala Glu Thr Pro Leu His Glu Ile
        195   200   205
Trp Ala Asp His Phe Thr Ile Gly Asn Ile Tyr Thr Pro Gly Phe Arg
    210   215   220
Thr Asp Ile Arg Gly Glu Val Leu Ala His His Phe Asn Val Ile Thr
225   230   235   240
Ala Glu Asn Ile Met Lys Pro Asp His Leu Gln Arg Glu Gln Gly Ile
                245   250   255
Phe Thr Phe Ser Ala Ser Asn Asp Met Met Glu Phe Ala Arg Ala Asn
            260   265   270
Asn Gln Glu Val Ile Gly His Thr Leu Val Trp His Ser Gln Ser Phe
        275   280   285
Pro Trp Phe Glu Ala Leu Asn Pro Thr Arg Asp Glu Ala Ile Ala Ile
    290   295   300
Met His Ala His Ile Glu Thr Val Met Gly His Phe Asn Glu Asn Tyr
305   310   315   320
Pro Gly Val Ile Thr Gly Trp Asp Val Leu Asn Glu Ala Ile Gln Pro
                325   330   335
Arg Gln Gly Gln Asp Pro Glu Asn Trp Arg Leu His Leu Arg Asp Thr
            340   345   350
Lys Trp Leu Arg Ala Ile Gly Asp Asp Tyr Ile Ala Ile Ala Phe Asn
        355   360   365
Lys Ala His Glu Met Asp Pro Asp Ala Ile Leu Tyr Tyr Asn Asp Tyr
    370   375   380
Asn Asp Asn Asp Tyr Phe Lys Ala Thr Ile Ile Lys Ala Met Val Gln
385   390   395   400
Glu Leu Arg Asn Glu Gly Val Pro Ile His Arg Ile Gly Met Gln Gly
                405   410   415
His Tyr Asn Leu Gln Thr Pro Leu Asn Ser Ile Arg Thr Ser Val Glu
            420   425   430
Arg Phe Ser Glu Ile Thr Gly His Glu Asp Leu Pro Pro Ile Gly Ile
        435   440   445
Ser Phe Thr Glu Ile Asp Val Thr Val Pro Gly Phe Glu Ser Ala Ala
    450   455   460
Arg Leu Pro Glu Glu Val Glu Ile Arg Gln Ala Gln Phe Tyr Ala Gln
465   470   475   480
Leu Met Gln Ile Leu Arg Asp Asn Ser Asp Val Ile His Arg Val Thr
                485   490   495
Phe Trp Gly Met Ser Asp Arg Glu Ser Trp Arg Ala Asp Arg His Pro
            500   505   510
Asn Met Leu Asp Pro Gln Tyr Gly Pro Lys His Val Phe His Ala Ile
        515   520   525
Ala Asn Pro Glu Ala Phe Leu Thr Ala Tyr Pro Leu Pro Glu Thr Pro

530 535 540
Asp Ala Gln Thr Ala Tyr Ala Ser Gln Gly Gln Pro Val Val Gly Gln
545 550 555 560
Phe Asn Leu Asp Ala Tyr Gln Asn Ser Glu Val Ile Pro Val Ala Asn
565 570 575
Gln Met Thr Ala His Asn Gly Ala Thr Ala Val Ala Arg Val Val Trp
580 585 590
His Glu Asp Ala Ile Tyr Ile Leu Ala Asn Val Ser Asp Ala Thr Pro
595 600 605
Asn Val Ala Ala Ser Ala Ala His Glu Gln Asp Ser Leu Glu Val Phe
610 615 620
Ile Ser Asn Thr Asp Ser Arg Ile Ser Asn Tyr Met Pro Gly Asp Tyr
625 630 635 640
Gln Leu Arg Phe Asn Arg Ala Gly Val His Thr Tyr Gly Ser Thr Gly
645 650 655
Ser Ile Glu Gly Met Thr Phe Ala Val Gln Asp Gly Pro Ile Gly Tyr
660 665 670
Gln Val Glu Val Arg Ile Pro Leu Glu Asn Glu Val Tyr Val Gly Arg
675 680 685
Arg Leu Gly Phe Asp Leu Gln Val Asn Asp Ala Trp Glu Val Gly Gly
690 695 700
Thr Ser Gly Arg Gln Ala Phe Ala Lys Trp Asn Asp His Thr Asp Asn
705 710 715 720
Gly Trp Gln Ser Thr Glu Phe Trp Gly Trp Leu Leu Leu Gln Gly Asp
725 730 735
Ala Ala Pro Val Leu Pro Val Val Leu Val Glu Glu Gly Phe Glu Thr
740 745 750
Asp Leu Gly Ser Phe Gln Pro Arg Gly Ser Ser Thr Leu Thr Arg Thr
755 760 765
Gln Glu Val Ser His Glu Gly Asp Tyr Ser Val Leu Val Ser Asn Arg
770 775 780
Val Asn Asn Trp Asn Gly Ala Ser Leu Pro Leu Thr Gly Ile Val Gln
785 790 795 800
Pro Gly Asn Thr Tyr Glu Phe Val Gly Tyr Ile Arg Ala Lys Ala Asp
805 810 815
Val Thr Gly Ser Tyr Ile Met Ser Gly Glu Phe Asn Asn Gly Ser Gly
820 825 830
Val Leu Glu Asn Gly Ser Ile Asn Arg Trp Pro Trp Leu Ser Asn Arg
835 840 845
Ser Leu Thr Ile Ala Asp Gly Phe Val Glu Phe Lys Ser Glu Leu Thr
850 855 860
Ile Pro Ser Asp Met Thr Thr Phe Asn Leu Asn Phe Glu His Gln Asn
865 870 875 880
Ala Glu Val Glu Phe Tyr Leu Asp Ala Val Gln Val Thr Leu Ile Ala
885 890 895
Glu Ala Asp Val Thr Pro Val Asp Pro Pro Val Asp Pro Pro Val Glu
900 905 910
Pro Glu Ile Thr Val Val Tyr Ser Met Val Asp Asp Ala Ala Ile Gln
915 920 925
Gly Ile Glu Val Gly Thr Thr Gly Thr Ala Glu Asp Phe Ser Asp Ile
930 935 940
Ser Glu Ala Leu Leu Val Ser Gly Ser Pro Val Val Thr Ala Val Ala
945 950 955 960
His Pro Glu Glu Ala Gly Lys Ile Gly Ile Glu Leu Ser Asn Arg Ala
965 970 975
Glu Asn Trp His Ala Leu Asp Phe Met Phe Pro Ala Ile Gly Val Gln
980 985 990
Arg Gly Gly Ser Tyr Arg Phe Val Ala Ser Gly Arg Met Ala Glu Gly
995 1000 1005
Thr Gly Asn Ser Asn Arg Arg Met Gln Trp Asn Gln Thr Asp Ala Pro
1010 1015 1020
Trp Ser Glu Ile Ser Gly Ser Arg Thr Asn Val Ala Pro Ala Ala Thr
1025 1030 1035 1040
Thr Trp Thr Ile Asp Val Thr Leu Ser Arg Leu Gln Ile Asn Thr Leu
1045 1050 1055
Leu Asn Ala Gly Gln Arg Gly Leu Arg Ile Gln Thr Gly Asn Ala Pro
1060 1065 1070
Thr Val Thr Ile Thr Ile Asp Asp Val Phe Val Tyr Gln Ile Gly Asp
1075 1080 1085

Ile Asp Thr Ala Gly Leu Pro Leu Pro Pro Gln Trp Asn Phe Asp Leu
    1090   1095   1100
Pro Arg Leu Ser Glu Leu Phe Glu Pro Tyr Phe Gly Leu Gly Asn Ile
1105   1110   1115   1120
Tyr Ser Thr Glu Thr Leu Met Asn Ala Asn Glu Thr Lys Arg Ala Phe
                1125   1130   1135
Leu His His Phe Asn Val Ile Thr Ala Glu Asn Gly His Lys Pro Ser
            1140   1145   1150
Ser Ile Ala Gly Pro Glu Asn Ser Phe Thr Val Pro Glu Pro Glu Gln
        1155   1160   1165
Phe Asn Phe Thr Asp Ala Asp Arg Ile Val Asn Phe Ala Val Glu Asn
    1170   1175   1180
Asp Ile Glu Leu Val Gly His Ala Leu Val Trp His Ser Gln Ser Pro
1185   1190   1195   1200
Asn Trp Leu Phe Arg Ser Ala Ala Asn Thr Pro Leu Thr Arg Ala Glu
                1205   1210   1215
Ala Lys Glu Arg Met Ala Tyr Tyr Met Lys Thr Val Ser Glu His Phe
            1220   1225   1230
Glu Ala Gln Gly Thr Leu Gly Ala Phe Tyr Gly Trp Asp Val Val Asn
        1235   1240   1245
Glu Ala Ile Ala Ser Gly Gly Gly Thr Phe Val Asp Gln Pro Gly His
    1250   1255   1260
Trp Arg Thr Gln Met Arg Thr Ser Ser Pro Trp Phe Gln Ala Phe Asn
1265   1270   1275   1280
Asn Gly Leu Asp Val Glu Ala Gly Glu His Ala Ser Asp Tyr Ile Phe
                1285   1290   1295
Tyr Ala Tyr Tyr Tyr Ala Arg Lys Tyr Phe Pro Thr Ser Ile Leu Tyr
            1300   1305   1310
Tyr Asn Asp Tyr Asn Asp Glu Ile Pro Asn Lys Arg Asp Asn Ile Ala
        1315   1320   1325
Gln Met Val Glu Glu Ile Asn Ala Leu Trp Glu Ala His Glu Glu Tyr
    1330   1335   1340
Asp Gly Arg Leu Leu Ile Glu Ser Ile Gly Met Gln Ser His Tyr His
1345   1350   1355   1360
Met Glu Gly Trp Thr Thr Ser Val Asp Asn Val Arg Ala Ala Leu Asp
                1365   1370   1375
Arg Tyr Ile Ala Thr Gly Ala Arg Val Ser Val Thr Glu Leu Asp Ile
            1380   1385   1390
Thr Tyr Gly Gly His Gly Ser Asn Ala Tyr Ala Ser Leu Thr Pro Glu
        1395   1400   1405
Gln Leu Ala Ala Gln Ala Glu Arg Tyr Ala Glu Ile Phe Thr Leu Tyr
    1410   1415   1420
Leu Glu Arg Ala Asp Gln Leu Ser Arg Val Ser Ile Trp Gly Met Ser
1425   1430   1435   1440
Asp Ala Asn Ser Trp Arg Ser Ser Gly Phe Pro Leu Leu Phe Asp Ser
                1445   1450   1455
Ser Leu Asn Ala Lys Pro Ala Phe Asn Ala Ile Val Glu Leu Val Lys
            1460   1465   1470
Asn Trp Glu Thr Pro Thr Val Val Ala Pro Val Ile Gln Thr Arg Thr
        1475   1480   1485
Leu Ala Pro Leu Glu Ser Gly Glu Arg Val Phe Thr Met Leu Asp Val
    1490   1495   1500
Val Arg Gly Ser Asn Ala Pro Val Trp Phe Ser Ile Thr Asp Gly Ala
1505   1510   1515   1520
Leu Pro Glu Gly Ile Ile Leu His Ser Arg Thr Gly Ile Leu Glu Gly
                1525   1530   1535
Thr Pro Val Glu Asp Gly His Tyr Ser Phe Thr Val Thr Ala Arg Asn
            1540   1545   1550
Tyr Gly Gly Ser Thr Ser Gln Ala Leu Thr Leu Thr Val Gly His Pro
        1555   1560   1565
Val Ala Pro Pro Val Thr Pro Pro Val Thr Pro Pro Thr Val Ile Ile
    1570   1575   1580
Asp Glu Ser Asp Ile Pro Gln Ala Gly Pro Gly Leu Arg Ala Pro Gln
1585   1590   1595   1600
Ile Val Val Thr Val Gln Glu Gly Ser Glu Val Thr Phe Asp Leu Glu
                1605   1610   1615
Lys Leu Glu Glu Val Met Ala Ser Leu Ser Ser Gln Val Pro Leu Val
            1620   1625   1630
Leu Asp Val Glu Leu Glu Asp Ser Ile Ile Thr Leu Asp Gln Thr Leu

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        1635                1640                1645
Leu Lys Arg Leu Thr Asp Lys Ala Ala Gly Ile Glu Ile Gln Ala Asp
    1650                1655                1660
Gly Phe Ser Tyr Met Leu Pro Ala Glu Val Leu Glu Ala Ile Leu Trp
1665                1670                1675                1680
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<210> 363
<211> 1317
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 363

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tgtgtcgcgc tgttgagcgc ctgcggcagt agtagtagct ccctggatga tccgggtgct    180
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caggtggcca attgggagcc tttcagcctg tttaccgcgc ccgatgccgc tgcgcgtcag    360
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cgcgccaatg gcatcaaagt gcacggtcac gcactggtct ggcatgcgga ttatcaggtg    540
ccaaatgtgt ttcgtgacta cgaaggggac aattggcagg ggcttttaac cgagcatgtc    600
gagggcgtta tggggctgtt tgacgacacc gtggtaagtt gggatgtcgt aaacgaagcg    660
gttgataccg gctcacctga cggctggcgc cggtcgattt tctataattt tgcgccgccg    720
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cagatgcacg cctatatgaa ctacccgagt attgcgcagt ttcgcaatgc ctttcaggaa    960
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ggtgtccgtt actgccagat tgccgaggcc tatctggatg tcgttcctgc cgagctgcgg   1140
ggtggtttca ccgtctgggg cctgaccgat gacgacagct ggctgatggg agcgttcgcg   1200
tccgcaaccg gcgcccaata cgaccaggtc tatccggtgt tgtttgacga taatctgcaa   1260
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<210> 364
<211> 438
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 364

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Arg Cys Gly Trp Glu Lys Leu Ser Leu Asp Ala Ile Ala Arg Ala Leu
            20                  25                  30
Gly Arg Phe Gly Ser Leu Ala Leu Cys Val Ala Leu Leu Ser Ala Cys
        35                  40                  45
Gly Ser Ser Ser Ser Ser Leu Asp Asp Pro Gly Ala Gly Ser Ser Ser
    50                  55                  60
Ser Ser Ser Glu Ser Ser Gln Ser Ser Ser Ala Ser Ser Gln Ala Asp
65                  70                  75                  80
Gly Asp Gly Thr Gln Asp Ser Leu Tyr Ala Gln Ala Asp Phe Pro Val
                85                  90                  95
Gly Val Ala Val Gln Val Ala Asn Trp Glu Pro Phe Ser Leu Phe Thr
            100                 105                 110
Ala Pro Asp Ala Ala Ala Arg Gln Asn Leu Val Ala Arg His Phe Ser
        115                 120                 125
Glu Val Thr Ala Thr Asn Val Met Lys Met Ser Tyr Met Arg Thr Asn
    130                 135                 140
Ser Gly Gly Phe Thr Asp Ala Pro Ala Arg Pro Leu Ile Asp Phe Ala
145                 150                 155                 160
Arg Ala Asn Gly Ile Lys Val His Gly His Ala Leu Val Trp His Ala
                165                 170                 175
```

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Asp Tyr Gln Val Pro Asn Val Phe Arg Asp Tyr Glu Gly Asp Asn Trp
            180                 185                 190
Gln Gly Leu Leu Thr Glu His Val Glu Gly Val Met Gly Leu Phe Asp
        195                 200                 205
Asp Thr Val Val Ser Trp Asp Val Val Asn Glu Ala Val Asp Thr Gly
    210                 215                 220
Ser Pro Asp Gly Trp Arg Arg Ser Ile Phe Tyr Asn Phe Ala Pro Pro
225                 230                 235                 240
Glu Ala Gly Gln Val Pro Glu Tyr Ile Glu Val Ala Tyr Gln Ala Ala
                245                 250                 255
Arg Glu Ala Asn Pro Glu Val Thr Leu Tyr Tyr Asn Asp Phe Asp Asn
            260                 265                 270
Thr Ala Asn Thr Gly Arg Leu Asn Lys Thr Leu Glu Ile Ala Asp Arg
        275                 280                 285
Leu Lys Glu Leu Asp Ala Ile Asp Gly Ile Gly Phe Gln Met His Ala
    290                 295                 300
Tyr Met Asn Tyr Pro Ser Ile Ala Gln Phe Arg Asn Ala Phe Gln Glu
305                 310                 315                 320
Val Val Asp Arg Asp Leu Lys Val Lys Val Thr Glu Leu Asp Ile Ala
                325                 330                 335
Ile Val Asn Pro Tyr Gly Ser Ser Thr Pro Pro Pro Leu Pro Glu Phe
            340                 345                 350
Asp Gln Ala Leu Ala Asp Ala Gln Gly Val Arg Tyr Cys Gln Ile Ala
        355                 360                 365
Glu Ala Tyr Leu Asp Val Val Pro Ala Glu Leu Arg Gly Gly Phe Thr
    370                 375                 380
Val Trp Gly Leu Thr Asp Asp Asp Ser Trp Leu Met Gly Ala Phe Ala
385                 390                 395                 400
Ser Ala Thr Gly Ala Gln Tyr Asp Gln Val Tyr Pro Val Leu Phe Asp
                405                 410                 415
Asp Asn Leu Gln Ala Lys Pro Ala Phe Phe Gly Val Lys Arg Ala Leu
            420                 425                 430
Arg Gly Glu Pro Cys Glu
        435
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<210> 365
<211> 3246
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 365

```
atgaaccact tcgcttcaaa atcgctgcgc atggcgtggc aacccggact gcttgcgaca      60
accgtgctgc cgttggcggc tgccgcccca ataccagcgc cgaatacgga taccaaagtg     120
agcaatactt cgtccatcac cactccggct gcggctccac agtcgcagcc acaaccaacg     180
caagacgcaa acgctcccgc accgcttaaa gcggctttcc gggataagtt tctcatcggc     240
gcggtgctga gtgacgctgc gctgcgaggc agtgcgcccg acaaggtggc gatagccacc     300
acgcacttta acgcgctcac cgccgaaaac gccatgaagc cagacgcgat gcaaccgcgc     360
gaagggcagt tcaacttcgc tgcaggcgat cggctcgtcg aactcgccga aaaaagcggc     420
ggtgtgccca tcggccacac gctggtgtgg cacgcgcaaa caccgaagtg gtttttgaa      480
gggccggatg gacagcccgc gacgcgcgaa ctggctttgg agcgcatgcg caaacacatt     540
tccactgtgg tggggcgcta caaagggcgc atcaaggagt gggatgtggt gaacgaagcc     600
atcaacgacg gacccggtgt gctgcgtccc tctccctggc tcaaagccat cggcgaagat     660
tacatcgccg aagccttccg cgccgcgcac gccgccgacc ccgacgcgat tttgatttat     720
aacgattaca acatcgaact gggctacaaa cggcccaaag cgctgcaact cctaaaatcg     780
ctcattgacc agaaagtgcc gattcacgcc gtgggcattc agggtcactg gcgcatggac     840
aacccgaact tcgccgaagt ggaacaggcc atcaaagagt tttcggcgct ggggttgaaa     900
gtcatgatca ccgaactcga catcggcgtg ctgccgacgc gttatcaggg cgcggatatt     960
tcagcgaccg aaaccatgac gcccgaacag cgcgccgtga tgaaccccta tacggacgga    1020
ttgccggacg atgtggcgca aaagcacgcc gagcgctatc gccaggcgtt tgagatgttc    1080
ctgcggcaca aagacaaaat cagtcgtgtg acattttggg gtgtggacga cggcacttcg    1140
tggctgaacg gtttcccggt gcgcggccgc accgattatc cgctgctatt tgatcgtcag    1200
ggcaagccaa aacccgcctt tttcgcggtg caaaacgcgg cgatgggcgc aacagcgcaa    1260
ccgagcgcca gcgctcccgc aacgcatggc gccgctcctg catccaccaa cattcgcggc    1320
gccgagtttc ctcgcgtgga aagcgacggg cgggtgacgt ttcgcatcaa agcgcctgac    1380
gcgcaaaaag tgcaatttga tttaggtaag ccttacgacg ccacccgcga cgccgagggc    1440
aactggacgg cgaccacaga gccacaagtg cccggcttcc attattattt tttgattgtc    1500
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gatggagtgc gcgtggccga cccggcgagc gaaacctttt acggtgcggg ccgccagatg 1560
agcggcatcg aaattcccga tcccgacagc gcgttttatt cgccgcaaaa cgtgccgcat 1620
ggcgaagtgc gcgaacgctg gtatttttcc aacaccacgc aggcgtggcg gcgcatcttc 1680
atttatacgc cgccgggtta cgacaccgat caggccatgc gttttcctgt gctgtatttg 1740
cagcacggcg gtggcgaaga cgaacgcggc tggcccaatc aggggcgcgt gagctttatc 1800
atggacaatc tcatcgcgca gggcaaagcc aaaccgatgc tggtggtgat ggagcaaggc 1860
tatgcgcgca agcccgatga accgcaggtg ccgctgcgcc cgcccggaag caacgccgga 1920
gcgatgccgc ccgactttaa tcgcatgttc gccacgctgg gcgaagtgtt caccaaagac 1980
ctgattccgt ttattgacgc aaattaccgc accaaaaccg agcgcgaaaa ccgcgcgatg 2040
gccggacttt cgatgggtgg aatgcaaagt ttcatcatcg gcctggcgaa caccgatcta 2100
ttcgcgcacc tcggcggttt cagcggcgcg ggtggtggtt ttggcggcgg cgccttcgac 2160
gccaaaaccg cgcacggcgg tgtgatggcc gatgccgatg ccttcaacaa aaaagttcgc 2220
acgatgtttc tcagcatcgg cactgccgag aacgagcgtt ttcagagcag cgtgcgcggt 2280
taccgcgacg cgctgaccaa agcgggcatc aaaaccacgt tctacgaatc gcccggcact 2340
tcgcacgagt ggctgacatg gcgccgcagc ctgcgcgaat tcgcgccgct cttgtttcaa 2400
gaggccaaca cgcagatcga gcgcggcccc aatgcccgcc cgattgcgcc gcagccgatt 2460
gttcttggcc cgggcgacaa gcccgccttc cctccggcgc cctccggttt cgatgcgcgg 2520
cgcgatggca ttccgcacgg cgaaattaaa cttgtggaat acccttctgc cacggtcggc 2580
accacgcgca agatgcaggt ctatacgccg ccgggctaca acccgcaaga agaatatccc 2640
gtgctctatt tgctgcacgg catcggcggc gacgagtggg aatggaaaaa tggcggcacg 2700
cccgaagtga ttctcgacaa cctctacgct gagaagaaac tccagccgat gatcgtggtg 2760
atgcccaatg ggcgcgcgca aaaagacgac cgtcctatcg gcaacgtgtt cgcttccgct 2820
ccggcgtttg cgacgtttga gaaagatttg ctgaacgaca ttatcccctt tgttgagaag 2880
aattacccga ccaaaaccgg cccgcaaaat cgcgctttgg ccggtctttc gatgggcggc 2940
gggcaatctc tcaactttgg cctcggcaac ctcgacacct tcgcgtgggt tggcggcttt 3000
tcgtccgcgc ccaacacgcg cagcggcgca agtctactgg ccaatcccga cgacgccaaa 3060
aagaagctga agctgctgtg ggtttcgtgc ggcgataaag acaatttgat gtttatcagc 3120
cagcgcacgc accgttatct tgccgagaat aacgtgccgc acatctggca tgtacagccc 3180
ggcggacacg acttcaaggt gtggaagcaa gacctgtata acttcgccca actgctattc 3240
cgttaa 3246

<210> 366
<211> 1081
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(65)

<400> 366
Met Asn His Phe Ala Ser Lys Ser Leu Arg Met Ala Trp Gln Pro Gly
1 5 10 15
Leu Leu Ala Thr Thr Val Leu Pro Leu Ala Ala Ala Ala Pro Ile Pro
20 25 30
Ala Pro Asn Thr Asp Thr Lys Val Ser Asn Thr Ser Ser Ile Thr Thr
35 40 45
Pro Ala Ala Ala Pro Gln Ser Gln Pro Gln Pro Thr Gln Asp Ala Asn
50 55 60
Ala Pro Ala Pro Leu Lys Ala Ala Phe Arg Asp Lys Phe Leu Ile Gly
65 70 75 80
Ala Val Leu Ser Asp Ala Ala Leu Arg Gly Ser Ala Pro Asp Lys Val
85 90 95
Ala Ile Ala Thr Thr His Phe Asn Ala Leu Thr Ala Glu Asn Ala Met
100 105 110
Lys Pro Asp Ala Met Gln Pro Arg Glu Gly Gln Phe Asn Phe Ala Ala
115 120 125
Gly Asp Arg Leu Val Glu Leu Ala Glu Lys Ser Gly Gly Val Pro Ile
130 135 140
Gly His Thr Leu Val Trp His Ala Gln Thr Pro Lys Trp Phe Phe Glu
145 150 155 160
Gly Pro Asp Gly Gln Pro Ala Thr Arg Glu Leu Ala Leu Glu Arg Met
165 170 175
Arg Lys His Ile Ser Thr Val Val Gly Arg Tyr Lys Gly Arg Ile Lys
180 185 190
Glu Trp Asp Val Val Asn Glu Ala Ile Asn Asp Gly Pro Gly Val Leu
195 200 205

Arg Pro Ser Pro Trp Leu Lys Ala Ile Gly Glu Asp Tyr Ile Ala Glu
210 215 220
Ala Phe Arg Ala Ala His Ala Ala Asp Pro Asp Ala Ile Leu Ile Tyr
225 230 235 240
Asn Asp Tyr Asn Ile Glu Leu Gly Tyr Lys Arg Pro Lys Ala Leu Gln
245 250 255
Leu Leu Lys Ser Leu Ile Asp Gln Lys Val Pro Ile His Ala Val Gly
260 265 270
Ile Gln Gly His Trp Arg Met Asp Asn Pro Asn Phe Ala Glu Val Glu
275 280 285
Gln Ala Ile Lys Glu Phe Ser Ala Leu Gly Leu Lys Val Met Ile Thr
290 295 300
Glu Leu Asp Ile Gly Val Leu Pro Thr Arg Tyr Gln Gly Ala Asp Ile
305 310 315 320
Ser Ala Thr Glu Thr Met Thr Pro Glu Gln Arg Ala Val Met Asn Pro
325 330 335
Tyr Thr Asp Gly Leu Pro Asp Asp Val Ala Gln Lys His Ala Glu Arg
340 345 350
Tyr Arg Gln Ala Phe Glu Met Phe Leu Arg His Lys Asp Lys Ile Ser
355 360 365
Arg Val Thr Phe Trp Gly Val Asp Asp Gly Thr Ser Trp Leu Asn Gly
370 375 380
Phe Pro Val Arg Gly Arg Thr Asp Tyr Pro Leu Leu Phe Asp Arg Gln
385 390 395 400
Gly Lys Pro Lys Pro Ala Phe Phe Ala Val Gln Asn Ala Ala Met Gly
405 410 415
Ala Thr Ala Gln Pro Ser Ala Ser Ala Pro Ala Thr His Gly Ala Ala
420 425 430
Pro Ala Ser Thr Asn Ile Arg Gly Ala Glu Phe Pro Arg Val Glu Ser
435 440 445
Asp Gly Arg Val Thr Phe Arg Ile Lys Ala Pro Asp Ala Gln Lys Val
450 455 460
Gln Phe Asp Leu Gly Lys Pro Tyr Asp Ala Thr Arg Asp Ala Glu Gly
465 470 475 480
Asn Trp Thr Ala Thr Thr Glu Pro Gln Val Pro Gly Phe His Tyr Tyr
485 490 495
Phe Leu Ile Val Asp Gly Val Arg Val Ala Asp Pro Ala Ser Glu Thr
500 505 510
Phe Tyr Gly Ala Gly Arg Gln Met Ser Gly Ile Glu Ile Pro Asp Pro
515 520 525
Asp Ser Ala Phe Tyr Ser Pro Gln Asn Val Pro His Gly Glu Val Arg
530 535 540
Glu Arg Trp Tyr Phe Ser Asn Thr Thr Gln Ala Trp Arg Arg Ile Phe
545 550 555 560
Ile Tyr Thr Pro Pro Gly Tyr Asp Thr Asp Gln Ala Met Arg Phe Pro
565 570 575
Val Leu Tyr Leu Gln His Gly Gly Gly Glu Asp Glu Arg Gly Trp Pro
580 585 590
Asn Gln Gly Arg Val Ser Phe Ile Met Asp Asn Leu Ile Ala Gln Gly
595 600 605
Lys Ala Lys Pro Met Leu Val Val Met Glu Gln Gly Tyr Ala Arg Lys
610 615 620
Pro Asp Glu Pro Gln Val Pro Leu Arg Pro Pro Gly Ser Asn Ala Gly
625 630 635 640
Ala Met Pro Pro Asp Phe Asn Arg Met Phe Ala Thr Leu Gly Glu Val
645 650 655
Phe Thr Lys Asp Leu Ile Pro Phe Ile Asp Ala Asn Tyr Arg Thr Lys
660 665 670
Thr Glu Arg Glu Asn Arg Ala Met Ala Gly Leu Ser Met Gly Gly Met
675 680 685
Gln Ser Phe Ile Ile Gly Leu Ala Asn Thr Asp Leu Phe Ala His Leu
690 695 700
Gly Gly Phe Ser Gly Ala Gly Gly Gly Phe Gly Gly Gly Ala Phe Asp
705 710 715 720
Ala Lys Thr Ala His Gly Gly Val Met Ala Asp Ala Asp Ala Phe Asn
725 730 735
Lys Lys Val Arg Thr Met Phe Leu Ser Ile Gly Thr Ala Glu Asn Glu
740 745 750
Arg Phe Gln Ser Ser Val Arg Gly Tyr Arg Asp Ala Leu Thr Lys Ala

755 760 765
Gly Ile Lys Thr Thr Phe Tyr Glu Ser Pro Gly Thr Ser His Glu Trp
770 775 780
Leu Thr Trp Arg Arg Ser Leu Arg Glu Phe Ala Pro Leu Leu Phe Gln
785 790 795 800
Glu Ala Asn Thr Gln Ile Glu Arg Gly Pro Asn Ala Arg Pro Ile Ala
805 810 815
Pro Gln Pro Ile Val Leu Gly Pro Gly Asp Lys Pro Ala Phe Pro Pro
820 825 830
Ala Pro Ser Gly Phe Asp Ala Arg Arg Asp Gly Ile Pro His Gly Glu
835 840 845
Ile Lys Leu Val Glu Tyr Pro Ser Ala Thr Val Gly Thr Thr Arg Lys
850 855 860
Met Gln Val Tyr Thr Pro Pro Gly Tyr Asn Pro Gln Glu Glu Tyr Pro
865 870 875 880
Val Leu Tyr Leu Leu His Gly Ile Gly Gly Asp Glu Trp Glu Trp Lys
885 890 895
Asn Gly Gly Thr Pro Glu Val Ile Leu Asp Asn Leu Tyr Ala Glu Lys
900 905 910
Lys Leu Gln Pro Met Ile Val Val Met Pro Asn Gly Arg Ala Gln Lys
915 920 925
Asp Asp Arg Pro Ile Gly Asn Val Phe Ala Ser Ala Pro Ala Phe Ala
930 935 940
Thr Phe Glu Lys Asp Leu Leu Asn Asp Ile Ile Pro Phe Val Glu Lys
945 950 955 960
Asn Tyr Pro Thr Lys Thr Gly Pro Gln Asn Arg Ala Leu Ala Gly Leu
965 970 975
Ser Met Gly Gly Gly Gln Ser Leu Asn Phe Gly Leu Gly Asn Leu Asp
980 985 990
Thr Phe Ala Trp Val Gly Gly Phe Ser Ser Ala Pro Asn Thr Arg Ser
995 1000 1005
Gly Ala Ser Leu Leu Ala Asn Pro Asp Asp Ala Lys Lys Lys Leu Lys
1010 1015 1020
Leu Leu Trp Val Ser Cys Gly Asp Lys Asp Asn Leu Met Phe Ile Ser
1025 1030 1035 1040
Gln Arg Thr His Arg Tyr Leu Ala Glu Asn Asn Val Pro His Ile Trp
1045 1050 1055
His Val Gln Pro Gly Gly His Asp Phe Lys Val Trp Lys Gln Asp Leu
1060 1065 1070
Tyr Asn Phe Ala Gln Leu Leu Phe Arg
1075 1080

<210> 367
<211> 1338
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 367
atgaaaagaa ttggattact atttatggcg ttggcgctaa ccgcatttat ggcgcagcat 60
tcgtccgctc aaaggatttg caataaccaa acagggaccc atggtggatt ctactacaca 120
tggtggagtg atgggggtgg atctgcatgt ataacaatgg gcgatggcgg taactacagc 180
acccaatgga gcaataccgg taactttgta ggcggtaagg gttggagcac aggaagatcc 240
aaccgcgtaa ttagttacaa tgctggtaac tggtcgccat cgggtaatgc ttacctatgt 300
ttatatggct ggactaccaa cccgcttgtt gagtactacg tagttgatag ctggggttct 360
tggagacctc ccggagcaac atcgcaggga acagtaaata ctgatggtgg cacctatgag 420
atatacagaa ctcagcgtgt aaaccagcca tctattcagg ggaatactac tttctatcag 480
tattggagcg ttagaacctc taaaagggcc actggaagca atgctaccat caccttccag 540
aaccacgtaa atgcttgggc aagtaggggt tggaacttgg gagctcatag ctatcaggta 600
ctggctaccg agggttatca gagcagcgga agttcaaata ttactgtttg ggaaggtggt 660
tcaagtggag gttcttcagg tggaagcacc ggaggcagca ctggaggtgg atcacacgag 720
atcattgtaa gagcccgtgg tgtagtaggt tcagagcaaa ttaggcttag ggttggcaat 780
acaaccgttg caacttggac ccttactacc ggttataggg actatagggc tactacctca 840
gctactggtg gtattctggt agagtacttc aatgatagcg gcaaccgtga tgttcagatt 900
gattacatta gggtaaacgg ctcaactcgt caatctgaga acatgtcgta caatacaggg 960
gtatggcaga atggctcatg cggcggctcc aatagcgagt ggctacactg caacggagct 1020
attggctacg gcgatgtggt tactggcaga tcaaccgctg ttgaggaagc atttactgct 1080

```
gccgaggatt gtggctgtga acctaaggca accctattcc ccaaccctgc tggcagtacc     1140
ctcagtatta tgctagacag gcaaccctat ggcgatgtaa gtattagaat atataatacg     1200
gtaggtgcag ttgttcgcac catcaacaat ccagacctac tcactgaggt tgatgtcagt     1260
gcattaaatt ctggaatcta ctttgtagag cttaggtccg aaggacatgt aagcaactac     1320
aaatttatta aaaagtag                                                   1338

<210> 368
<211> 445
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(23)

<400> 368
Met Lys Arg Ile Gly Leu Leu Phe Met Ala Leu Ala Leu Thr Ala Phe
 1               5                  10                  15
Met Ala Gln His Ser Ser Ala Gln Arg Ile Cys Asn Asn Gln Thr Gly
            20                  25                  30
Thr His Gly Gly Phe Tyr Tyr Thr Trp Trp Ser Asp Gly Gly Gly Ser
        35                  40                  45
Ala Cys Ile Thr Met Gly Asp Gly Gly Asn Tyr Ser Thr Gln Trp Ser
    50                  55                  60
Asn Thr Gly Asn Phe Val Gly Gly Lys Gly Trp Ser Thr Gly Arg Ser
65                  70                  75                  80
Asn Arg Val Ile Ser Tyr Asn Ala Gly Asn Trp Ser Pro Ser Gly Asn
                85                  90                  95
Ala Tyr Leu Cys Leu Tyr Gly Trp Thr Thr Asn Pro Leu Val Glu Tyr
            100                 105                 110
Tyr Val Val Asp Ser Trp Gly Ser Trp Arg Pro Pro Gly Ala Thr Ser
        115                 120                 125
Gln Gly Thr Val Asn Thr Asp Gly Gly Thr Tyr Glu Ile Tyr Arg Thr
    130                 135                 140
Gln Arg Val Asn Gln Pro Ser Ile Gln Gly Asn Thr Thr Phe Tyr Gln
145                 150                 155                 160
Tyr Trp Ser Val Arg Thr Ser Lys Arg Ala Thr Gly Ser Asn Ala Thr
                165                 170                 175
Ile Thr Phe Gln Asn His Val Asn Ala Trp Ala Ser Arg Gly Trp Asn
            180                 185                 190
Leu Gly Ala His Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln Ser
        195                 200                 205
Ser Gly Ser Ser Asn Ile Thr Val Trp Glu Gly Gly Ser Ser Gly Gly
    210                 215                 220
Ser Ser Gly Gly Ser Thr Gly Gly Ser Thr Gly Gly Gly Ser His Glu
225                 230                 235                 240
Ile Ile Val Arg Ala Arg Gly Val Val Gly Ser Glu Gln Ile Arg Leu
                245                 250                 255
Arg Val Gly Asn Thr Thr Val Ala Thr Trp Thr Leu Thr Thr Gly Tyr
            260                 265                 270
Arg Asp Tyr Arg Ala Thr Thr Ser Ala Thr Gly Gly Ile Leu Val Glu
        275                 280                 285
Tyr Phe Asn Asp Ser Gly Asn Arg Asp Val Gln Ile Asp Tyr Ile Arg
    290                 295                 300
Val Asn Gly Ser Thr Arg Gln Ser Glu Asn Met Ser Tyr Asn Thr Gly
305                 310                 315                 320
Val Trp Gln Asn Gly Ser Cys Gly Gly Ser Asn Ser Glu Trp Leu His
                325                 330                 335
Cys Asn Gly Ala Ile Gly Tyr Gly Asp Val Val Thr Gly Arg Ser Thr
            340                 345                 350
Ala Val Glu Glu Ala Phe Thr Ala Ala Glu Asp Cys Gly Cys Glu Pro
        355                 360                 365
Lys Ala Thr Leu Phe Pro Asn Pro Ala Gly Ser Thr Leu Ser Ile Met
    370                 375                 380
Leu Asp Arg Gln Pro Tyr Gly Asp Val Ser Ile Arg Ile Tyr Asn Thr
385                 390                 395                 400
Val Gly Ala Val Val Arg Thr Ile Asn Asn Pro Asp Leu Leu Thr Glu
```

```
                405                     410                     415
Val Asp Val Ser Ala Leu Asn Ser Gly Ile Tyr Phe Val Glu Leu Arg
            420                     425                 430
Ser Glu Gly His Val Ser Asn Tyr Lys Phe Ile Lys Lys
        435                     440                 445
```

<210> 369
<211> 1077
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 369

```
atgaaatcat ttatcactgg caaaaaaatt gctgctggac taattactgc agctgctttg      60
agcgcatcta tggtgagcgc gcaaaccctg acttcaaatt ctcaaggcac ccacgacgga     120
tttttctact ctttctggaa ggactcaggc aacgcctcaa tgaacttatt ggcgggcggc     180
cgttatcagt ctagctggaa caccggcacc aacaactggg taggcggtaa aggctggaac     240
ccaggcacta acaaccgtgt aattaactac tctggttact acggtgtgga caactcccaa     300
aactcttacg tcgcgcttta cggctggacc agaaacccat tggttgagta ctacgtgatt     360
gagagctacg gctcatacaa ccctgctagc tgctctggcg gcaccgattt cggtagcttc     420
caaagtgacg gcgccaccta caacgtgcgt cgttgccagc gcgtgcaaca gccttcgatc     480
gatggcaccc agactttcta ccaatacttc agcgtgagaa atccgaaaaa agggtttggg     540
aacatttctg gcaccatcac ctttgctaac cacgtaaact actggagaag cagagggatg     600
aatcttggta accacgatta ccaagttctc gctactgaag gctacagaag cacgggttct     660
tctgacctca ccatcagcca aggcgcaagc aacaacggcg gtggcggcag tagctcaagt     720
gctccatctg ctgggggcgg tagcaagaca atcgtcgtgc gggcacgcgg gactaccgga     780
caagagcaaa tccgtttgcg ggtgaacaac actattgttc agacctggac cttgtccacc     840
accatgcgcg actacaccgt caacactaac ttggcaggcg ggtcattggt tgaatacttc     900
aatgacagcg gcaaccgcga cgtccaagtt gattacatca gcgtaaatgg caatgttcgc     960
caatccgaaa accaaaccta caacaccggt gtctaccaga acggtgcgtg tggcggcggt    1020
aacggccgga gcgagtggct ccattgcaac ggtgcaatcg ggtacggcga tatctaa       1077
```

<210> 370
<211> 358
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(27)

<400> 370

```
Met Lys Ser Phe Ile Thr Gly Lys Lys Ile Ala Ala Gly Leu Ile Thr
 1               5                  10                  15
Ala Ala Ala Leu Ser Ala Ser Met Val Ser Ala Gln Thr Leu Thr Ser
            20                  25                  30
Asn Ser Gln Gly Thr His Asp Gly Phe Phe Tyr Ser Phe Trp Lys Asp
        35                  40                  45
Ser Gly Asn Ala Ser Met Asn Leu Leu Ala Gly Gly Arg Tyr Gln Ser
    50                  55                  60
Ser Trp Asn Thr Gly Thr Asn Asn Trp Val Gly Gly Lys Gly Trp Asn
65                  70                  75                  80
Pro Gly Thr Asn Asn Arg Val Ile Asn Tyr Ser Gly Tyr Tyr Gly Val
                85                  90                  95
Asp Asn Ser Gln Asn Ser Tyr Val Ala Leu Tyr Gly Trp Thr Arg Asn
            100                 105                 110
Pro Leu Val Glu Tyr Tyr Val Ile Glu Ser Tyr Gly Ser Tyr Asn Pro
        115                 120                 125
Ala Ser Cys Ser Gly Gly Thr Asp Phe Gly Ser Phe Gln Ser Asp Gly
    130                 135                 140
Ala Thr Tyr Asn Val Arg Arg Cys Gln Arg Val Gln Gln Pro Ser Ile
145                 150                 155                 160
Asp Gly Thr Gln Thr Phe Tyr Gln Tyr Phe Ser Val Arg Asn Pro Lys
                165                 170                 175
Lys Gly Phe Gly Asn Ile Ser Gly Thr Ile Thr Phe Ala Asn His Val
```

```
                180                 185                 190
Asn Tyr Trp Arg Ser Arg Gly Met Asn Leu Gly Asn His Asp Tyr Gln
            195                 200                 205
Val Leu Ala Thr Glu Gly Tyr Arg Ser Thr Gly Ser Ser Asp Leu Thr
    210                 215                 220
Ile Ser Gln Gly Ala Ser Asn Asn Gly Gly Gly Gly Ser Ser Ser Ser
225                 230                 235                 240
Ala Pro Ser Ala Gly Gly Gly Ser Lys Thr Ile Val Val Arg Ala Arg
                245                 250                 255
Gly Thr Thr Gly Gln Glu Gln Ile Arg Leu Arg Val Asn Asn Thr Ile
            260                 265                 270
Val Gln Thr Trp Thr Leu Ser Thr Thr Met Arg Asp Tyr Thr Val Asn
        275                 280                 285
Thr Asn Leu Ala Gly Gly Ser Leu Val Glu Tyr Phe Asn Asp Ser Gly
    290                 295                 300
Asn Arg Asp Val Gln Val Asp Tyr Ile Ser Val Asn Gly Asn Val Arg
305                 310                 315                 320
Gln Ser Glu Asn Gln Thr Tyr Asn Thr Gly Val Tyr Gln Asn Gly Ala
                325                 330                 335
Cys Gly Gly Gly Asn Gly Arg Ser Glu Trp Leu His Cys Asn Gly Ala
            340                 345                 350
Ile Gly Tyr Gly Asp Ile
        355
```

<210> 371
<211> 1245
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 371

```
gtgaccggga tcgcgagaaa aggcgtatgg tccgtgattt ccggaacttt cactgccggg      60
gattacgatt cctacctgct gtatgtcgaa acacaggacc agggcggcgg acacccgacg     120
ctgagctttg aaatccggaa cttcagactg acggcaccgg aaggcatcgc tccgccgaag     180
gcgacagaag aaccggctga cgcggcagag gcgacgcctg ttccggcact gagcgagatt     240
ccgggcctga aggacgtcta cgcggactac tttgacttcg gcgctgcggc gccgcagtat     300
gcattcggcc tcggccagac ccagctgcag gacctgatga tcagccagtt cagcatcctg     360
acccctgaaa acgaactgaa accggacagc gtgcttgatg tccagacgag taaaaaactg     420
gcggcagaag acgaaaccgc ggtggcgatc aggctgaacg ccgcaacgcc gctgctgaag     480
ttcgcgcaga agaacggcat caaagtgcac ggccatgtgc tggtatggca cagccagacg     540
ccggaagctt tcttccatga aggatacgat accaagaaac cctatgtgac gagagaggtt     600
atgctcggcc gcctggaaaa ctatatccgt gaagtgctga cgcagacaga ggaacagttc     660
ccgggcgtga tcgtcagctg ggacgtcgtg aacgaggcga tcgacgacgg tactcactgg     720
ctgcggaaga cttccagctg gtacaaagtc gtcggcgagg atttcctgaa cagggctttt     780
gaatacgcca ggaaatacgc cgcggagggc gtgctgctgt actacaacga ttacagcacg     840
gcaaattcgg ctaaactgat gggcatcacg aagctgctga agcagctgat tccagacggg     900
aatatcgacg gctacggatt ccagatgcac catgacctcg gctggccgag catcgacctt     960
atggcggcag ctgtgaagca gattgccggc ctggggctga aactgcgcgt cagcgaactg    1020
gatatcggcg tatccaagaa caatcaggaa aactatgaca aacaggccaa acgctacaag    1080
gaaatgctga acctgatgct gcagtacgcg gaccagacgg aagccgtgca ggtctggggc    1140
ctgacggaca acatgagctg gagaaccggc aaatacccgc tgctgttcga cagcgcggca    1200
aaaccgaaaa aggcgttctt cgcggtgatt gaagccgcag aggaa                    1245
```

<210> 372
<211> 415
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 372

```
Met Thr Gly Ile Ala Arg Lys Gly Val Trp Ser Val Ile Ser Gly Thr
1               5                   10                  15
Phe Thr Ala Gly Asp Tyr Asp Ser Tyr Leu Leu Tyr Val Glu Thr Gln
            20                  25                  30
Asp Gln Gly Gly Gly His Pro Thr Leu Ser Phe Glu Ile Arg Asn Phe
```

35 40 45
Arg Leu Thr Ala Pro Glu Gly Ile Ala Pro Pro Lys Ala Thr Glu Glu
50 55 60
Pro Ala Asp Ala Ala Glu Ala Thr Pro Val Pro Ala Leu Ser Glu Ile
65 70 75 80
Pro Gly Leu Lys Asp Val Tyr Ala Asp Tyr Phe Asp Phe Gly Ala Ala
85 90 95
Ala Pro Gln Tyr Ala Phe Gly Leu Gly Gln Thr Gln Leu Gln Asp Leu
100 105 110
Met Ile Ser Gln Phe Ser Ile Leu Thr Pro Glu Asn Glu Leu Lys Pro
115 120 125
Asp Ser Val Leu Asp Val Gln Thr Ser Lys Lys Leu Ala Ala Glu Asp
130 135 140
Glu Thr Ala Val Ala Ile Arg Leu Asn Ala Ala Thr Pro Leu Leu Lys
145 150 155 160
Phe Ala Gln Lys Asn Gly Ile Lys Val His Gly His Val Leu Val Trp
165 170 175
His Ser Gln Thr Pro Glu Ala Phe Phe His Glu Gly Tyr Asp Thr Lys
180 185 190
Lys Pro Tyr Val Thr Arg Glu Val Met Leu Gly Arg Leu Glu Asn Tyr
195 200 205
Ile Arg Glu Val Leu Thr Gln Thr Glu Glu Gln Phe Pro Gly Val Ile
210 215 220
Val Ser Trp Asp Val Val Asn Glu Ala Ile Asp Asp Gly Thr His Trp
225 230 235 240
Leu Arg Lys Thr Ser Ser Trp Tyr Lys Val Val Gly Glu Asp Phe Leu
245 250 255
Asn Arg Ala Phe Glu Tyr Ala Arg Lys Tyr Ala Ala Glu Gly Val Leu
260 265 270
Leu Tyr Tyr Asn Asp Tyr Ser Thr Ala Asn Ser Ala Lys Leu Met Gly
275 280 285
Ile Thr Lys Leu Leu Lys Gln Leu Ile Pro Asp Gly Asn Ile Asp Gly
290 295 300
Tyr Gly Phe Gln Met His His Asp Leu Gly Trp Pro Ser Ile Asp Leu
305 310 315 320
Met Ala Ala Ala Val Lys Gln Ile Ala Gly Leu Gly Leu Lys Leu Arg
325 330 335
Val Ser Glu Leu Asp Ile Gly Val Ser Lys Asn Asn Gln Glu Asn Tyr
340 345 350
Asp Lys Gln Ala Lys Arg Tyr Lys Glu Met Leu Asn Leu Met Leu Gln
355 360 365
Tyr Ala Asp Gln Thr Glu Ala Val Gln Val Trp Gly Leu Thr Asp Asn
370 375 380
Met Ser Trp Arg Thr Gly Lys Tyr Pro Leu Leu Phe Asp Ser Ala Ala
385 390 395 400
Lys Pro Lys Lys Ala Phe Phe Ala Val Ile Glu Ala Ala Glu Glu
405 410 415

<210> 373
<211> 1539
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 373
ttgattggct gcgtcatgtc gccgccggaa gcgggaagtc cccgttttga tcttttaacc 60
cggcacttta atgtcatcac cgcggaaaac gccatgaagc ccgcgtcgtt gcagcgcgaa 120
aagggggtgt ttacttttga acaggcggac atgatggtgg acgcggtatt ggagcgggga 180
ctgaagatcc acggacatac tctggcctgg caccagcagt ctccggagtg gatgaatcat 240
gaggggattt cccgggacga agccgtggaa aatctcaccg tccacgccaa aaccgcggcc 300
gctcatttta gggggcgggt catatcctgg gatgtactca acgaggcgat cattgacaat 360
ccccccaacc ccggggattg gcgggcatcc ctcaggcaaa gcccctggta caaagccata 420
ggcccggatt acgtggagct tgtgttcaag gcggccaggg aggcggaccc ggaggcaaaa 480
ctttattata acgattacaa ccttgataac cggaacaagg ccctggcggt ttacaacatg 540
gtcagggaac tgaacgaaaa gaatccgaat ccgggcggca ggcccctcat cgacggcgtg 600
ggcatgcagg gccattaccg cctgaatacc aataccgata acgtgaggct gtcgctggaa 660
cggtttattt ccctgggggt cgaggtcagc atcacggagc tcgatataca ggccggttcg 720

gattcaaacc agacagagcg gcagcgggtg gaacagggcc tggtctatgc cgctttgttt 780
accattttcc gggaacacgc ggcaaacata ggccgggtaa ctttttgggg acttgacgac 840
ggggcaagct ggcgttccgc ggcgagtccc tgcctctttg ataaaaacct caacgcaaaa 900
cctgcctttt acgcggtcct ggacccggat tcctttattg cggaaaacag cgccctgctg 960
atcagggaag cgaaagaggg agaggcttat tatggtacgc ctgctttagg cgccgtccct 1020
gatcccctct gggacagggc gccttccctc ccggtggatc agtacctcat ggcctggcag 1080
ggcgcttcgg gaagggcaaa agtcctctgg gacgaaaaaa atctctatgt gctggtccgg 1140
gttgaaaacg cggaaataaa caaggacagt tccaacagct acgaacagga ttcggtcgaa 1200
atttttattg atgaggataa ccggaaaagt tccttttca gggaggatga cgggcagtac 1260
cgggtcaatt ttgccaacga ggcgggcttt aacccctcgt ccgccggggc ggggtttgtt 1320
tcggccgccg cggtggatgg aaaatcctat accgttacca tgaagattcc ctttaaaaca 1380
atagtccccg gagcggggac gcgtatcggg tttgatgtcc agatcaacgg cgcgtcggcc 1440
agggggatac gggagagcgt ggcggtatgg aatgatacca cgggcaattc atttcaggat 1500
acctcaggtt acggggtact gcggttagta aaaaagtaa 1539

<210> 374
<211> 512
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 374
Met Ile Gly Cys Val Met Ser Pro Pro Glu Ala Gly Ser Pro Arg Phe
1 5 10 15
Asp Leu Leu Thr Arg His Phe Asn Val Ile Thr Ala Glu Asn Ala Met
20 25 30
Lys Pro Ala Ser Leu Gln Arg Glu Lys Gly Val Phe Thr Phe Glu Gln
35 40 45
Ala Asp Met Met Val Asp Ala Val Leu Glu Arg Gly Leu Lys Ile His
50 55 60
Gly His Thr Leu Ala Trp His Gln Gln Ser Pro Glu Trp Met Asn His
65 70 75 80
Glu Gly Ile Ser Arg Asp Glu Ala Val Glu Asn Leu Thr Val His Ala
85 90 95
Lys Thr Ala Ala Ala His Phe Arg Gly Arg Val Ile Ser Trp Asp Val
100 105 110
Leu Asn Glu Ala Ile Ile Asp Asn Pro Pro Asn Pro Gly Asp Trp Arg
115 120 125
Ala Ser Leu Arg Gln Ser Pro Trp Tyr Lys Ala Ile Gly Pro Asp Tyr
130 135 140
Val Glu Leu Val Phe Lys Ala Ala Arg Glu Ala Asp Pro Glu Ala Lys
145 150 155 160
Leu Tyr Tyr Asn Asp Tyr Asn Leu Asp Asn Arg Asn Lys Ala Leu Ala
165 170 175
Val Tyr Asn Met Val Arg Glu Leu Asn Glu Lys Asn Pro Asn Pro Gly
180 185 190
Gly Arg Pro Leu Ile Asp Gly Val Gly Met Gln Gly His Tyr Arg Leu
195 200 205
Asn Thr Asn Thr Asp Asn Val Arg Leu Ser Leu Glu Arg Phe Ile Ser
210 215 220
Leu Gly Val Glu Val Ser Ile Thr Glu Leu Asp Ile Gln Ala Gly Ser
225 230 235 240
Asp Ser Asn Gln Thr Glu Arg Gln Arg Val Glu Gln Gly Leu Val Tyr
245 250 255
Ala Ala Leu Phe Thr Ile Phe Arg Glu His Ala Ala Asn Ile Gly Arg
260 265 270
Val Thr Phe Trp Gly Leu Asp Asp Gly Ala Ser Trp Arg Ser Ala Ala
275 280 285
Ser Pro Cys Leu Phe Asp Lys Asn Leu Asn Ala Lys Pro Ala Phe Tyr
290 295 300
Ala Val Leu Asp Pro Asp Ser Phe Ile Ala Glu Asn Ser Ala Leu Leu
305 310 315 320
Ile Arg Glu Ala Lys Glu Gly Glu Ala Tyr Tyr Gly Thr Pro Ala Leu
325 330 335
Gly Ala Val Pro Asp Pro Leu Trp Asp Arg Ala Pro Ser Leu Pro Val
340 345 350
Asp Gln Tyr Leu Met Ala Trp Gln Gly Ala Ser Gly Arg Ala Lys Val

Leu Trp Asp Glu Lys Asn Leu Tyr Val Leu Val Arg Val Glu Asn Ala
355 360 365
370 375 380
Glu Ile Asn Lys Asp Ser Ser Asn Ser Tyr Glu Gln Asp Ser Val Glu
385 390 395 400
Ile Phe Ile Asp Glu Asp Asn Arg Lys Ser Ser Phe Phe Arg Glu Asp
405 410 415
Asp Gly Gln Tyr Arg Val Asn Phe Ala Asn Glu Ala Gly Phe Asn Pro
420 425 430
Ser Ser Ala Gly Ala Gly Phe Val Ser Ala Ala Ala Val Asp Gly Lys
435 440 445
Ser Tyr Thr Val Thr Met Lys Ile Pro Phe Lys Thr Ile Val Pro Gly
450 455 460
Ala Gly Thr Arg Ile Gly Phe Asp Val Gln Ile Asn Gly Ala Ser Ala
465 470 475 480
Arg Gly Ile Arg Glu Ser Val Ala Val Trp Asn Asp Thr Thr Gly Asn
485 490 495
Ser Phe Gln Asp Thr Ser Gly Tyr Gly Val Leu Arg Leu Val Lys Lys
500 505 510

<210> 375
<211> 570
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated polynucleotide

<400> 375
atggccctta tggcttcgac attctactgg cacttgtgga ctgatggtat agggacagta 60
aatgctacca atggatctga tggcaattac agcgtttcat ggtcaaattg cgggaatttt 120
gttgttggta aaggctggac taccggatca gcaactaggg taataaacta taatgcccac 180
gccttttcgg tagtgggtaa tgcttatttg gctctttatg ggtggacgag aaattcactc 240
atagaatatt acgtcgttga tagctggggg acttatagac ctactggaac ttataaaggc 300
actgtgacta gtgatggagg gacttatgac atatacacga ctacacgaac caacgcacct 360
tccattgacg gcaataatac aactttcacc cagttctgga gtgttaggca gtcgaagaga 420
ccgattggta ccaacaatac catcaccttt agcaaccatg ttaacgcctg gaagagtaaa 480
ggaatgaatt tggggagtag ttggtcttat caggtattag caacagaggg ctatcaaagt 540
agtgggtact ctaacgtaac ggtctggtaa 570

<210> 376
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated polypeptide

<400> 376
Met Ala Leu Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly
1 5 10 15
Ile Gly Thr Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val
20 25 30
Ser Trp Ser Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr
35 40 45
Gly Ser Ala Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val
50 55 60
Val Gly Asn Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu
65 70 75 80
Ile Glu Tyr Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly
85 90 95
Thr Tyr Lys Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr
100 105 110
Thr Thr Thr Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr
115 120 125
Phe Thr Gln Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr
130 135 140
Asn Asn Thr Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys
145 150 155 160

Gly Met Asn Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu
165 170 175
Gly Tyr Gln Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 377
<211> 570
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated polynucleotide

<400> 377
atggccctta tggcttcgac attctactgg cacttgtgga ctgatggtat agggacagta 60
aatgctacca atggatctga tggcaattac agcgtttcat ggtcaaattg cgggaatttt 120
gttgttggta aaggctggac taccggatca gcaactaggg taataaacta taatgcccac 180
gccttttcgg tagtgggtaa tgcttatttg gctctttatg ggtggacgag aaatccactc 240
atagaatatt acgtcgttga tagctggggg acttatagac ctactggaac ttataaaggc 300
actgtgacta gtgatggagg gacttatgac atatacacga ctacacgaac caacgcacct 360
tccattgacg gcaataatac aactttcacc cagttctgga gtgttaggca gtcgaagaga 420
ccgattggta ccaacaatac catcaccttt agcaaccatg ttaacgcctg gaagagtaaa 480
ggaatgaatt tggggagtag ttggtcttat caggtattag caacagaggg ctatcaaagt 540
agtgggtact ctaacgtaac ggtctggtaa 570

<210> 378
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated polypeptide

<400> 378
Met Ala Leu Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly
1 5 10 15
Ile Gly Thr Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val
20 25 30
Ser Trp Ser Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr
35 40 45
Gly Ser Ala Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val
50 55 60
Val Gly Asn Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Pro Leu
65 70 75 80
Ile Glu Tyr Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly
85 90 95
Thr Tyr Lys Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr
100 105 110
Thr Thr Thr Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr
115 120 125
Phe Thr Gln Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr
130 135 140
Asn Asn Thr Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys
145 150 155 160
Gly Met Asn Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu
165 170 175
Gly Tyr Gln Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 379
<211> 570
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated polynucleotide.

<400> 379
atggccctta tggcttcgac attctactgg cacaattgga ctgatggtat agggacagta 60

aatgctacca atggatctga tggcaattac agcgtttcat ggtcaaattg cgggaatttt 120
gttgttggta aaggctggac taccggatca gcaactaggg taataaacta taatgcccac 180
gccttttcgc cggtgggtaa tgcttatttg gctctttatg ggtggacgag aaattcactc 240
atagaatatt acgtcgttga tagctggggg acttatagac ctactggaac ttataaaggc 300
actgtgacta gtgatggagg gacttatgac atatacacga ctacacgaac caacgcacct 360
tccattgacg gcaataatac aactttcacc cagttctgga gtgttaggca gtcgaagaga 420
ccgattggta ccaacaatac catcaccttt agcaaccatg ttaacgcctg gaagagtaaa 480
ggaatgaatt tggggagtag ttggtcttat caggtattag caacagaggg ctatcaaagt 540
agtgggtact ctaacgtaac ggtctggtaa 570

<210> 380
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated polypeptide.

<400> 380
Met Ala Leu Met Ala Ser Thr Phe Tyr Trp His Asn Trp Thr Asp Gly
1 5 10 15
Ile Gly Thr Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val
20 25 30
Ser Trp Ser Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr
35 40 45
Gly Ser Ala Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Pro
50 55 60
Val Gly Asn Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu
65 70 75 80
Ile Glu Tyr Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly
85 90 95
Thr Tyr Lys Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr
100 105 110
Thr Thr Thr Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr
115 120 125
Phe Thr Gln Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr
130 135 140
Asn Asn Thr Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys
145 150 155 160
Gly Met Asn Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu
165 170 175
Gly Tyr Gln Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185